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385                               390                               395                               400
Arg Asn Asn Leu Asn Asn Arg Val Asn Ser Gly Ser Ser Ser Asn Ile
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Ser Asn Thr Ala Ala Asn His Pro Tyr Gly Ala Pro Glu Phe Asn Met
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Ile Ala Asn Asn Thr Pro Ala Ala Leu Thr Tyr Asn Arg Ala His Phe
      435                               440                               445

Pro Ala Ile Thr Pro Leu Ser Arg Gln Asn Ser Leu Asn Met Ala Pro
      450                               455                               460

Ser Asn Ser Gly Ser Pro Ile Ile Ile Ala Asp His Phe Ser Gly Asn
      465                               470                               475                               480

Asn Asn Ile Ala Pro Asn Tyr Arg Tyr Asn Asn Asn Ile Asn Asn Asn
      485                               490                               495

Asn Asn Asn Ile Asn Asn Met Thr Asn Asn Arg Tyr Asn Ile Asn Asn
      500                               505                               510

Asn Ile Asn Gly Asn Gly Asn Gly Asn Gly Asn Asn Ser Asn Asn Asn
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Asn Asn His Asn Asn Asn His Asn Asn Asn His His Asn Gly Ser Ile
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Asn Ser Asn Ser Asn Thr Asn Asn Asn Asn Asn Asn Asn Asn Gly Asn
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Asn Met Pro Phe Arg Ala Gly Asp Trp Lys Cys Ser Thr Cys Thr Tyr
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His Asn Phe Ala Lys Asn Val Val Cys Leu Arg Cys Gly Gly Pro Lys
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Ser Ile Ser Gly Asp Ala Ser Glu Thr Asn His Tyr Ile Asp Ser Ser
      610                               615                               620

Thr Phe Gly Pro Ala Ser Arg Thr Pro Ser Asn Asn Asn Ile Ser Val
      625                               630                               635                               640

Asn Thr Asn Gly Gly Ser Asn Ala Gly Arg Thr Asp Gly Asn Asp Asn

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645

650

655

Lys Gly Arg Asp Ile Ser Leu Met Glu Phe Met Ser Pro Pro Leu Ser  
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Met Ala Thr Lys Ser Met Lys Glu Gly Asp Gly Asn Gly Ser Ser Phe  
 675 680 685

Asn Glu Phe Lys Ser Asp Lys Ala Asn Val Asn Phe Ser Asn Val Gly  
 690 695 700

Asp Asn Ser Ala Phe Gly Asn Gly Phe Asn Ser Ser Ile Arg Trp  
 705 710 715

&lt;210&gt; 47

&lt;211&gt; 578

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 47

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&lt;210&gt; 48

&lt;211&gt; 25

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 48

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Arg Arg Lys Val Arg Ala Arg Ser Lys  
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<210> 49  
 <211> 1354  
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 <213> *Saccharomyces cerevisiae*

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 <211> 120  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

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 Val Gln Lys Leu Ser Arg Pro Ser Leu Pro Lys Ile Lys Thr Val Arg  
 35 40 45  
 Lys Ser Ile Ala Cys Val Leu Thr Val Ile Asn Glu Gln Gln Arg Glu  
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Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu  
 65 70 75 80

Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu  
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Ala Ser Gln Val Thr Glu Lys Gln Arg Lys Lys Gln Ile Ala Phe Pro  
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Gln Arg Lys Tyr Ala Ile Lys Ala  
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&lt;210&gt; 51

&lt;211&gt; 3254

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 51

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&lt;210&gt; 52

&lt;211&gt; 917

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 52

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Met Met Glu Thr Pro Thr Asp Asn Ile Val Ser Pro Phe His Asn Phe
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Gly Ser Ser Thr Gln Tyr Ser Gly Thr Leu Ser Arg Thr Pro Asn Gln
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Ile Ile Glu Leu Glu Lys Pro Ser Thr Leu Ser Pro Leu Ser Arg Gly
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Lys Lys Trp Thr Glu Lys Leu Ala Arg Phe Gln Arg Ser Ser Ala Lys
          50                   55                   60

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Lys Lys Arg Phe Ser Pro Ser Pro Ile Ser Ser Ser Thr Phe Ser Phe  
 65 70 75 80

Ser Pro Lys Ser Arg Val Thr Ser Ser Asn Ser Ser Gly Asn Glu Asp  
 85 90 95

Gly Asn Leu Met Asn Thr Pro Ser Thr Val Ser Thr Asp Tyr Leu Pro  
 100 105 110

Gln His Pro His Arg Thr Ser Ser Leu Pro Arg Pro Asn Ser Asn Leu  
 115 120 125

Phe His Ala Ser Asn Ser Asn Leu Ser Arg Ala Asn Glu Pro Pro Arg  
 130 135 140

Ala Glu Asn Leu Ser Asp Asn Ile Pro Pro Lys Val Ala Pro Phe Gly  
 145 150 155 160

Tyr Pro Ile Gln Arg Thr Ser Ile Lys Lys Ser Phe Leu Asn Ala Ser  
 165 170 175

Cys Thr Leu Cys Asp Glu Pro Ile Ser Asn Arg Arg Lys Gly Glu Lys  
 180 185 190

Ile Ile Glu Leu Ala Cys Gly His Leu Ser His Gln Glu Cys Leu Ile  
 195 200 205

Ile Ser Phe Gly Thr Thr Ser Lys Ala Asp Val Arg Ala Leu Phe Pro  
 210 215 220

Phe Cys Thr Lys Cys Lys Lys Asp Thr Asn Lys Ala Val Gln Cys Ile  
 225 230 235 240

Pro Glu Asn Asp Glu Leu Lys Asp Ile Leu Ile Ser Asp Phe Leu Ile  
 245 250 255

His Lys Ile Pro Asp Ser Glu Leu Ser Ile Thr Pro Gln Ser Arg Phe  
 260 265 270

Pro Pro Tyr Ser Pro Leu Leu Pro Pro Phe Gly Leu Ser Tyr Thr Pro  
 275 280 285

Val Glu Arg Gln Thr Ile Tyr Ser Gln Ala Pro Ser Leu Asn Pro Asn  
 290 295 300

Leu Ile Leu Ala Ala Pro Pro Lys Glu Arg Asn Gln Ile Pro Gln Lys  
 305 310 315 320

Lys Ser Asn Tyr Thr Phe Leu His Ser Pro Leu Gly His Arg Arg Ile  
 325 330 335  
 Pro Ser Gly Ala Asn Ser Ile Leu Ala Asp Thr Ser Val Ala Leu Ser  
 340 345 350  
 Ala Asn Asp Ser Ile Ser Ala Val Ser Asn Ser Val Arg Ala Lys Asp  
 355 360 365  
 Asp Glu Thr Lys Thr Thr Leu Pro Leu Leu Arg Ser Tyr Phe Ile Gln  
 370 375 380  
 Ile Leu Leu Asn Asn Phe Gln Glu Glu Leu Gln Asp Trp Arg Ile Asp  
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 Gly Asp Tyr Gly Leu Leu Arg Leu Val Asp Lys Leu Met Ile Ser Lys  
 405 410 415  
 Asp Gly Gln Arg Tyr Ile Gln Cys Trp Cys Phe Leu Phe Glu Asp Ala  
 420 425 430  
 Phe Val Ile Ala Glu Val Asp Asn Asp Val Asp Val Leu Glu Ile Arg  
 435 440 445  
 Leu Lys Asn Leu Glu Val Phe Thr Pro Ile Ala Asn Leu Arg Met Thr  
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 Thr Leu Glu Ala Ser Val Leu Lys Cys Thr Leu Asn Lys Gln His Cys  
 465 470 475 480  
 Ala Asp Leu Ser Asp Leu Tyr Ile Val Gln Asn Ile Asn Ser Asp Glu  
 485 490 495  
 Ser Thr Thr Val Gln Lys Trp Ile Ser Gly Ile Leu Asn Gln Asp Phe  
 500 505 510  
 Val Phe Asn Glu Asp Asn Ile Thr Ser Thr Leu Pro Ile Leu Pro Ile  
 515 520 525  
 Ile Lys Asn Phe Ser Lys Asp Val Gly Asn Gly Arg His Glu Thr Ser  
 530 535 540  
 Thr Phe Leu Gly Leu Ile Asn Pro Asn Lys Val Val Glu Val Gly Asn  
 545 550 555 560  
 Val His Asp Asn Asp Thr Val Ile Ile Arg Arg Gly Phe Thr Leu Asn  
 565 570 575

Ser Gly Glu Cys Ser Arg Gln Ser Thr Val Asp Ser Ile Gln Ser Val  
 580 585 590

Leu Thr Thr Ile Ser Ser Ile Leu Ser Leu Lys Arg Glu Lys Pro Asp  
 595 600 605

Asn Leu Ala Ile Ile Leu Gln Ile Asp Phe Thr Lys Leu Lys Glu Glu  
 610 615 620

Asp Ser Leu Ile Val Val Tyr Asn Ser Leu Lys Ala Leu Thr Ile Lys  
 625 630 635 640

Phe Ala Arg Leu Gln Phe Cys Phe Val Asp Arg Asn Asn Tyr Val Leu  
 645 650 655

Asp Tyr Gly Ser Val Leu His Lys Ile Asp Ser Leu Asp Ser Ile Ser  
 660 665 670

Asn Leu Lys Ser Lys Ser Ser Ser Thr Gln Phe Ser Pro Ile Trp Leu  
 675 680 685

Lys Asn Thr Leu Tyr Pro Glu Asn Ile His Glu His Leu Gly Ile Val  
 690 695 700

Ala Val Ser Asn Ser Asn Met Glu Ala Lys Lys Ser Ile Leu Phe Gln  
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Asp Tyr Arg Cys Phe Thr Ser Phe Gly Arg Arg Arg Pro Asn Glu Leu  
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Lys Ile Lys Val Gly Tyr Leu Asn Val Asp Tyr Ser Asp Lys Ile Asp  
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Glu Leu Val Glu Ala Ser Ser Trp Thr Phe Val Leu Glu Thr Leu Cys  
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Tyr Ser Phe Gly Leu Ser Phe Asp Glu His Asp Asp Asp Asp Glu Glu  
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Asp Asn Asp Asp Ser Thr Asp Asn Glu Leu Asp Asn Ser Ser Gly Ser  
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Leu Ser Asp Ala Glu Ser Thr Thr Thr Ile His Ile Asp Ser Pro Phe  
 805 810 815

Asp Asn Glu Asn Ala Thr Ala Asn Met Val Asn Asp Arg Asn Leu Leu  
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Thr Glu Gly Glu His Ser Asn Ile Glu Asn Leu Glu Thr Val Ala Ser  
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 Ser Val Gln Pro Ala Leu Ile Pro Asn Ile Arg Phe Ser Leu His Ser  
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ga

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&lt;210&gt; 54

&lt;211&gt; 973

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 54

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Met Thr Ser Leu Ser Ser Gln Pro Ala Tyr Thr Leu Val Phe Asp Pro
  1                      5                      10                      15

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Ser Pro Ser Met Glu Thr Tyr Ser Ser Thr Asp Phe Gln Lys Ala Leu

```

20	25	30
Glu Lys Gly Ser Asp Glu Gln Lys Ile Asp Thr Met Lys Ser Ile Leu		
35	40	45
Val Thr Met Leu Glu Gly Asn Pro Met Pro Glu Leu Leu Met His Ile		
50	55	60
Ile Arg Phe Val Met Pro Ser Lys Asn Lys Glu Leu Lys Lys Leu Leu		
65	70	75 80
Tyr Phe Tyr Trp Glu Ile Val Pro Lys Leu Ala Glu Asp Gly Lys Leu		
85	90	95
Arg His Glu Met Ile Leu Val Cys Asn Ala Ile Gln His Asp Leu Gln		
100	105	110
His Pro Asn Glu Tyr Ile Arg Gly Asn Thr Leu Arg Phe Leu Thr Lys		
115	120	125
Leu Arg Glu Ala Glu Leu Leu Glu Gln Met Val Pro Ser Val Leu Ala		
130	135	140
Cys Leu Glu Tyr Arg His Ala Tyr Val Arg Lys Tyr Ala Ile Leu Ala		
145	150	155 160
Val Phe Ser Ile Phe Lys Val Ser Glu His Leu Leu Pro Asp Ala Lys		
165	170	175
Glu Ile Ile Asn Ser Phe Ile Val Ala Glu Thr Asp Pro Ile Cys Lys		
180	185	190
Arg Asn Ala Phe Ile Gly Leu Ala Glu Leu Asp Arg Glu Asn Ala Leu		
195	200	205
His Tyr Leu Glu Asn Asn Ile Ala Asp Ile Glu Asn Leu Asp Pro Leu		
210	215	220
Leu Gln Ala Val Phe Val Gln Phe Ile Arg Gln Asp Ala Asn Arg Thr		
225	230	235 240
Pro Ala Leu Lys Ala Gln Tyr Ile Glu Leu Leu Met Glu Leu Leu Ser		
245	250	255
Thr Thr Thr Ser Asp Glu Val Ile Phe Glu Thr Ala Leu Ala Leu Thr		
260	265	270
Val Leu Ser Ala Asn Pro Asn Val Leu Val Pro Ala Val Asn Lys Leu		

275

280

285

Ile Asp Leu Ala Val Lys Val Ser Asp Asn Asn Ile Lys Leu Ile Val		
290	295	300
Leu Asp Arg Ile Gln Asp Ile Asn Ala Asn Asn Val Gly Ala Leu Glu		
305	310	315 320
Glu Leu Thr Leu Asp Ile Leu Arg Val Leu Asn Ala Glu Asp Leu Asp		
	325	330 335
Val Arg Ser Lys Ala Leu Asp Ile Ser Met Asp Leu Ala Thr Ser Arg		
	340	345 350
Asn Ala Glu Asp Val Val Gln Leu Leu Lys Lys Glu Leu Gln Thr Thr		
	355	360 365
Val Asn Asn Pro Asp Gln Asp Lys Ala Met Gln Tyr Arg Gln Leu Leu		
	370	375 380
Ile Lys Thr Ile Arg Thr Val Ala Val Asn Phe Val Glu Met Ala Ala		
385	390	395 400
Ser Val Val Ser Leu Leu Leu Asp Phe Ile Gly Asp Leu Asn Ser Val		
	405	410 415
Ala Ala Ser Gly Ile Ile Ala Phe Ile Lys Glu Val Ile Glu Lys Tyr		
	420	425 430
Pro Gln Leu Arg Ala Asn Ile Leu Glu Asn Met Val Gln Thr Leu Asp		
	435	440 445
Lys Val Arg Ser Ala Lys Ala Tyr Arg Gly Ala Leu Trp Ile Met Gly		
	450	455 460
Glu Tyr Ala Glu Gly Glu Ser Glu Ile Gln His Cys Trp Lys His Ile		
465	470	475 480
Arg Asn Ser Val Gly Glu Val Pro Ile Leu Gln Ser Glu Ile Lys Lys		
	485	490 495
Leu Thr Gln Asn Gln Glu His Thr Glu Glu Asn Glu Val Asp Ala Thr		
	500	505 510
Ala Lys Pro Thr Gly Pro Val Ile Leu Pro Asp Gly Thr Tyr Ala Thr		
	515	520 525
Glu Ser Ala Phe Asp Val Lys Thr Ser Gln Lys Ser Val Thr Asp Glu		



530                                      535                                      540  
 Glu Arg Asp Ser Arg Pro Pro Ile Arg Arg Phe Val Leu Ser Gly Asp  
 545                                      550                                      555                                      560  
 Phe Tyr Thr Ala Ala Ile Leu Ala Asn Thr Ile Ile Lys Leu Val Leu  
                                     565                                      570                                      575  
 Lys Phe Glu Asn Val Ser Lys Asn Lys Thr Val Ile Asn Ala Leu Lys  
                                     580                                      585                                      590  
 Ala Glu Ala Leu Leu Ile Leu Val Ser Ile Val Arg Val Gly Gln Ser  
                                     595                                      600                                      605  
 Ser Leu Val Glu Lys Lys Ile Asp Glu Asp Ser Leu Glu Arg Val Met  
                                     610                                      615                                      620  
 Thr Ser Ile Ser Ile Leu Leu Asp Glu Val Asn Pro Glu Glu Lys Lys  
                                     625                                      630                                      635                                      640  
 Glu Glu Val Lys Leu Leu Glu Val Ala Phe Leu Asp Thr Thr Lys Ser  
                                     645                                      650                                      655  
 Ser Phe Lys Arg Gln Ile Glu Ile Ala Lys Lys Asn Lys His Lys Arg  
                                     660                                      665                                      670  
 Ala Leu Lys Asp Ser Cys Lys Asn Ile Glu Pro Ile Asp Thr Pro Ile  
                                     675                                      680                                      685  
 Ser Phe Arg Gln Phe Ala Gly Val Asp Ser Thr Asn Val Gln Lys Asp  
                                     690                                      695                                      700  
 Ser Ile Glu Glu Asp Leu Gln Leu Ala Met Lys Gly Asp Ala Ile His  
                                     705                                      710                                      715                                      720  
 Ala Thr Ser Ser Ser Ser Ile Ser Lys Leu Lys Lys Ile Val Pro Leu  
                                     725                                      730                                      735  
 Cys Gly Phe Ser Asp Pro Val Tyr Ala Glu Ala Cys Ile Thr Asn Asn  
                                     740                                      745                                      750  
 Gln Phe Asp Val Val Leu Asp Val Leu Leu Val Asn Gln Thr Lys Glu  
                                     755                                      760                                      765  
 Thr Leu Lys Asn Leu His Val Gln Phe Ala Thr Leu Gly Asp Leu Lys  
                                     770                                      775                                      780  
 Ile Ile Asp Thr Pro Gln Lys Thr Asn Val Ile Pro His Gly Phe His

785                                      790                                      795                                      800  
 Lys Phe Thr Val Thr Val Lys Val Ser Ser Ala Asp Thr Gly Val Ile  
    805                                      810                                      815  
 Phe Gly Asn Ile Ile Tyr Asp Gly Ala His Gly Glu Asp Ala Arg Tyr  
    820                                      825                                      830  
 Val Ile Leu Asn Asp Val His Val Asp Ile Met Asp Tyr Ile Lys Pro  
    835                                      840                                      845  
 Ala Thr Ala Asp Asp Glu His Phe Arg Thr Met Trp Asn Ala Phe Glu  
    850                                      855                                      860  
 Trp Glu Asn Lys Ile Ser Val Lys Ser Gln Leu Pro Thr Leu His Ala  
 865                                      870                                      875                                      880  
 Tyr Leu Arg Glu Leu Val Lys Gly Thr Asn Met Gly Ile Leu Thr Pro  
    885                                      890                                      895  
 Ser Glu Ser Leu Gly Glu Asp Asp Cys Arg Phe Leu Ser Cys Asn Leu  
    900                                      905                                      910  
 Tyr Ala Lys Ser Ser Phe Gly Glu Asp Ala Leu Ala Asn Leu Cys Ile  
    915                                      920                                      925  
 Glu Lys Asp Ser Lys Thr Asn Asp Val Ile Gly Tyr Val Arg Ile Arg  
    930                                      935                                      940  
 Ser Lys Gly Gln Gly Leu Ala Leu Ser Leu Gly Asp Arg Val Ala Leu  
 945                                      950                                      955                                      960  
 Ile Ala Lys Lys Thr Asn Lys Leu Ala Leu Thr His Val  
    965                                      970

<210> 55  
 <211> 1652  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 55  
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 aatgatttct gatactcttt gattccattc tgtcatactt ttttctgcat ttgaaacgct 180  
 aattaagtat ttcttggtcc tgcttctttt ccttttgatt tcttttttta ttctcaagtt 240  
 ttttaatttct ggagaatctc tttttttgtt tattttgtta acacagtttag tggagccttg 300

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tagtattcgag agtagactat ctttgaaaag caatgcgagt tgagagattg tggagtgtac 360
tacagaacca atattaaaca caatctttcc tcaaactgta acaccgagtt tttttcccca 420
ccaatcgtga atccgatagc atatactttt gtctagaaat ttcaataaac aacagaataa 480
cgaagagtgc taagggacaa atgcaaaacc ctccgttgat tcgtcccgat atgtataatc 540
agggaagcag ctcaatggct acttataatg cctctgagaa gaatctaaat gagcatcctt 600
ctccgcaaat tgcacagccc agcacgtccc aaaagttacc ttatagaata aatcctacaa 660
ccactaatgg ggacaccgac atatctgtta acagcaatcc tatccagcct cctttgccaa 720
acttgatgca tctatctggg ccgtctgact atagatcgat gcatcaaagt cctatacatc 780
catcttatat catccctccg cattcaaag aaagaaaaca atcagcttct tacaacagac 840
ctcaaaatgc tcatgttagt attcaacctt ccgtgggtatt cccccctaaa agttattcca 900
tatcttatgc accttatcaa ataaatcccc ctttaccaaa tggacttccg aaccagagca 960
tatctttgaa taaggagtat attgcagagg agcaactatc aaccctccca tctcgcaata 1020
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ctgataataa tgataataat gataatgtaa ccaaacctgt tcttgataaa gacacccaac 1140
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taagaagtga gtatgatgtc ttatgtaacg aaaacaacat gttgaagaat gagaatagta 1440
taataaaaaa tgaacacaac atgtcaagaa atgaaaatga aaacctaaaa cttgagaata 1500
aacgcttcca cgctgaatat atacgaatga tcgaggatat tgaaaatact aaaagaaagg 1560
aacaagaaca acgagatgaa atagagcaac taaaaaaaaa aataagatcc ctggaggaaa 1620
tagtagggag acactcggat agtgccacgt aa 1652

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&lt;210&gt; 56

&lt;211&gt; 383

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 56

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Met Gln Asn Pro Pro Leu Ile Arg Pro Asp Met Tyr Asn Gln Gly Ser
  1              5              10              15

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Ser Ser Met Ala Thr Tyr Asn Ala Ser Glu Lys Asn Leu Asn Glu His
          20              25              30

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Pro Ser Pro Gln Ile Ala Gln Pro Ser Thr Ser Gln Lys Leu Pro Tyr
          35              40              45

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Arg Ile Asn Pro Thr Thr Thr Asn Gly Asp Thr Asp Ile Ser Val Asn
          50              55              60

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Ser Asn Pro Ile Gln Pro Pro Leu Pro Asn Leu Met His Leu Ser Gly
          65              70              75              80

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Pro Ser Asp Tyr Arg Ser Met His Gln Ser Pro Ile His Pro Ser Tyr
          85              90              95

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Ile Ile Pro Pro His Ser Asn Glu Arg Lys Gln Ser Ala Ser Tyr Asn
      100                      105                      110

Arg Pro Gln Asn Ala His Val Ser Ile Gln Pro Ser Val Val Phe Pro
      115                      120                      125

Pro Lys Ser Tyr Ser Ile Ser Tyr Ala Pro Tyr Gln Ile Asn Pro Pro
      130                      135                      140

Leu Pro Asn Gly Leu Pro Asn Gln Ser Ile Ser Leu Asn Lys Glu Tyr
      145                      150                      155                      160

Ile Ala Glu Glu Gln Leu Ser Thr Leu Pro Ser Arg Asn Thr Ser Val
      165                      170                      175

Thr Thr Ala Pro Pro Ser Phe Gln Asn Ser Ala Asp Thr Ala Lys Asn
      180                      185                      190

Ser Ala Asp Asn Asn Asp Asn Asn Asp Asn Val Thr Lys Pro Val Pro
      195                      200                      205

Asp Lys Asp Thr Gln Leu Ile Ser Ser Ser Gly Lys Thr Leu Arg Asn
      210                      215                      220

Thr Arg Arg Ala Ala Gln Asn Arg Thr Ala Gln Lys Ala Phe Arg Gln
      225                      230                      235                      240

Arg Lys Glu Lys Tyr Ile Lys Asn Leu Glu Gln Lys Ser Lys Ile Phe
      245                      250                      255

Asp Asp Leu Leu Ala Glu Asn Asn Asn Phe Lys Ser Leu Asn Asp Ser
      260                      265                      270

Leu Arg Asn Asp Asn Asn Ile Leu Ile Ala Gln His Glu Ala Ile Arg
      275                      280                      285

Asn Ala Ile Thr Met Leu Arg Ser Glu Tyr Asp Val Leu Cys Asn Glu
      290                      295                      300

Asn Asn Met Leu Lys Asn Glu Asn Ser Ile Ile Lys Asn Glu His Asn
      305                      310                      315                      320

Met Ser Arg Asn Glu Asn Glu Asn Leu Lys Leu Glu Asn Lys Arg Phe
      325                      330                      335

His Ala Glu Tyr Ile Arg Met Ile Glu Asp Ile Glu Asn Thr Lys Arg
      340                      345                      350

```

Lys Glu Gln Glu Gln Arg Asp Glu Ile Glu Gln Leu Lys Lys Lys Ile  
 355 360 365

Arg Ser Leu Glu Glu Ile Val Gly Arg His Ser Asp Ser Ala Thr  
 370 375 380

&lt;210&gt; 57

&lt;211&gt; 2270

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 57

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aaaagaagta gcctgtataa tatagagaga ttttatatac tttcttaatg aattagactg 180
tttctacaag tatttgacac tggaaaaaaa gagaaagtac atagagattg gccaaatatt 240
taaatctaca cagttgccta tcgtttatcg ccttattcct cagaaacatt tcatcaacta 300
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tgattgaaaa aattggtata ttttcagtac acatataaat aaaaccctca atttgcctct 420
ccaaccgtta taactattcc agatcctcct taccgagcaa gtaggctagc ttctgtaaag 480
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ggtagggcat gccaatcat ttactaaggg aagaaggcga ctttgcccag tttatgattc 600
taaccatcaa cgaattaaaa atagccatac atgggtacct cagaaatacc ccatggtaca 660
acatgttgaa ggattatttg tttgtgatct tttgttaca gctaataagt aatttttttt 720
atctgttgaa agtttatggg ccggtgaggt tagcagttag aacatacgag catagtcca 780
gaagattgtt tcgttggtta ttggactcac catttttgag gggtagcgta gaaaaggaag 840
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aattgaacga cttgatacca catacccaat ggaaggaagg aaagggtctt ggtgccgttt 1020
accacgggtg tgatgatttg atccacttac aaacaatcgc atacgaaaaa tattgcgttg 1080
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gtggtacaga atccttgctt ttagcatgtc tgagcgctaa aatgtatgcc cttcatcatc 1260
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aatataaact tcctttacac gtgcacagtt gtctagggtc ctttattgtt tcatttatgg 1560
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ctatgggtcaa catgggtgaa aatgggtaca ttgagtcgtg ccaagaaata gtcggtgcag 1860
caatgaagtt taaaaaatac atccaggaaa acattccaga cctgaatata atgggcaacc 1920
ctagatattc agtcatttca ttttcttcaa agaccttgaa catacacgaa ctatctgaca 1980

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 ccttcacgag attgagcgt catgttgtgg atgagatctg cgacatttta cgtactaccg 2100  
 tgcaagagtt gaagagcgaa tcaaattcta aaccatcccc agacggaact agcgtcttat 2160  
 atggtgtcgc cgggagcgtt aaaactgctg gcgttgcaga caaattgatt gtgggattcc 2220  
 tagacgcatt atacaagttg ggtccaggag aggataccgc caccaagtag 2270

<210> 58

<211> 589

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 58

Met Ser Gly Val Ser Asn Lys Thr Val Ser Ile Asn Gly Trp Tyr Gly  
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Met Pro Ile His Leu Leu Arg Glu Glu Gly Asp Phe Ala Gln Phe Met  
 20 25 30

Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg  
 35 40 45

Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe  
 50 55 60

Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly  
 65 70 75 80

Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu  
 85 90 95

Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys  
 100 105 110

Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser  
 115 120 125

Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro  
 130 135 140

Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro  
 145 150 155 160

His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly  
 165 170 175

Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys  
 180 185 190

```

Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met
    195                                200                                205

Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser
    210                                215                                220

Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu
    225                                230                                235                                240

Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile
                245                                250                                255

Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp
                260                                265                                270

Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
                275                                280                                285

Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
    290                                295                                300

Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
    305                                310                                315                                320

Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys
                325                                330                                335

Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe
                340                                345                                350

Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val
                355                                360                                365

Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
    370                                375                                380

Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
    385                                390                                395                                400

His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
                405                                410                                415

Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
                420                                425                                430

Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
    435                                440                                445

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Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn  
 450 455 460  
 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser  
 465 470 475 480  
 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser  
 485 490 495  
 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His  
 500 505 510  
 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp  
 515 520 525  
 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys  
 530 535 540  
 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val  
 545 550 555 560  
 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala  
 565 570 575  
 Leu Tyr Lys Leu Gly Pro Gly Glu Asp Thr Ala Thr Lys  
 580 585

&lt;210&gt; 59

&lt;211&gt; 3470

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 59

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 tatatttaga agagaggaaa ttatttttct catgtccttt ttaaateccct ttgggtggcg 300  
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 caagcaattg taatcaataa gccaccaatt agaaggctac tcaaaagaat aaagttacta 480  
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 cacaggccgt tagaaaatat ccagttggag gtatattcca tggttatgaa gtgagaagaa 600  
 ttctaccggt tccggagctg agactcactg cggtagattt ggtgcactcc cagacaggag 660  
 ccgagcattt gcatattgat agagacgaca agaataatgt gttcagcatt gcttttaaaa 720



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ccaaccctcc agattccact ggggtccctc atattctaga gcatacaacg ttgtgtgggt 780
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aagatttcgc taatttaaga ggtgtttatt tagactccac cttgaatccg ctacttaaac 960
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gagatcctat gaaaattaca gacttgagat acggcgatct cttggatttc catcacaaaa 1200
attaccatcc ctccaatgca aaaactttca cgtacggtaa cttgccattg gtggatacgt 1260
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tccgcttatt agcatcttca aacacatctt ctgtagcaga tgccggtcat gcatttgcaa 2580
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caaaattcat ggagagatta cctcatggca gctgcttgcc caatggacca aagacttcag 2880
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gtgcttatgg tgggtgtgct tcttatagcg ccttagcggg tattttcagt ttctattcct 3120
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cagacgatat gaaacaagca agaagggaac aactcttaga cgtatctctc ctggacgttc 3360
atagagtcgc cgaaaaatat ctactaaaca aagaaggggt ggtacgggtc attggacctg 3420
gaatcgaggg gaagactgtt tcaccaaatt gggaggtgaa ggaactgtag 3470
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<210> 60  
 <211> 989  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 60

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Met Leu Arg Phe Gln Arg Phe Ala Ser Ser Tyr Ala Gln Ala Gln Ala
 1             5             10             15

Val Arg Lys Tyr Pro Val Gly Gly Ile Phe His Gly Tyr Glu Val Arg
             20             25             30

Arg Ile Leu Pro Val Pro Glu Leu Arg Leu Thr Ala Val Asp Leu Val
             35             40             45

His Ser Gln Thr Gly Ala Glu His Leu His Ile Asp Arg Asp Asp Lys
             50             55             60

Asn Asn Val Phe Ser Ile Ala Phe Lys Thr Asn Pro Pro Asp Ser Thr
             65             70             75             80

Gly Val Pro His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Val Lys
             85             90             95

Tyr Pro Val Arg Asp Pro Phe Phe Lys Met Leu Asn Lys Ser Leu Ala
             100            105            110

Asn Phe Met Asn Ala Met Thr Gly Pro Asp Tyr Thr Phe Phe Pro Phe
             115            120            125

Ser Thr Thr Asn Pro Gln Asp Phe Ala Asn Leu Arg Gly Val Tyr Leu
             130            135            140

Asp Ser Thr Leu Asn Pro Leu Leu Lys Gln Glu Asp Phe Asp Gln Glu
             145            150            155            160

Gly Trp Arg Leu Glu His Lys Asn Ile Thr Asp Pro Glu Ser Asn Ile
             165            170            175

Val Phe Lys Gly Val Val Tyr Asn Glu Met Lys Gly Gln Ile Ser Asn
             180            185            190

Ala Asn Tyr Tyr Phe Trp Ser Lys Phe Gln Gln Ser Ile Tyr Pro Ser
             195            200            205

Leu Asn Asn Ser Gly Gly Asp Pro Met Lys Ile Thr Asp Leu Arg Tyr
             210            215            220

```

Gly Asp Leu Leu Asp Phe His His Lys Asn Tyr His Pro Ser Asn Ala  
225 230 235 240

Lys Thr Phe Thr Tyr Gly Asn Leu Pro Leu Val Asp Thr Leu Lys Gln  
245 250 255

Leu Asn Glu Gln Phe Ser Gly Tyr Gly Lys Arg Ala Arg Lys Asp Lys  
260 265 270

Leu Leu Met Pro Ile Asp Leu Lys Lys Asp Ile Asp Val Lys Leu Leu  
275 280 285

Gly Gln Ile Asp Thr Met Leu Pro Pro Glu Lys Gln Thr Lys Ala Ser  
290 295 300

Met Thr Trp Ile Cys Gly Ala Pro Gln Asp Thr Tyr Asp Thr Phe Leu  
305 310 315 320

Leu Lys Val Leu Gly Asn Leu Leu Met Asp Gly His Ser Ser Val Met  
325 330 335

Tyr Gln Lys Leu Ile Glu Ser Gly Ile Gly Leu Glu Phe Ser Val Asn  
340 345 350

Ser Gly Val Glu Pro Thr Thr Ala Val Asn Leu Leu Thr Val Gly Ile  
355 360 365

Gln Gly Val Ser Asp Ile Glu Ile Phe Lys Asp Thr Val Asn Asn Ile  
370 375 380

Phe Gln Asn Leu Leu Glu Thr Glu His Pro Phe Asp Arg Lys Arg Ile  
385 390 395 400

Asp Ala Ile Ile Glu Gln Leu Glu Leu Ser Lys Lys Asp Gln Lys Ala  
405 410 415

Asp Phe Gly Leu Gln Leu Leu Tyr Ser Ile Leu Pro Gly Trp Thr Asn  
420 425 430

Lys Ile Asp Pro Phe Glu Ser Leu Leu Phe Glu Asp Val Leu Gln Arg  
435 440 445

Phe Arg Gly Asp Leu Glu Thr Lys Gly Asp Thr Leu Phe Gln Asp Leu  
450 455 460

Ile Arg Lys Tyr Ile Val His Lys Pro Cys Phe Thr Phe Ser Ile Gln  
465 470 475 480

Gly Ser Glu Glu Phe Ser Lys Ser Leu Asp Asp Glu Glu Gln Thr Arg  
 485 490 495  
 Leu Arg Glu Lys Ile Thr Ala Leu Asp Glu Gln Asp Lys Lys Asn Ile  
 500 505 510  
 Phe Lys Arg Gly Ile Leu Leu Gln Glu Lys Gln Asn Glu Lys Glu Asp  
 515 520 525  
 Leu Ser Cys Leu Pro Thr Leu Gln Ile Lys Asp Ile Pro Arg Ala Gly  
 530 535 540  
 Asp Lys Tyr Ser Ile Glu Gln Lys Asn Asn Thr Met Ser Arg Ile Thr  
 545 550 555 560  
 Asp Thr Asn Gly Ile Thr Tyr Val Arg Gly Lys Arg Leu Leu Asn Asp  
 565 570 575  
 Ile Ile Pro Phe Glu Leu Phe Pro Tyr Leu Pro Leu Phe Ala Glu Ser  
 580 585 590  
 Leu Thr Asn Leu Gly Thr Thr Thr Glu Ser Phe Ser Glu Ile Glu Asp  
 595 600 605  
 Gln Ile Lys Leu His Thr Gly Gly Ile Ser Thr His Val Glu Val Thr  
 610 615 620  
 Ser Asp Pro Asn Thr Thr Glu Pro Arg Leu Ile Phe Gly Phe Asp Gly  
 625 630 635 640  
 Trp Ser Leu Asn Ser Lys Thr Asp His Ile Phe Glu Phe Trp Ser Lys  
 645 650 655  
 Ile Leu Leu Glu Thr Asp Phe His Lys Asn Ser Asp Lys Leu Lys Val  
 660 665 670  
 Leu Ile Arg Leu Leu Ala Ser Ser Asn Thr Ser Ser Val Ala Asp Ala  
 675 680 685  
 Gly His Ala Phe Ala Arg Gly Tyr Ser Ala Ala His Tyr Arg Ser Ser  
 690 695 700  
 Gly Ala Ile Asn Glu Thr Leu Asn Gly Ile Glu Gln Leu Gln Phe Ile  
 705 710 715 720  
 Asn Arg Leu His Ser Leu Leu Asp Asn Glu Glu Thr Phe Gln Arg Glu  
 725 730 735

```

Val Val Asp Lys Leu Thr Glu Leu Gln Lys Tyr Ile Val Asp Thr Asn
      740                      745                      750

Asn Met Asn Phe Phe Ile Thr Ser Asp Ser Asp Val Gln Ala Lys Thr
      755                      760                      765

Val Glu Ser Gln Ile Ser Lys Phe Met Glu Arg Leu Pro His Gly Ser
      770                      775                      780

Cys Leu Pro Asn Gly Pro Lys Thr Ser Asp Tyr Pro Leu Ile Gly Ser
      785                      790                      795                      800

Lys Cys Lys His Thr Leu Ile Lys Phe Pro Phe Gln Val His Tyr Thr
      805                      810                      815

Ser Gln Ala Leu Leu Gly Val Pro Tyr Thr His Lys Asp Gly Ser Ala
      820                      825                      830

Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu
      835                      840                      845

Val Arg Glu Lys Gly Gly Ala Tyr Gly Gly Gly Ala Ser Tyr Ser Ala
      850                      855                      860

Leu Ala Gly Ile Phe Ser Phe Tyr Ser Tyr Arg Asp Pro Gln Pro Leu
      865                      870                      875                      880

Lys Ser Leu Glu Thr Phe Lys Asn Ser Gly Arg Tyr Ile Leu Asn Asp
      885                      890                      895

Ala Lys Trp Gly Val Thr Asp Leu Asp Glu Ala Lys Leu Thr Ile Phe
      900                      905                      910

Gln Gln Val Asp Ala Pro Lys Ser Pro Lys Gly Glu Gly Val Thr Tyr
      915                      920                      925

Phe Met Ser Gly Val Thr Asp Asp Met Lys Gln Ala Arg Arg Glu Gln
      930                      935                      940

Leu Leu Asp Val Ser Leu Leu Asp Val His Arg Val Ala Glu Lys Tyr
      945                      950                      955                      960

Leu Leu Asn Lys Glu Gly Val Ser Thr Val Ile Gly Pro Gly Ile Glu
      965                      970                      975

Gly Lys Thr Val Ser Pro Asn Trp Glu Val Lys Glu Leu
      980                      985

```

<210> 61  
 <211> 1612  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 61  
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 ctctaatagt tactctatta ttgctgttaa ttgacaatgt ttagtcacgt gcaacacaat 180  
 tcaagtcacg tggaaaggcc ttcacatggg gatccatctt ctacatcttc atcgggtcctg 240  
 cataaagtca taatatgggg ctactggaat gtatgcactt aacagtacta ttatatgggtg 300  
 aggctgtaat gcttaccgtt ttgtggctat tctcgtattc tgtaggcccc ccatacaca 360  
 tttttcggta actgcggcat atagatgaaa gttgaaatga atattcaaaa gaatatatat 420  
 aataatgcag gagatcaagg aagaattaga tatgtataag agtgatggta gaggcaaaaa 480  
 ataaaaagta agcaggagaa tgaatcgtgt tggatatagac gtagatcata tgataggggt 540  
 cctgcttctg gccgtagtgg tgggtgtttg ggttggcgct tctgttttga ctaatgaatt 600  
 gctcgagaca aacgcgtaca ataaaccttt ctctcttact tatctaaaca tatcatcggt 660  
 tgctctttat ttgacgccag atctatggag gataatccaa tcaagaagga agagcttgca 720  
 ggaacggaca gaacgaacat tacctattca cacacaagaa tctttttcag agttcctacc 780  
 tttactatct tcaactcctt ctacttcttc aaatttgtct tcgatagcgg acacgaaagt 840  
 gaaggataca atgaggttga gtctgctatt ttgcgtcttg tggttcgtgg caaatttggc 900  
 ggctaacgct gctttgtcgt ataccacagt ggcttcgtca acaattcttt catcgacatc 960  
 ctcatTTTTT accttatttc ttgccactag tctaggaata gaaactTTTT cgacaaaaaa 1020  
 actgctgggg ttatttgtgt ctttgttttg aattatctta attgtgatgc aatcctcgaa 1080  
 gcaacaggat tctgtgagtg ctctctcctt tttggtagg aacactttag cactgctggg 1140  
 gtcattgggt tacagtgtct atacaaccct tttgaaatac gaaatatcat ccaaaggctc 1200  
 cagactagac attcagatgt ttcttggtta tgttggtatc ttcacgtttc tgttggtttg 1260  
 gccaatTTTA ataactctgg atataacaca tatggaaact tttgaactac caagtaactt 1320  
 ccacatttct tttcttgtca tgttaaattg tatcattatc tttgttagtg actatttttg 1380  
 gtgtaaagcc ctcatTTTga catcacctt ggtggttacc gttgccttaa cttttactat 1440  
 ccggttagcc atgttcgctg attttgtatg gcgagaggca ttttttacgc cttggtatat 1500  
 cattggtgtt attttcattt ttgtttcatt ctttctagtt aaccatcggg gagaatctgc 1560  
 tgttgaaaag gactgtgctg cggttgaaaa aggacctatc ttggatgcct aa 1612

<210> 62  
 <211> 370  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 62  
 Met Asn Arg Val Gly Ile Asp Val Asp His Met Ile Gly Val Leu Leu  
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 Leu Ala Val Val Val Val Phe Trp Val Gly Ala Ser Cys Leu Thr Asn  
 20 25 30

Glu Leu Leu Glu Thr Asn Ala Tyr Asn Lys Pro Phe Phe Leu Thr Tyr  
           35                          40                          45  
 Leu Asn Ile Ser Ser Phe Ala Leu Tyr Leu Thr Pro Asp Leu Trp Arg  
           50                          55                          60  
 Ile Ile Gln Ser Arg Arg Lys Ser Leu Gln Glu Arg Thr Glu Arg Thr  
           65                          70                          75                          80  
 Leu Pro Ile His Thr Gln Glu Ser Phe Ser Glu Phe Leu Pro Leu Leu  
                           85                          90                          95  
 Ser Ser Thr Pro Ser Thr Ser Ser Asn Leu Ser Ser Ile Ala Asp Thr  
                           100                          105                          110  
 Lys Val Lys Asp Thr Met Arg Leu Ser Leu Leu Phe Cys Val Leu Trp  
           115                          120                          125  
 Phe Val Ala Asn Leu Ala Ala Asn Ala Ala Leu Ser Tyr Thr Thr Val  
           130                          135                          140  
 Ala Ser Ser Thr Ile Leu Ser Ser Thr Ser Ser Phe Phe Thr Leu Phe  
           145                          150                          155                          160  
 Leu Ala Thr Ser Leu Gly Ile Glu Thr Phe Ser Thr Lys Lys Leu Leu  
                           165                          170                          175  
 Gly Leu Phe Val Ser Leu Phe Gly Ile Ile Leu Ile Val Met Gln Ser  
                           180                          185                          190  
 Ser Lys Gln Gln Asp Ser Val Ser Ala Ser Ser Phe Leu Val Gly Asn  
           195                          200                          205  
 Thr Leu Ala Leu Leu Gly Ser Leu Gly Tyr Ser Val Tyr Thr Thr Leu  
           210                          215                          220  
 Leu Lys Tyr Glu Ile Ser Ser Lys Gly Leu Arg Leu Asp Ile Gln Met  
           225                          230                          235                          240  
 Phe Leu Gly Tyr Val Gly Ile Phe Thr Phe Leu Leu Phe Trp Pro Ile  
                           245                          250                          255  
 Leu Ile Ile Leu Asp Ile Thr His Met Glu Thr Phe Glu Leu Pro Ser  
           260                          265                          270  
 Asn Phe His Ile Ser Phe Leu Val Met Leu Asn Cys Ile Ile Ile Phe  
           275                          280                          285

Val Ser Asp Tyr Phe Trp Cys Lys Ala Leu Ile Leu Thr Ser Pro Leu  
 290 295 300

Val Val Thr Val Ala Leu Thr Phe Thr Ile Pro Leu Ala Met Phe Ala  
 305 310 315 320

Asp Phe Val Trp Arg Glu Ala Phe Phe Thr Pro Trp Tyr Ile Ile Gly  
 325 330 335

Val Ile Phe Ile Phe Val Ser Phe Phe Leu Val Asn His Arg Gly Glu  
 340 345 350

Ser Ala Val Glu Lys Asp Cys Ala Ala Val Glu Lys Gly Pro Ile Leu  
 355 360 365

Asp Ala  
 370

<210> 63

<211> 1376

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 63

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 ggccattata tccaaaactt ttttaaaata gcatccacat cacttactgg cgtacagttt 120  
 cgtgtctggc aacaaaaaag tacatttaat ttcaatgatt aaaaagacat taaacatccg 180  
 tacattacgc acccatgcat gctatctgaa aatattctac atgctgcttt tagaaatttg 240  
 aagcggcata tgggtgtttcc ttgcggagac ggcgcgtcag gggaactgcg attccgaaag 300  
 atgcctttcc cagteccata tgcccatccc aagatcatgc ccgggagagc aaatgtcgcc 360  
 ccagccaggt cggacacatc tgtcattcga ccactaagta ttgtcaaagc tagggttaat 420  
 tgaagatagc tctacatggt attagtagag tttttaaacg ttgagatact agtgaacgta 480  
 tacacaagag cggataaaag atgtctttag ttgtccaaga acaaggttcc ttccaacaca 540  
 ttttacggta tgtttattat tactagttag ctatgacaaa atcggctaaa aacttaaaaa 600  
 tatgacagac aagaaaggaa attcattcac ctctttaatc gtggcgatta ttcgctaacg 660  
 acgtgattaa atataataat gatgttcccc ggctggacta agaacgtaat aataaggctg 720  
 atgaacaaat ttatggttta tgcataaaaa aggaacatga atttggcata agcgcacata 780  
 attacggaac attgcaatag cggtcggagg taaagtaccg ggaatgcttt acaatgaatc 840  
 agctattggc ggatattgac caaccaacac taaaatttta tatcctgctc cgatttttgt 900  
 cttggccgtg aaatccatta tgcacatttt ttactaacgt ttatcaataa gttcggtttc 960  
 ccgtctaaat ttttttacgc agtttggtga acactaacgt tgacggtaac attaagatcg 1020  
 tttacgcttt gaccactatc aagggtgttg gtcgtcgta ctccaacttg gtctgtaaga 1080  
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 ttgttcaaat tatgcaaaac ccaactcact acaaaatccc agcttggttc ttgaaccgtc 1200  
 aaaatgacat cactgatggt aaggactacc acactttggc taacaacgct gaatccaaat 1260



tgagagatga cttggaaaga ttaaagaaaa tcagagctca tcgtggtatc agacacttct 1320  
 ggggtttgcg tgtagaggt caacacacca agaccactgg tagaagaaga gcttaa 1376

<210> 64

<211> 146

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 64

Met Ser Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg  
 1 5 10 15

Leu Leu Asn Thr Asn Val Asp Gly Asn Ile Lys Ile Val Tyr Ala Leu  
 20 25 30

Thr Thr Ile Lys Gly Val Gly Arg Arg Tyr Ser Asn Leu Val Cys Lys  
 35 40 45

Lys Ala Asp Val Asp Leu His Lys Arg Ala Gly Glu Leu Thr Gln Glu  
 50 55 60

Glu Leu Glu Arg Ile Val Gln Ile Met Gln Asn Pro Thr His Tyr Lys  
 65 70 75 80

Ile Pro Ala Trp Phe Leu Asn Arg Gln Asn Asp Ile Thr Asp Gly Lys  
 85 90 95

Asp Tyr His Thr Leu Ala Asn Asn Val Glu Ser Lys Leu Arg Asp Asp  
 100 105 110

Leu Glu Arg Leu Lys Lys Ile Arg Ala His Arg Gly Ile Arg His Phe  
 115 120 125

Trp Gly Leu Arg Val Arg Gly Gln His Thr Lys Thr Thr Gly Arg Arg  
 130 135 140

Arg Ala  
 145

<210> 65

<211> 1289

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 65

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aaaccagggc acatctgtcc cttgagagcc gctgatggcg gtgttttgca gagaagaggc 180
cacactgagg ccggtgtcga tttgtgtaaa ctaagtggac taagtcccgt cgctgttatt 240
ggcgaattgg ttaacgatga cgaacaagga actatgatga gattaaatga ctgccaaagcg 300
tttggttaaga aacatggcat tcctttgatc tccatcgaag aattggccca atatttgaag 360
aaataatctg gtgaacattt tctccattca ttctatcaca acagactcac acatatatac 420
atgtatatat ttgtaacttt gtatatatct tttgtttttt gacctttttc ttctctatg 480
tttttcagcc atacaaaaat atgggatttt tagcaagaga aaaagtacat ctaaaaaaag 540
tagtaatagg aggaagccaa gattggttga aacacagtta taaactcttc aaggcaatta 600
tgaacaggat ttctggatat gggaacaaaa agagccatga tcagctctta caagagtcga 660
atcagtccat gaatcaggcc caacaatcac tatcgaacag aatatcccag ttagatactc 720
aaatcgccca gttaaacttc cagctgcaaa atattcaaaa gaatttgcaa agatcaaaca 780
acaagcaacc ctcgttaaga aaacaggctt tgaagatttt aaataaacgt aaacagttag 840
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gcgagctcga cgacattagt gatgcagagc tggatgcaga gctggatgct ctggcacaag 1140
aggatttcac tttgccaaac agcgaaaact cattaggtta cgatatgcc agttacttac 1200
taggtgcgaa tgcgccaccg gctttttatt atgaagagcc aaacttagat actgaagaca 1260
aaaataaagc tttagaaagc gctcagtga 1289

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&lt;210&gt; 66

&lt;211&gt; 262

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 66

```

Met Gly Phe Leu Ala Arg Glu Lys Val His Leu Lys Lys Val Val Ile
  1                      5                      10                      15

```

```

Gly Gly Ser Gln Asp Trp Leu Lys His Ser Tyr Lys Leu Phe Lys Ala
      20                      25                      30

```

```

Ile Met Asn Arg Ile Phe Gly Tyr Gly Asn Lys Lys Ser His Asp Gln
      35                      40                      45

```

```

Leu Leu Gln Glu Ser Asn Gln Ser Met Asn Gln Ala Gln Gln Ser Leu
      50                      55                      60

```

```

Ser Asn Arg Ile Ser Gln Leu Asp Thr Gln Ile Ala Gln Leu Asn Phe
      65                      70                      75                      80

```

```

Gln Leu Gln Asn Ile Gln Lys Asn Leu Gln Arg Ser Asn Asn Lys Gln
      85                      90                      95

```

Pro Ser Leu Arg Lys Gln Ala Leu Lys Ile Leu Asn Lys Arg Lys Gln  
 100 105 110  
 Leu Glu Asn Met Lys Asp Ser Leu Asp Ser Gln Ser Trp Ser Met Thr  
 115 120 125  
 Gln Ala Gln Leu Thr Asn Asp Asn Leu Gln Asn Thr Met Ile Thr Ile  
 130 135 140  
 Asn Ala Leu Lys Gln Thr Asn Asn Ala Met Lys Ala Gln Tyr Gly Lys  
 145 150 155 160  
 Ile Asn Ile Asp Lys Leu Gln Asp Met Gln Asp Glu Met Leu Asp Leu  
 165 170 175  
 Ile Glu Gln Gly Asp Glu Leu Gln Glu Val Leu Ala Met Asn Asn Asn  
 180 185 190  
 Ser Gly Glu Leu Asp Asp Ile Ser Asp Ala Glu Leu Asp Ala Glu Leu  
 195 200 205  
 Asp Ala Leu Ala Gln Glu Asp Phe Thr Leu Pro Thr Ser Glu Asn Ser  
 210 215 220  
 Leu Gly Asn Asp Met Pro Ser Tyr Leu Leu Gly Ala Asn Ala Pro Pro  
 225 230 235 240  
 Ala Phe Ile Asp Glu Glu Pro Asn Leu Asp Thr Glu Asp Lys Asn Lys  
 245 250 255  
 Ala Leu Glu Ser Ala Gln  
 260

&lt;210&gt; 67

&lt;211&gt; 1295

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 67

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 cttaccaatt tgaagactat gtttttaaac acccaatcat tttccacca cacatatatt 180  
 accctttttt tgggtgaaga gaagtagtat tttgtttttc atgggagtg aagtcctttc 240  
 aaaactaatc cgagcagtag tgctgtctag gcggagatta ttgaaagtcg gcattggctg 300  
 cagctagcgt tttgtttttg gtactacctg tcaaaaccgg cgtctgccta gattgcgcg 360  
 agggtagcgt gaaacttttg cctttccacg tcagtttata atatcaaaag cagcaatata 420

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cacatttaaat ggtttgccct tagtgactat tagggcggtt tggtgaaaag aaagagtcgc 480
tcaaagaaat caatataacc atggctaaat ttttgaaagc aggtaaagtt ggtacgtaaa 540
tttaacagag caaacgctct aattaagata tcgaataaaa ggggactttc aggtgcataa 600
gatgggaaat tgtacaatct gagggacaaa caatatggaa agcagtacat gattgtattg 660
tcattgtagg aggtaccaat tgtgccagta aaaaagagag ggcccgggga gcaccacatt 720
cacgaccaat cgtgtcgatc tgcaaaaaag gcacatggaa aatgtaattt atcagtgttc 780
aacactgagt tgaacagata gctatctaata caatgttaac tttccaggga acaaaaagct 840
aaatccactt ctcttttatt tcaaaatata attagaaata gaaaaattta ctaacaaatt 900
ttcgtattat cgtagctgtc gttgttcgtg gtcgttacgc tggtaagaag gttgtgatcg 960
ttaagccaca cgatgagggt tctaaatctc atccattcgg tcacgctttg gttgccggta 1020
ttgaaaggta cccatcaaag gtcaccaaga agcacgggtc caagaaggtc gctaagagaa 1080
ctaaaatcaa gccattcatc aaagtcgtca actacaacca cttattgcca accagataca 1140
ccttggaatg tgaagctttc aagagcgttg tatctacaga gacttttgaa caaccatccc 1200
aacgtgaaga agccaagaag gttgtaaaga aggcatttga agaaagacat caagctggta 1260
aaaaccaatg gttcttctcc aagttgagat tctaa 1295

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<210> 68

<211> 136

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 68

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Met Ala Lys Phe Leu Lys Ala Gly Lys Val Ala Val Val Val Arg Gly
  1              5              10              15

Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly
          20              25              30

Ser Lys Ser His Pro Phe Gly His Ala Leu Val Ala Gly Ile Glu Arg
      35              40              45

Tyr Pro Ser Lys Val Thr Lys Lys His Gly Ala Lys Lys Val Ala Lys
      50              55              60

Arg Thr Lys Ile Lys Pro Phe Ile Lys Val Val Asn Tyr Asn His Leu
      65              70              75              80

Leu Pro Thr Arg Tyr Thr Leu Asp Val Glu Ala Phe Lys Ser Val Val
          85              90              95

Ser Thr Glu Thr Phe Glu Gln Pro Ser Gln Arg Glu Glu Ala Lys Lys
      100             105             110

Val Val Lys Lys Ala Phe Glu Glu Arg His Gln Ala Gly Lys Asn Gln
      115             120             125

Trp Phe Phe Ser Lys Leu Arg Phe

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130

135

&lt;210&gt; 69

&lt;211&gt; 2744

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 69

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&lt;210&gt; 70

&lt;211&gt; 747

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 70

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Ile Leu Leu Glu Leu Gly Thr Arg Pro Pro Arg Phe Thr Gln Ile Pro
      20              25              30

Pro Ser Ser Ala Ala Leu Gln Thr Gln Ile Pro Thr Thr Leu Glu Val
      35              40              45

Thr Thr Thr Thr Leu Asn Asn Lys Gln Ser Lys Asn Asp Asn Gln Leu
      50              55              60

Val Asn Gln Leu Asn Lys Ala Gln Gly Glu Ala Ser Met Leu Arg Asp
      65              70              75              80

Lys Ile Asn Phe Leu Asn Ile Glu Arg Glu Lys Glu Lys Asn Ile Gln
      85              90              95

Ala Val Lys Val Asn Glu Leu Gln Val Lys His Leu Gln Glu Leu Ala
      100              105              110

Lys Leu Lys Gln Glu Leu Gln Lys Leu Glu Asp Glu Lys Lys Phe Leu
      115              120              125

Gln Met Glu Ala Arg Gly Lys Ser Lys Arg Glu Val Ile Thr Asn Val
      130              135              140

Lys Pro Pro Ser Thr Thr Leu Ser Thr Asn Thr Asn Thr Ile Thr Pro
      145              150              155              160

Asp Ser Ser Ser Val Ala Ile Glu Ala Lys Pro Gln Ser Pro Gln Ser
      165              170              175

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Lys Lys Arg Lys Ile Ser Asp Asn Leu Leu Lys Lys Asn Met Val Pro
      180                      185                      190

Leu Asn Pro Asn Arg Ile Ile Pro Asp Glu Thr Ser Leu Phe Leu Glu
      195                      200                      205

Ser Ile Leu Leu His Gln Ile Ile Gly Ala Asp Leu Ser Thr Ile Glu
      210                      215                      220

Ile Leu Asn Arg Leu Lys Leu Asp Tyr Ile Thr Glu Phe Lys Phe Lys
      225                      230                      235                      240

Asn Phe Val Ile Ala Lys Gly Ala Pro Ile Gly Lys Ser Ile Val Ser
      245                      250                      255

Leu Leu Leu Arg Cys Lys Lys Thr Leu Thr Leu Asp Arg Phe Ile Asp
      260                      265                      270

Thr Leu Leu Glu Asp Ile Ala Val Leu Ile Lys Glu Ile Ser Val His
      275                      280                      285

Pro Asn Glu Ser Lys Leu Ala Val Pro Phe Leu Val Ala Leu Met Tyr
      290                      295                      300

Gln Ile Val Gln Phe Arg Pro Ser Ala Thr His Asn Leu Ala Leu Lys
      305                      310                      315                      320

Asp Cys Phe Leu Phe Ile Cys Asp Leu Ile Arg Ile Tyr His His Val
      325                      330                      335

Leu Lys Val Pro Ile His Glu Ser Asn Met Asn Leu His Val Glu Pro
      340                      345                      350

Gln Ile Phe Gln Tyr Glu Leu Ile Asp Tyr Leu Ile Ile Ser Tyr Ser
      355                      360                      365

Phe Asp Leu Leu Glu Gly Ile Leu Arg Val Leu Gln Ser His Pro Lys
      370                      375                      380

Gln Thr Tyr Met Glu Phe Phe Asp Glu Asn Ile Leu Lys Ser Phe Glu
      385                      390                      395                      400

Phe Val Tyr Lys Leu Ala Leu Thr Ile Ser Tyr Lys Pro Met Val Asn
      405                      410                      415

Val Ile Phe Ser Ala Val Glu Val Val Asn Ile Ile Thr Ser Ile Ile
      420                      425                      430

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Leu Asn Met Asp Asn Ser Ser Asp Leu Lys Ser Leu Ile Ser Gly Ser  
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Trp Trp Arg Asp Cys Ile Thr Arg Leu Tyr Ala Leu Leu Glu Lys Glu  
 450 455 460

Ile Lys Ser Gly Asp Val Tyr Asn Glu Asn Val Asp Thr Thr Thr Leu  
 465 470 475 480

His Met Ser Lys Tyr His Asp Phe Phe Gly Leu Ile Arg Asn Ile Gly  
 485 490 495

Asp Asn Glu Leu Gly Gly Leu Ile Ser Lys Leu Ile Tyr Thr Asp Arg  
 500 505 510

Leu Gln Ser Val Pro Arg Val Ile Ser Lys Glu Asp Ile Gly Met Asp  
 515 520 525

Ser Asp Lys Phe Thr Ala Pro Ile Ile Gly Tyr Lys Met Glu Lys Trp  
 530 535 540

Leu Leu Lys Leu Lys Asp Glu Val Leu Asn Ile Phe Glu Asn Leu Leu  
 545 550 555 560

Met Ile Tyr Gly Asp Asp Ala Thr Ile Val Asn Gly Glu Met Leu Ile  
 565 570 575

His Ser Ser Lys Phe Leu Ser Arg Glu Gln Ala Leu Met Ile Glu Arg  
 580 585 590

Tyr Val Gly Gln Asp Ser Pro Asn Leu Asp Leu Arg Cys His Leu Ile  
 595 600 605

Glu His Thr Leu Thr Ile Ile Tyr Arg Leu Trp Lys Asp His Phe Lys  
 610 615 620

Gln Leu Arg Glu Glu Gln Ile Lys Gln Val Glu Ser Gln Leu Ile Met  
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Ser Leu Trp Arg Phe Leu Val Cys Gln Thr Glu Thr Val Thr Ala Asn  
 645 650 655

Glu Arg Glu Met Arg Asp His Arg His Leu Val Asp Ser Leu His Asp  
 660 665 670

Leu Thr Ile Lys Asp Gln Ala Ser Tyr Tyr Glu Asp Ala Phe Glu Asp  
 675 680 685



Leu Pro Glu Tyr Ile Glu Glu Glu Leu Lys Met Gln Leu Asn Lys Arg  
 690 695 700  
 Thr Gly Arg Ile Met Gln Val Lys Tyr Asp Glu Lys Phe Gln Glu Met  
 705 710 715 720  
 Ala Arg Thr Ile Leu Glu Ser Lys Ser Phe Asp Leu Thr Thr Leu Glu  
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 Glu Ala Asp Ser Leu Tyr Ile Ser Met Gly Leu  
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&lt;210&gt; 71

&lt;211&gt; 3929

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 71

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<210> 72

<211> 1142

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 72

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Val Gln Leu Ala Arg Asn Gly Ser Thr Gly Gln Glu Ala Ala Val Lys	35	40	45
Val Ile Ser Lys Ala Val Phe Asn Thr Gly Asn Val Ser Gly Thr Ser	50	55	60
Ile Val Gly Ser Thr Thr Pro Asp Ala Leu Pro Tyr Gly Ile Glu Arg	65	70	75 80
Glu Ile Ile Ile Met Lys Leu Leu Asn His Pro Asn Val Leu Arg Leu	85	90	95
Tyr Asp Val Trp Glu Thr Asn Thr Asp Leu Tyr Leu Val Leu Glu Tyr	100	105	110
Ala Glu Lys Gly Glu Leu Phe Asn Leu Leu Val Glu Arg Gly Pro Leu	115	120	125
Pro Glu His Glu Ala Ile Arg Phe Phe Arg Gln Ile Ile Ile Gly Val	130	135	140
Ser Tyr Cys His Ala Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu	145	150	155 160
Asn Leu Leu Leu Asp His Lys Tyr Asn Ile Lys Ile Ala Asp Phe Gly	165	170	175
Met Ala Ala Leu Glu Thr Glu Gly Lys Leu Leu Glu Thr Ser Cys Gly	180	185	190
Ser Pro His Tyr Ala Ala Pro Glu Ile Val Ser Gly Ile Pro Tyr Gln	195	200	205
Gly Phe Ala Ser Asp Val Trp Ser Cys Gly Val Ile Leu Phe Ala Leu	210	215	220
Leu Thr Gly Arg Leu Pro Phe Asp Glu Glu Asp Gly Asn Ile Arg Thr	225	230	235 240
Leu Leu Leu Lys Val Gln Lys Gly Glu Phe Glu Met Pro Ser Asp Asp	245	250	255
Glu Ile Ser Arg Glu Ala Gln Asp Leu Ile Arg Lys Ile Leu Thr Val			

260

265

270

Asp Pro Glu Arg Arg Ile Lys Thr Arg Asp Ile Leu Lys His Pro Leu  
 275 280 285

Leu Gln Lys Tyr Pro Ser Ile Arg Asp Ser Lys Ser Ile Arg Gly Leu  
 290 295 300

Pro Arg Glu Asp Thr Tyr Leu Thr Pro Leu Ser Glu Ser Asn Ser Ser  
 305 310 315 320

Ile Asp Ala Thr Ile Leu Gln Asn Leu Val Ile Leu Trp His Gly Arg  
 325 330 335

Asp Pro Glu Gly Ile Lys Glu Lys Leu Arg Glu Pro Gly Ala Asn Ala  
 340 345 350

Glu Lys Thr Leu Tyr Ala Leu Leu Tyr Arg Phe Lys Cys Asp Thr Gln  
 355 360 365

Lys Glu Leu Ile Lys Gln Gln Gln Val Lys Lys Arg Gln Ser Ile Ser  
 370 375 380

Ser Val Ser Val Ser Pro Ser Lys Lys Val Ser Thr Thr Pro Gln Arg  
 385 390 395 400

Arg Arg Asn Arg Glu Ser Leu Ile Ser Val Thr Ser Ser Arg Lys Lys  
 405 410 415

Pro Ile Ser Phe Asn Lys Phe Thr Ala Ser Ser Ala Ser Ser Ser Asn  
 420 425 430

Leu Thr Thr Pro Gly Ser Ser Lys Arg Leu Ser Lys Asn Phe Ser Ser  
 435 440 445

Lys Lys Lys Leu Ser Thr Ile Val Asn Gln Ser Ser Pro Thr Pro Ala  
 450 455 460

Ser Arg Asn Lys Arg Ala Ser Val Ile Asn Val Glu Lys Asn Gln Lys  
 465 470 475 480

Arg Ala Ser Ile Phe Ser Thr Thr Lys Lys Asn Lys Arg Ser Ser Arg  
 485 490 495

Ser Ile Lys Arg Met Ser Leu Ile Pro Ser Met Lys Arg Glu Ser Val  
 500 505 510

Thr Thr Lys Leu Met Ser Thr Tyr Ala Lys Leu Ala Glu Asp Asp Asp

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Thr Leu Ile Asp Glu Ile Phe Glu Tyr Glu Lys Tyr Glu Gln Ile Arg		
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Lys Glu Lys Glu Glu Leu Glu Arg Lys Val Arg Glu Ala Lys Ala Arg		
565	570	575
Glu Glu Leu Glu Arg Arg Arg Arg Lys Gln Glu Glu Lys Glu Arg Ala		
580	585	590
Arg Lys Leu Leu Glu Lys Glu Asp Leu Lys Arg Lys Gln Glu Glu Leu		
595	600	605
Lys Lys Gln Ile Glu Ile Asp Ile Ser Asp Leu Glu Gln Glu Leu Ser		
610	615	620
Lys His Lys Glu Glu Lys Leu Asp Gly Asn Ile Arg Ser Ile Ser Ala		
625	630	635
Pro Met Glu Asn Glu Glu Lys Asn Ile Asn His Leu Glu Val Asp Ile		
645	650	655
Asp Asn Ile Leu Arg Arg Arg Asn Phe Ser Leu Gln Thr Arg Pro Val		
660	665	670
Ser Arg Leu Asp Pro Gly Ile Met Phe Ser Ser Pro Thr Glu Glu Val		
675	680	685
Ser Pro Val Glu Pro Lys Arg Thr Glu Asn Glu Arg Leu Thr Thr Glu		
690	695	700
Lys Lys Ile Leu Glu Thr Ile Arg Arg Ser Lys Phe Leu Gly Ser Ser		
705	710	715
Phe Asn Ile Asp Lys Glu Leu Lys Leu Ser Lys Met Glu Tyr Pro Ser		
725	730	735
Ile Ile Ala Pro Gln Arg Leu Ser Glu Glu Arg Val Val Ser Asp Ser		
740	745	750
Asn Asp Gly Tyr Glu Ser Leu Ile Leu Pro Lys Asp Gly Asn Gly Val		
755	760	765
Ser Gln Leu Lys Asp Ser Thr Ala Thr Thr Ala Pro Val Ser Asp Gly		

770	775	780
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Ser Arg His Phe Ser Glu Ser Asn Lys Arg Leu Ser Val Leu Ser Met 805	810	815
Tyr Ser Thr Lys Glu Ser Phe Thr Asn Leu Val Asp Ile Leu Lys Asn 820	825	830
Gly Asn Leu Asp Val Asn Asn Gln Gln Ser Gln Arg Ile Pro Thr Pro 835	840	845
Arg Ser Ala Asp Asp Ser Glu Phe Leu Phe Glu Thr Val Asn Glu Glu 850	855	860
Ala Glu Tyr Thr Gly Asn Ser Ser Asn Asp Glu Arg Leu Tyr Asp Val 865	870	875 880
Gly Asp Ser Thr Ile Lys Asp Lys Ser Ala Leu Lys Leu Asn Phe Ala 885	890	895
Asp Arg Phe Asn Gly Ser Asn Glu Ala Lys Gln Thr Asp Asn Leu His 900	905	910
Leu Pro Ile Leu Pro Pro Leu Asn Gly Asp Asn Glu Leu Arg Lys Gln 915	920	925
Asn Ser Gln Glu Gly Asp Gln Ala His Pro Lys Ile Lys Ser Met Ile 930	935	940
Pro Glu Ser Gly Ser Ser Ser His Thr Glu Lys Glu Glu Glu Asn Glu 945	950	955 960
Glu Lys Glu Glu Lys Lys Pro Glu Gln His Lys Gln Glu Glu Asp Gln 965	970	975
Glu Lys Arg Glu Lys Val Val Asp Asp Met Glu Pro Pro Leu Asn Lys 980	985	990
Ser Val Gln Lys Ile Arg Glu Lys Asn Ala Gly Ser Gln Ala Lys Asp 995	1000	1005
His Ser Lys Asp His Leu Lys Glu His Lys Gln Asp Lys Asn Thr Ala 1010	1015	1020
Ile Gly Asn Gly Ser Phe Phe Arg Lys Phe Ser Lys Ser Ser Asp Lys		

1025                      1030                      1035                      1040  
 Thr Met Glu Leu Tyr Ala Lys Ile Ser Ala Lys Gln Leu Phe Asn Gly  
                          1045                      1050                      1055  
 Leu Glu Lys Leu Leu Arg Gly Trp Thr Gln Tyr Gly Leu Lys Asn Ile  
                          1060                      1065                      1070  
 Lys Ser His Pro Asn Asn Leu Thr Leu Thr Gly Lys Leu Ser Ser Asp  
                          1075                      1080                      1085  
 Asn Ile Phe Ser Leu Arg Ser Thr Leu Phe Glu Val Asn Ile Tyr Pro  
                          1090                      1095                      1100  
 Arg Gly Lys Met Ser Val Val Gln Phe Lys Lys Val Ser Gly Ser Phe  
 1105                      1110                      1115                      1120  
 Lys Ala Val Lys Lys Leu Val Asn Glu Val Glu Asn Val Leu Asn Lys  
                          1125                      1130                      1135  
 Glu Gly Val Leu Gln Lys  
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&lt;210&gt; 73

&lt;211&gt; 1844

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 73

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&lt;210&gt; 74

&lt;211&gt; 447

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 74

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Met Ser Ser Gln Asn Leu Asn Asp Asn Pro Lys Asn Thr Ser Ser Ala
  1              5              10              15

```

```

Ala Glu Asp Lys Lys Lys Gln Thr Ser Ser Leu Lys Leu Ala Pro Ile
      20              25              30

```

```

Pro Thr Thr Ser Pro Trp Lys Ser Ser Ser Pro Asp Ser Asn Thr Val
      35              40              45

```

```

Ile Pro Val Glu Glu Leu Arg Asp Ile Ser Lys Thr Ala Lys Pro Ser
      50              55              60

```

```

Lys Asn Gly Ser Gly Ser Ile Lys Leu Thr Ser Asn Thr Lys Trp Thr
      65              70              75              80

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```

Pro Ile Thr Pro Ser Val Ile Ile Ser Gly Ser Lys Asp Thr Asn Ser
      85              90              95

```

```

Lys Ser Gly Lys Asn Ser Lys Asn Ser Lys Thr Asn Lys Lys Met Lys
      100              105              110

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```

Lys Arg Gly Lys Tyr Asn Asn Asp Ile Asn Lys Lys Asp Phe Asn Gly
      115              120              125

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Gln Thr Asn Ser Thr Ser Glu Ile Ser Asn Val Ser Asn Leu Glu Ser
      130              135              140

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Lys Pro Leu Asp Ala Asn Ala Lys Val Asn Ile His Ser Ser Ser Gly  
 145 150 155 160  
 Ala Thr Ala Asn Gly Asn Ile Lys Arg Ile Thr Asn Asn Asn Ser  
 165 170 175  
 Thr Asn Gly Arg Gln Ser Arg Asn Tyr Gln Asn Arg Asn Gly Lys Thr  
 180 185 190  
 Arg Tyr Asn Asn Asn Ser Arg His Ser Gln Ala Ala Asn Asn Ala Ile  
 195 200 205  
 Ser Phe Pro Asn Asn Tyr Gln Ala Arg Pro Glu Tyr Ile Pro Asn Ala  
 210 215 220  
 Ser His Trp Leu Asn Asn Asn Ser Arg Asn Ser Tyr Lys Gln Leu Ser  
 225 230 235 240  
 Tyr Phe Arg Gln Gln Gln Tyr Tyr Asn Asn Ile Asn Tyr Gln Gln Gln  
 245 250 255  
 Leu Gln Thr Pro Tyr Tyr Tyr Ser Met Glu Pro Ile Phe Lys Ser Ile  
 260 265 270  
 Glu Ser Ile Lys Asn Gln Ile Glu Phe Tyr Phe Ser Glu Glu Asn Leu  
 275 280 285  
 Lys Thr Asp Glu Phe Leu Arg Ser Lys Phe Lys Lys Ala Asn Asp Gly  
 290 295 300  
 Phe Ile Pro Met Ser Leu Ile Gly Lys Phe Tyr Arg Met Val Asn Leu  
 305 310 315 320  
 Ser Leu Gly Gly Asp Pro Asn Leu Ile Leu Ala Ser Met Arg Glu Val  
 325 330 335  
 Leu Gln His Lys Glu Thr Asn His Leu Glu Ile Ala Leu Gly Ser Ile  
 340 345 350  
 Glu Gly Ala Gln Lys Asn Met Ala Asp Asp Phe Asn Pro Leu Glu Asn  
 355 360 365  
 Tyr Phe Ile Arg Arg Glu Asn Trp Ala Glu Tyr Ala Met Glu Ser Asn  
 370 375 380  
 Phe Asp Glu Asn Asp Asp Glu Thr Glu Lys Tyr Asn Ile Glu Lys Leu  
 385 390 395 400

Leu Gly Pro Asn Asp Leu Asp Asn Tyr Ser Tyr Met Gly Tyr Pro Asn  
 405 410 415

Phe Phe Pro Ser Asn Glu Asn Gly Lys Lys Ser Gln Ser Tyr Asp Gln  
 420 425 430

Gly Glu Ile Ser Arg Gln Phe Glu Gln Asn Leu Gln Ile Asn Asp  
 435 440 445

<210> 75  
 <211> 2054  
 <212> DNA  
 <213> *Saccharomyces cerevisiae* .

<400> 75

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<210> 76

<211> 517

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 76

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Phe Ala Ser Phe Thr Leu Ala Glu Asn Ser Ala Arg Ala Thr Pro Gly

20 25 30

Ser Asp Leu Leu Val Leu Thr Glu Lys Lys Phe Lys Ser Phe Ile Glu

35 40 45

Ser His Pro Leu Val Leu Val Glu Phe Phe Ala Pro Trp Cys Leu His

50 55 60

Ser Gln Ile Leu Arg Pro His Leu Glu Glu Ala Ala Ser Ile Leu Lys

65 70 75 80

Glu His Asn Val Pro Val Val Gln Ile Asp Cys Glu Ala Asn Ser Met

85 90 95

Val Cys Leu Gln Gln Thr Ile Asn Thr Tyr Pro Thr Leu Lys Ile Phe

100 105 110

Lys Asn Gly Arg Ile Phe Asp Gly Gln Val Tyr Arg Gly Val Lys Ile

115 120 125

Thr Asp Glu Ile Thr Gln Tyr Met Ile Gln Leu Tyr Glu Ala Ser Val

130 135 140

Ile Tyr Leu Asn Ser Glu Asp Glu Ile Gln Pro Tyr Leu Glu Asn Ala

145 150 155 160

Thr Leu Pro Val Val Ile Asn Arg Gly Leu Thr Gly Leu Asn Glu Thr

165 170 175

Tyr Gln Glu Val Ala Leu Asp Leu Ala Glu Asp Tyr Val Phe Leu Ser

180 185 190

Leu Leu Asp Ser Glu Asp Lys Ser L u Ser Ile His Leu Pro Asn Thr  
 195 200 205  
 Thr Glu Pro Ile Leu Phe Asp Gly Asn Val Asp Ser Leu Val Gly Asn  
 210 215 220  
 Ser Val Ala Leu Thr Gln Trp Leu Lys Val Val Ile Leu Pro Tyr Phe  
 225 230 235 240  
 Thr Asp Ile Glu Pro Asp Leu Phe Pro Lys Tyr Ile Ser Ser Asn Leu  
 245 250 255  
 Pro Leu Ala Tyr Phe Phe Tyr Thr Ser Glu Glu Glu Leu Glu Asp Tyr  
 260 265 270  
 Thr Asp Leu Phe Thr Gln Leu Gly Lys Glu Asn Arg Gly Gln Ile Asn  
 275 280 285  
 Phe Ile Ala Leu Asn Ser Thr Met Phe Pro His His Val Arg Phe Leu  
 290 295 300  
 Asn Met Arg Glu Gln Phe Pro Leu Phe Ala Ile His Asn Met Ile Asn  
 305 310 315 320  
 Asn Leu Lys Tyr Gly Leu Pro Gln Leu Pro Glu Glu Glu Tyr Ala Lys  
 325 330 335  
 Leu Glu Lys Pro Gln Pro Leu Asp Arg Asp Met Ile Val Gln Leu Val  
 340 345 350  
 Lys Asp Tyr Arg Glu Gly Thr Ala Lys Pro Ile Val Lys Ser Glu Glu  
 355 360 365  
 Ile Pro Lys Glu Gln Lys Ser Asn Val Tyr Lys Ile Val Gly Lys Thr  
 370 375 380  
 His Asp Asp Ile Val His Asp Asp Asp Lys Asp Val Leu Val Lys Tyr  
 385 390 395 400  
 Tyr Ala Thr Trp Cys Ile His Ser Lys Arg Phe Ala Pro Ile Tyr Glu  
 405 410 415  
 Glu Ile Ala Asn Val Leu Ala Ser Asp Glu Ser Val Arg Asp Lys Ile  
 420 425 430  
 Leu Ile Ala Glu Val Asp Ser Gly Ala Asn Asp Ile Leu Ser Phe Pro  
 435 440 445

Val Thr Gly Tyr Pro Thr Ile Ala Leu Tyr Pro Ala Gly Asn Asn Ser  
450 455 460

Lys Pro Ile Il Phe Asn Lys Ile Arg Asn Leu Glu Asp Val Phe Glu  
465 470 475 480

Phe Ile Lys Glu Ser Gly Thr His His Ile Asp Gly Gln Ala Ile Tyr  
485 490 495

Asp Lys Leu His Gln Ala Lys Asp Ser Glu Val Ser Thr Glu Asp Thr  
500 505 510

Val His Asp Glu Leu  
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<210> 77

<211> 908

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 77

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caccag gcca aggatt ctga agtgc tact gaagata ccg tacat gatga attata atca 240
ataaataa ag catat ataat gcacat tttt aacat ctgat tactc gcatc gtttc tggaa 300
gaaaatag ct aatatt cgtt atttat ggca tcacg attat tctc accagt taccg ttta 360
tgctc ttgaa gagatt tagc attact gcca gcgc atctt aaata cacagg ttat atgaga 420
cccatt acta taacc ctaag aagag aaaaa ggagt gctt cgttt tcaat cacatt cttag 480
tttac agtaa ttgagt ctg atgat gtta atatt tacct tttc gtcact ttttt tcca 540
ccattc ttgc aggtt cctg tcagatt tgg aaatc ggtat tatca agaga atacc ggtag 600
aagatt gctt aatta aggca atgcc aggtg ataa agtta gggtc attat acagg atctt 660
tattaga atc gggaact gta ttgact caa gttatt caag aggc tctcct atcg cttttg 720
aactt ggcgt tggcag agta attaa aggtt gggat caagg tgttg ccggc atgtg cgttg 780
gcgaaaaa ag aaagct gcaa attcca agtt ctttg gccta cggaga aaga ggtgt cccag 840
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<210> 78

<211> 135

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 78

Met Met Phe Asn Ile Tyr Leu Phe Val Thr Phe Phe Ser Thr Ile Leu  
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Ala Gly Ser Leu Ser Asp Leu Glu Ile Gly Ile Ile Lys Arg Ile Pro  
 20 25 30

Val Glu Asp Cys Leu Ile Lys Ala Met Pro Gly Asp Lys Val Lys Val  
 35 40 45

His Tyr Thr Gly Ser Leu Leu Glu Ser Gly Thr Val Phe Asp Ser Ser  
 50 55 60

Tyr Ser Arg Gly Ser Pro Ile Ala Phe Glu Leu Gly Val Gly Arg Val  
 65 70 75 80

Ile Lys Gly Trp Asp Gln Gly Val Ala Gly Met Cys Val Gly Glu Lys  
 85 90 95

Arg Lys Leu Gln Ile Pro Ser Ser Leu Ala Tyr Gly Glu Arg Gly Val  
 100 105 110

Pro Gly Val Ile Pro Pro Ser Ala Asp Leu Val Phe Asp Val Glu Leu  
 115 120 125

Val Asp Val Lys Ser Ala Ala  
 130 135

&lt;210&gt; 79

&lt;211&gt; 1103

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 79

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 gtcaatccgg tagatgtgat gggtacatct tggaagggtga agaattagct ttctacctaa 1080  
 gaagattgac tgctaagaaa tag 1103

&lt;210&gt; 80

&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 80

Met Gly Ile Ser Arg Asp Ser Arg His Lys Arg Ser Ala Thr Gly Ala  
 1 5 10 15

Lys Arg Ala Gln Phe Arg Lys Lys Arg Lys Phe Glu Leu Gly Arg Gln  
 20 25 30

Pro Ala Asn Thr Lys Ile Gly Ala Lys Arg Ile His Ser Val Arg Thr  
 35 40 45

Arg Gly Gly Asn Lys Lys Tyr Arg Ala Leu Arg Ile Glu Thr Gly Asn  
 50 55 60

Phe Ser Trp Ala Ser Glu Gly Ile Ser Lys Lys Thr Arg Ile Ala Gly  
 65 70 75 80

Val Val Tyr His Pro Ser Asn Asn Glu Leu Val Arg Thr Asn Thr Leu  
 85 90 95

Thr Lys Ala Ala Ile Val Gln Ile Asp Ala Thr Pro Phe Arg Gln Trp  
 100 105 110

Phe Glu Ala His Tyr Gly Gln Thr Leu Gly Lys Lys Lys Asn Val Lys  
 115 120 125

Glu Glu Glu Thr Val Ala Lys Ser Lys Asn Ala Glu Arg Lys Trp Ala  
 130 135 140

Ala Arg Ala Ala Ser Ala Lys Ile Glu Ser Ser Val Glu Ser Gln Phe  
 145 150 155 160

Ser Ala Gly Arg Leu Tyr Ala Cys Ile Ser Ser Arg Pro Gly Gln Ser  
 165 170 175

Gly Arg Cys Asp Gly Tyr Ile Leu Glu Gly Glu Glu Leu Ala Phe Tyr

180

185

190

Leu Arg Arg Leu Thr Ala Lys Lys  
 195 200

<210> 81  
 <211> 1265  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 81  
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 ggatttccga gacatcggtg gcatttgggc ccgtcgaatt aaatcttttg gcctgaaaag 180  
 agatccatga cggatggggc cggggcaata ctatggttcg agcgggtggcc agtctggaag 240  
 aggcagcaaa ccttgacgtg acgagtcgag aggtgagttt gaacatcgtc ggggaggtta 300  
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 tttcatggct cggattactt ccgtactgct ggctaaaatc gaaatctcgg cctgctgaga 420  
 gtgttttgag caatcaaggg aacatctgaa cgtggaagag cagacgaggc attagctcga 480  
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<210> 82  
 <211> 254  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 82  
 Met Leu Thr Ile Thr Lys Arg Leu Val Thr Thr Asp Val Arg Ser Arg  
 1 5 10 15  
 Ile Leu Leu Ser Ser Leu Asn Gly Lys Met Ser Asp Ala Leu Ala Leu  
 20 25 30



Leu Arg Gln Gln Gln Gln Thr Ser Val Asp Val Glu Leu Leu His Thr  
 35 40 45

Met Leu Ala Arg Ala Ala Ala Leu Ala His Ala Asp Thr Ile Ala Tyr  
 50 55 60

Met Trp Tyr Gln His Val Met Pro Arg Arg Leu Pro Val Glu Gly Arg  
 65 70 75 80

Leu Leu Cys Glu Met Ala Gly Val Ala Leu Tyr Gln Asp Arg Leu Phe  
 85 90 95

Leu Pro Ala Gln Phe Leu Gln His Tyr Gln Ala Met Asn Arg Asp Arg  
 100 105 110

Arg Thr Ser Pro Glu Asp Glu Leu Ile Glu Tyr Glu Leu Arg Arg Ile  
 115 120 125

Lys Val Glu Ala Phe Ala Arg Gly Thr Met His Ser Thr Ala Leu Arg  
 130 135 140

Glu Lys Trp Lys Val Phe Leu Gln Glu Met Asp Thr Leu Pro Gly Gln  
 145 150 155 160

Pro Pro Leu Arg Leu Arg Asp Phe Pro Gln Met Thr Lys Ala Met Gly  
 165 170 175

Ile Ala Leu Met Gln Gln Asp Glu Gln Ala Ala Ala Leu Ala Leu Phe  
 180 185 190

Gly Arg Gln Pro Leu Val Ile Lys Asn Glu Trp Ser Leu Pro Leu Leu  
 195 200 205

Leu Ala Gly Val Leu Trp His Val Pro Gly Pro Ala Gln Ala Arg Arg  
 210 215 220

Val Leu Ala Glu Phe Arg Gln Ser Tyr Arg Gly Leu Pro Leu Leu Asp  
 225 230 235 240

Ala Glu Leu Val Ile Lys Arg Arg Gly Phe Glu Ile Asn Thr  
 245 250

<210> 83

<211> 830

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 83

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ctgacaaggc cgacaaggtc gctggtaagg ttcaaccaga agacaacaag ggtgtcttcc 660
aaggtgtcca cgactctgcc gaaaaaggca aggataacgc tgaaggtaa ggtgaatctt 720
tggcagacca agctagagat tacatgggag ccgccaagtc caagttgaac gatgccgtcg 780
aatatgtttc cggtcgtgtc cacggtgaag aagaccaac caagaagtaa 830

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<210> 84

<211> 109

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 84

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Met Ser Asp Ala Gly Arg Lys Gly Phe Gly Glu Lys Ala Ser Glu Ala
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Leu Lys Pro Asp Ser Gln Lys Ser Tyr Ala Glu Gln Gly Lys Glu Tyr
      20              25              30

Ile Thr Asp Lys Ala Asp Lys Val Ala Gly Lys Val Gln Pro Glu Asp
      35              40              45

Asn Lys Gly Val Phe Gln Gly Val His Asp Ser Ala Glu Lys Gly Lys
      50              55              60

Asp Asn Ala Glu Gly Gln Gly Glu Ser Leu Ala Asp Gln Ala Arg Asp
      65              70              75              80

Tyr Met Gly Ala Ala Lys Ser Lys Leu Asn Asp Ala Val Glu Tyr Val
      85              90              95

Ser Gly Arg Val His Gly Glu Glu Asp Pro Thr Lys Lys
      100              105

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<210> 85  
 <211> 995  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 85  
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 taccttggtc agcgtatgac ttttgagagt ctggcttcaa agcttcagaa gctttttcac 180  
 cgaatccttt tctacctgcy tcagacattg ttgtatttag ttttttttgt tttgagttgt 240  
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 ataagatcaa acgcaattga ggaagtagaa cgcaattcac cgtcctattt atacgtttta 360  
 atatagattt agagaaagac ctttcagatc aagaggggga cgaccggaac ctcaaagttg 420  
 accaaacgat tttccagggg ctgtagatct agttactctc cgtctagagt gcttctggtc 480  
 tgtgtttgtg ggttgattta atgcttgctg atacctttcc ttctttcaat ttctacgtca 540  
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 atgttatttt gtgccgcccc ctgcaagttg caacatatcc ccttaacaga tgccagcaat 660  
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 cttggatttg cgcgtccctt ttttttcttc attctctgac tccccctacc ttctccctact 900  
 tttctgtgta tcaagaggaa aagaaggaga aaaggagaac tccgaaaaat accgaacaag 960  
 agggtaacag aatgtgcatt tggatgagcg ggtaa 995

<210> 86  
 <211> 164  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 86  
 Met Leu Ala Tyr Thr Phe Pro Ser Phe Asn Phe Tyr Val Asn Gly Phe  
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 20 25 30  
 Phe Tyr Val Ile Leu Cys Arg Pro Leu Gln Val Ala Thr Tyr Pro Leu  
 35 40 45  
 Asn Arg Cys Gln Gln Tyr Ser Ser Leu Ala Ile Phe Thr Ala Ser Gly  
 50 55 60  
 Phe Trp Leu Leu Val Leu Val Pro Arg Ala Lys Gly Pro Ser Thr Arg  
 65 70 75 80  
 Arg His Cys Tyr Arg Gln Leu Ala Pro Thr His His Arg Pro Phe Phe  
 85 90 95

Ser Ile Phe Gly Trp Ala Val Ser Gly Ile Arg Pro Leu Pro Glu Ile  
 100 105 110

Phe Thr Trp Ile Cys Ala Ser Pro Phe Phe Leu His Ser Leu Thr Pro  
 115 120 125

Pro Thr Phe Ser His Phe Ser Val Tyr Gln Glu Glu Lys Lys Glu Lys  
 130 135 140

Arg Arg Thr Pro Lys Asn Thr Glu Gln Glu Gly Asn Arg Met Cys Ile  
 145 150 155 160

Trp Met Ser Gly

&lt;210&gt; 87

&lt;211&gt; 2702

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 87

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ag 2702

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&lt;210&gt; 88

&lt;211&gt; 733

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 88

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Met Gly Phe Ser Ser Gly Lys Ser Thr Lys Lys Lys Pro Leu Leu Phe
  1             5             10             15

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Asp Ile Arg Leu Lys Asn Val Asp Asn Asp Val Ile Leu Leu Lys Gly
          20             25             30

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Pro Pro Asn Glu Ala Pro Ser Val Leu Leu Ser Gly Cys Ile Val Leu
          35             40             45

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Ser Ile Asn Glu Pro Met Gln Ile Lys Ser Ile Ser Leu Arg Leu Tyr
          50             55             60

```

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Gly Lys Ile Gln Ile Asp Val Pro Leu Glu Arg Pro Gln Asp Ala Ser
          65             70             75             80

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Ser Ser Ser Leu Ser Ser Ser Pro Pro Lys Ile Arg Lys Tyr Asn Lys
          85             90             95

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Val Phe Tyr Asn Tyr Ala Trp Asp Asn Val Asn Leu Lys Glu Tyr Leu  
100 105 110

Ser Gly Leu Arg Gly Gln Ser Gly Leu Ala Gly Ser Ser Ser Ser  
115 120 125

Asn Ile Leu Gly Thr Arg Gln Arg Ala Gln Ser Thr Ser Ser Leu Lys  
130 135 140

Ser Leu Lys Gly Ser Ser Ser Pro Ser Ser Cys Thr Leu Asp Lys Gly  
145 150 155 160

Asn Tyr Asp Phe Pro Phe Ser Ala Ile Leu Pro Gly Ser Leu Pro Glu  
165 170 175

Ser Val Glu Ser Leu Pro Asn Cys Phe Val Thr Tyr Ser Met Glu Ser  
180 185 190

Val Ile Glu Arg Ser Lys Asn Tyr Ser Asp Leu Ile Cys Arg Lys Asn  
195 200 205

Ile Arg Val Leu Arg Thr Ile Ser Pro Ala Ala Val Glu Leu Ser Glu  
210 215 220

Thr Val Cys Val Asp Asn Ser Trp Pro Asp Lys Val Asp Tyr Ser Ile  
225 230 235 240

Ser Val Pro Asn Lys Ala Val Ala Ile Gly Ser Ala Thr Pro Ile Asn  
245 250 255

Ile Ser Ile Val Pro Leu Ser Lys Gly Leu Lys Leu Gly Ser Ile Lys  
260 265 270

Val Val Leu Phe Glu Asn Tyr Gln Tyr Cys Asp Pro Phe Pro Pro Val  
275 280 285

Ile Ser Glu Asn Arg Gln Val Thr Glu Leu Asn Leu Glu Asp Pro Leu  
290 295 300

Asn Glu Ser Ser Gly Glu Phe Asn Gly Asn Gly Cys Phe Val Asn Asn  
305 310 315 320

Pro Phe Phe Gln Pro Asp His Ser Phe Gln Asp Lys Trp Glu Ile Asp  
325 330 335

Thr Ile Leu Gln Ile Pro Asn Ser Leu Ser Asn Cys Val Gln Asp Cys  
340 345 350

Asp Val Arg Ser Asn Ile Lys Val Arg His Lys Leu Lys Phe Phe Ile  
 355 360 365

Ile Leu Ile Asn Pro Asp Gly His Lys Ser Glu Leu Arg Ala Ser Leu  
 370 375 380

Pro Ile Gln Leu Phe Ile Ser Pro Phe Val Ala Leu Ser Ile Lys Pro  
 385 390 395 400

Leu Ser Ser Ser Asn Leu Tyr Ser Leu Phe Ser Thr Thr Asn Gln Lys  
 405 410 415

Asp Glu Asn Ser Ser Gln Glu Glu Glu Glu Tyr Leu Phe Ser Arg  
 420 425 430

Ser Ala Ser Val Thr Gly Leu Glu Leu Leu Ala Asp Met Arg Ser Gly  
 435 440 445

Gly Ser Val Pro Thr Ile Ser Asp Leu Met Thr Pro Pro Asn Tyr Glu  
 450 455 460

Met His Val Tyr Asp Arg Leu Tyr Ser Gly Ser Phe Thr Arg Thr Ala  
 465 470 475 480

Val Glu Thr Ser Gly Thr Cys Thr Pro Leu Gly Ser Glu Cys Ser Thr  
 485 490 495

Val Glu Asp Gln Gln Gln Asp Leu Glu Asp Leu Arg Ile Arg Leu Thr  
 500 505 510

Lys Ile Arg Asn Gln Arg Asp Asn Leu Gly Leu Pro Pro Ser Ala Ser  
 515 520 525

Ser Ala Ala Ala Ser Arg Ser Leu Ser Pro Leu Leu Asn Val Pro Ala  
 530 535 540

Pro Glu Asp Gly Thr Glu Arg Ile Leu Pro Gln Ser Ala Leu Gly Pro  
 545 550 555 560

Asn Ser Gly Ser Val Pro Gly Val His Ser Asn Val Ser Pro Val Leu  
 565 570 575

Leu Ser Arg Ser Pro Ala Pro Ser Val Ser Ala His Glu Val Leu Pro  
 580 585 590

Val Pro Ser Gly Leu Asn Tyr Pro Glu Thr Gln Asn Leu Asn Lys Val  
 595 600 605

Pro Ser Tyr Gly Lys Ala Met Lys Tyr Asp Ile Ile Gly Glu Asp Leu  
 610 615 620  
 Pro Pro Ser Tyr Pro Cys Ala Ile Gln Asn Val Gln Pro Arg Lys Pro  
 625 630 635 640  
 Ser Arg Val His Ser Arg Asn Ser Ser Thr Thr Leu Ser Ser Ser Ile  
 645 650 655  
 Pro Thr Ser Phe His Ser Ser Ser Phe Met Ser Ser Thr Ala Ser Pro  
 660 665 670  
 Ile Ser Ile Ile Asn Gly Ser Arg Ser Ser Ser Ser Gly Val Ser Leu  
 675 680 685  
 Asn Thr Leu Asn Glu Leu Thr Ser Lys Thr Ser Asn Asn Pro Ser Ser  
 690 695 700  
 Asn Ser Met Lys Arg Ser Pro Thr Arg Arg Arg Ala Thr Ser Leu Ala  
 705 710 715 720  
 Gly Phe Met Gly Gly Phe Leu Ser Lys Gly Asn Lys Arg  
 725 730

<210> 89  
 <211> 1259  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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 tggatcaaaa cgttcttagg attgtggttg taaaacttgt aaaatccaag ctgagatctt 180  
 aaatccagca aaccttcgcc catatttatt cttttataac agaagaagag actatattct 240  
 caaaacctcg tatatttata tacatatcct ccaaacaac tccaagttt cactttcctg 300  
 gatttacctt ggcattcctt ttccccatcc tcttataatg gtaatcgga tccttaatta 360  
 tgatatcaca atagacgaag ggcacacacc aatttgccac cgtaaggata gagtaagtta 420  
 aatggctaac tcattataat cttcatgcta aatcatataa gggcagagac gaagcaaagc 480  
 gaaaaaaca tattacaatc atgtcgggtg ctgctgctgc atctgctgct gggttatgaca 540  
 ggcacatcac tatcttttcc cccgaggggtc gtttatatca agtagaatat gccttttaaag 600  
 cgactaatca aactaacata aactcactag cggtcagagg taaagattgt acagtgggtga 660  
 taagtcagaa aaaggctcct gataaactgt tggatccaac tactgtttcg tatatttttt 720  
 gtatttcaag aacaattggt atggtagtga acggaccaat accggatgca agaaatgcgg 780  
 ccctaagagc caaggctgag gctgcagaat tccgttataa atatggttat gatatgccat 840  
 gcgatgtatt ggctaagaga atggctaacc tttcccaaat ctatactcaa agagcatata 900  
 tgagaccatt aggtgttata ctcacatttg tttcggtaga tgaagaattg ggtccctcca 960



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 aacaacagga gatcacaca aacttagaaa accatttcaa aaagagtaaa atcgaccata 1080  
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 tgggtaccga attttcaaag aatgacttgg aagtcggtgt cgctacaaag gacaaattct 1200  
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<210> 90

<211> 252

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 90

Met Ser Gly Ala Ala Ala Ala Ser Ala Ala Gly Tyr Asp Arg His Ile  
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Thr Ile Phe Ser Pro Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Phe  
 20 25 30

Lys Ala Thr Asn Gln Thr Asn Ile Asn Ser Leu Ala Val Arg Gly Lys  
 35 40 45

Asp Cys Thr Val Val Ile Ser Gln Lys Lys Val Pro Asp Lys Leu Leu  
 50 55 60

Asp Pro Thr Thr Val Ser Tyr Ile Phe Cys Ile Ser Arg Thr Ile Gly  
 65 70 75 80

Met Val Val Asn Gly Pro Ile Pro Asp Ala Arg Asn Ala Ala Leu Arg  
 85 90 95

Ala Lys Ala Glu Ala Ala Glu Phe Arg Tyr Lys Tyr Gly Tyr Asp Met  
 100 105 110

Pro Cys Asp Val Leu Ala Lys Arg Met Ala Asn Leu Ser Gln Ile Tyr  
 115 120 125

Thr Gln Arg Ala Tyr Met Arg Pro Leu Gly Val Ile Leu Thr Phe Val  
 130 135 140

Ser Val Asp Glu Glu Leu Gly Pro Ser Ile Tyr Lys Thr Asp Pro Ala  
 145 150 155 160

Gly Tyr Tyr Val Gly Tyr Lys Ala Thr Ala Thr Gly Pro Lys Gln Gln  
 165 170 175

Glu Ile Thr Thr Asn Leu Glu Asn His Phe Lys Lys Ser Lys Ile Asp  
 180 185 190

115

His Ile Asn Glu Glu Ser Trp Glu Lys Val Val Glu Phe Ala Ile Thr  
 195 200 205

His Met Ile Asp Ala Leu Gly Thr Glu Phe Ser Lys Asn Asp Leu Glu  
 210 215 220

Val Gly Val Ala Thr Lys Asp Lys Phe Phe Thr Leu Ser Ala Glu Asn  
 225 230 235 240

Ile Glu Glu Arg Leu Val Ala Ile Ala Glu Gln Asp  
 245 250

<210> 91

<211> 968

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 91

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 agagcttcag atagccaata caccggaatt tagactttga caggattgtg gcttggtcca 180  
 gtataactta taatatatgt caacctttga gcaggaaacc caatgaaaat gcttcattac 240  
 atatatagca tatggagaag catgaaaaat aacagcgtga gatgttatcc atgttgcaag 300  
 aacctagtaa aatgaattct gaatttgcaa aaagtccata tttccacggt ctctctctcc 360  
 tacaattttg cgaacgcctg aacaaccatg cggattacca ttatttatat tgacaagatg 420  
 gctacctatg aaaagcatag acttactaac attttttttt tcaaatatgt ttgaaaaacg 480  
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 acccaggcag aggtaccttg tttgtccgtg gtgactccaa aatcttcaga ttccaaaact 600  
 ccaaactctgc ctctttgttc aagcaaagaa agaaccgaag aagaatcgct tggactgtct 660  
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 ctcgttaa 968

<210> 92

<211> 155

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 92

Met Lys Val Glu Ile Asp Ser Phe Ser Gly Ala Lys Ile Tyr Pro Gly  
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Arg Gly Thr Leu Phe Val Arg Gly Asp Ser Lys Ile Phe Arg Phe Gln  
                   20                  25                  30  
 Asn Ser Lys Ser Ala Ser Leu Phe Lys Gln Arg Lys Asn Pro Arg Arg  
                   35                  40                  45  
 Ile Ala Trp Thr Val Leu Phe Arg Lys His His Lys Lys Gly Ile Thr  
                   50                  55                  60  
 Glu Glu Val Ala Lys Lys Arg Ser Arg Lys Thr Val Lys Ala Gln Arg  
                   65                  70                  75                  80  
 Pro Ile Thr Gly Ala Ser Leu Asp Leu Ile Lys Glu Arg Arg Ser Leu  
                   85                  90                  95  
 Lys Pro Glu Val Arg Lys Ala Asn Arg Glu Glu Lys Leu Lys Ala Asn  
                   100                  105                  110  
 Lys Glu Lys Lys Lys Ala Glu Lys Ala Ala Arg Lys Ala Glu Lys Ala  
                   115                  120                  125  
 Lys Ser Ala Gly Thr Gln Ser Ser Lys Phe Ser Lys Gln Gln Ala Lys  
                   130                  135                  140  
 Gly Ala Phe Gln Lys Val Ala Ala Thr Ser Arg  
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&lt;210&gt; 93

&lt;211&gt; 764

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 93

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caactagcaa aggcagcccc ataaacacac agtatgtttt ttga

764

<210> 94  
 <211> 87  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 94  
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 Leu Ala Gln Glu Leu Thr Thr Ile Cys Glu Gln Ile Pro Ser Pro Thr  
                   20                  25                  30  
 Leu Glu Ser Thr Pro Tyr Ser Leu Ser Thr Thr Thr Ile Leu Ala Asn  
           35                  40                  45  
 Gly Lys Ala Met Gln Gly Val Phe Glu Tyr Tyr Lys Ser Val Thr Phe  
       50                  55                  60  
 Val Ser Asn Cys Gly Ser His Pro Ser Thr Thr Ser Lys Gly Ser Pro  
       65                  70                  75                  80  
 Ile Asn Thr Gln Tyr Val Phe  
                   85

<210> 95  
 <211> 1430  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 95  
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 tgcttcgaat gacaacgcct ttttgatata taatatccaa tttcattata gggaaatttt 360  
 caactcttac ccgccccact gtgctgatat gaccaagtga tcactcgatg atgggactac 420  
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 tccgcataag agcattcatc atggatagta aggaagtact ggtacatgtt aagaatctag 540  
 aaaagaacaa aagtaatgat gctgcagttc tagaaatctt acatgtcttg gataaagaat 600  
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 acgcaattaa taaaaataag cgttccaggc aagcacagca gcatcatcaa gatcatgcgc 780

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acaacgcaca ggggtgccacc atagaaaggc cagtcaccga tagatttaca tgtggtaaata 1320
gtaaagagaa gaaggtatct tactatcaat tgcaaacaa atctgcggtat gaaccattga 1380
ccactttctg tacatgtgaa gcatgtggta acagatggaa attctcttag 1430

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&lt;210&gt; 96

&lt;211&gt; 309

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 96

```

Met Asp Ser Lys Glu Val Leu Val His Val Lys Asn Leu Glu Lys Asn
  1              5              10              15

```

```

Lys Ser Asn Asp Ala Ala Val Leu Glu Ile Leu His Val Leu Asp Lys
          20              25              30

```

```

Glu Phe Val Pro Thr Glu Lys Leu Leu Arg Glu Thr Lys Val Gly Val
          35              40              45

```

```

Glu Val Asn Lys Phe Lys Lys Ser Thr Asn Val Glu Ile Ser Lys Leu
          50              55              60

```

```

Val Lys Lys Met Ile Ser Ser Trp Lys Asp Ala Ile Asn Lys Asn Lys
          65              70              75              80

```

```

Arg Ser Arg Gln Ala Gln Gln His His Gln Asp His Ala Pro Gly Asn
          85              90              95

```

```

Ala Glu Asp Lys Thr Thr Val Gly Glu Ser Val Asn Gly Val Gln Gln
          100              105              110

```

```

Pro Ala Ser Ser Gln Ser Asp Ala Met Lys Gln Asp Lys Tyr Val Ser
          115              120              125

```

```

Thr Lys Pro Arg Asn Ser Lys Asn Asp Gly Val Asp Thr Ala Ile Tyr
          130              135              140

```

```

His His Lys Leu Arg Asp Gln Val Leu Lys Ala Leu Tyr Asp Val Leu
          145              150              155              160

```

Ala Lys Glu Ser Glu His Pro Pro Gln Ser Ile Leu His Thr Ala Lys  
 165 170 175

Ala Ile Glu Ser Glu Met Asn Lys Val Asn Asn Cys Asp Thr Asn Glu  
 180 185 190

Ala Ala Tyr Lys Ala Arg Tyr Arg Ile Ile Tyr Ser Asn Val Ile Ser  
 195 200 205

Lys Asn Asn Pro Asp Leu Lys His Lys Ile Ala Asn Gly Asp Ile Thr  
 210 215 220

Pro Glu Phe Leu Ala Thr Cys Asp Ala Lys Asp Leu Ala Pro Ala Pro  
 225 230 235 240

Leu Lys Gln Lys Ile Glu Glu Ile Ala Lys Gln Asn Leu Tyr Asn Ala  
 245 250 255

Gln Gly Ala Thr Ile Glu Arg Ser Val Thr Asp Arg Phe Thr Cys Gly  
 260 265 270

Lys Cys Lys Glu Lys Lys Val Ser Tyr Tyr Gln Leu Gln Thr Arg Ser  
 275 280 285

Ala Asp Glu Pro Leu Thr Thr Phe Cys Thr Cys Glu Ala Cys Gly Asn  
 290 295 300

Arg Trp Lys Phe Ser  
 305

<210> 97

<211> 929

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 97

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 ttttcaaaag ttgtataata ttcaaaaacg ctaactgata atttgggtga ggtttcgaaa 180  
 gaattgccaa aatctcccta ggtatattat cttctggctt ccagatgtta actgcagtca 240  
 ttttgttttt cctgggtcttt acctcgaata ggttttcttg ttttgttatt tgttttcttt 300  
 ttggacccta tgtttatata tggattttga aaatctttta aaaaagcgat aaaagcggtg 360  
 ggatctgcca ctggttaactt caaaatagac aagacgaaaa aacggtgaaa atgggtgata 420  
 gaaataatac agaagtagat gttgaattag attaaactga agatatataa tttattggaa 480  
 aatacataga gtttttggtg atgcgcttaa gcatcaatt caacaacacc accagcagct 540

```

ctgatttttt cttcagccaa cttggagacg aatctagctt tgacgataac tggaacattt 600
ggaattctac ccttacccaa gatcttaccg taaccggctg ccaaagtgtc aataactgga 660
gcagtttcct tagaagcaga tttcaagtat tggctctctt tgtcttctgg gatcaatgtc 720
cacaatttgt ccaagttcaa gactggcttc cagaaatgag cttgttgctt gtggaagtat 780
ctcataccaa ccttacccaa ataacctgga tggattttat ccatgttaat tctgtggtga 840
tggtgaccac cggccatacc tctaccaccg ggggtgcttc tgtgcttacc gatacgacct 900
ttaccggctg tacaaaaaaa atattgtaa 929

```

&lt;210&gt; 98

&lt;211&gt; 142

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 98

```

Met Arg Leu Ser Asp Gln Phe Asn Asn Thr Thr Ser Ser Ser Asp Phe
  1             5             10             15

```

```

Phe Phe Ser Gln Leu Gly Asp Glu Ser Ser Phe Asp Asp Asn Trp Asn
      20             25             30

```

```

Ile Trp Asn Ser Thr Leu Thr Gln Asp Leu Thr Val Thr Gly Cys Gln
      35             40             45

```

```

Ser Val Asn Asn Trp Ser Ser Phe Leu Arg Ser Arg Phe Gln Val Leu
      50             55             60

```

```

Val Ser Leu Val Phe Trp Asp Gln Cys Pro Gln Phe Val Gln Val Gln
      65             70             75             80

```

```

Asp Trp Leu Pro Glu Met Ser Leu Leu Leu Val Glu Val Ser His Thr
      85             90             95

```

```

Asn Leu Thr Glu Ile Thr Trp Met Val Phe Ile His Val Asn Ser Val
      100            105            110

```

```

Val Met Leu Thr Thr Gly His Thr Ser Thr Thr Gly Val Leu Ser Val
      115            120            125

```

```

Leu Thr Asp Thr Thr Phe Thr Gly Cys Thr Lys Lys Ile Leu
      130            135            140

```

&lt;210&gt; 99

&lt;211&gt; 1461

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 99

```

aacaagctat aatattgtta aatatagttg atcaacagca ttgtaatgat tacaagagac 60
gaggttgaat gaaccttatg aaatgcgtat tatatataaa ctgtaataag agctaagttg 120
aattgaaatc tacgatactt gatgttgaca ttatagcaact agttcccagg aaaccctttc 180
gaaaaacaca gcaaaaacaa gagtactgta accaatgtaa catctgtaca ccagggaccc 240
acacattacc aaaatcaaaa ttatttttct aatgcctgtt atttttccta tttttcctct 300
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tgcgtatttt cccagatagg ttcaaactt tcatctgtat cccgtatatt taagatggcg 420
tttgctttct ccgttgattt ttttccttct tagtgatttt tttgcattaa atcccagaac 480
aatcatccaa ctaatcaaga atgccttcca gattcactaa gactagaaag cacagaggtc 540
acgtctcagg tatgtagttc catttggaag agggaatgaa agaaccaaga cggtgacttt 600
tttttttagtg ttgtgcaacc aatatgtcgt gtgtatatca tggtagagga gaatgtcaat 660
cagctaagtg tactcaacat atttctttgt gttttgattg cgaactttgt attaccatct 720
cactgttgag acggcttatt tgaggtaata gctcgagtaa atgtactctt ccatcgcaaa 780
ctgagcaaaa agaaagtgtg catagccttt gtcatacttc tcctttatta taccatgata 840
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aagcacagaa agcaccgccg tggtagaggt atggccgggt gtcaacatca ccacagaatt 1140
aacatggata aataccatcc aggttatatt ggtaagggtg gtatgagata cttccacaag 1200
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actttggcag ccggttacgg taagatcttg ggtaagggtg gaattccaaa tgttccagtt 1380
atcgtaaaag ctgattcgt ctccaagttg gctgaagaaa aaatcagagc tgctggtggt 1440
gttggtgaat tgatcgctta a 1461

```

&lt;210&gt; 100

&lt;211&gt; 149

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 100

```

Met Pro Ser Arg Phe Thr Lys Thr Arg Lys His Arg Gly His Val Ser
  1             5             10             15

Ala Gly Lys Gly Arg Ile Gly Lys His Arg Lys His Pro Gly Gly Arg
      20             25             30

Gly Met Ala Gly Gly Gln His His His Arg Ile Asn Met Asp Lys Tyr
      35             40             45

His Pro Gly Tyr Phe Gly Lys Val Gly Met Arg Tyr Phe His Lys Gln
      50             55             60

Gln Ala His Phe Trp Lys Pro Val Leu Asn Leu Asp Lys Leu Trp Thr

```



65                      70                      75                      80  
 Leu Ile Pro Glu Asp Lys Arg Asp Gln Tyr Leu Lys Ser Ala Ser Lys  
                                  85                      90                      95  
 Glu Thr Ala Pro Val Ile Asp Thr Leu Ala Ala Gly Tyr Gly Lys Ile  
                                  100                      105                      110  
 Leu Gly Lys Gly Arg Ile Pro Asn Val Pro Val Ile Val Lys Ala Arg  
                                  115                      120                      125  
 Phe Val Ser Lys Leu Ala Glu Glu Lys Ile Arg Ala Ala Gly Gly Val  
                                  130                      135                      140  
 Val Glu Leu Ile Ala  
 145

<210> 101  
 <211> 1880  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 101  
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 tgaactaatt tagtatctat ttccatttca ttataattca cgtttttagc agcctctctt 180  
 cttctaggta attggaaatc ttcttcttta ggcatacgct gaccagctga aaggcagatg 240  
 atctcaatat gtcccgatag gccaattttg ccaccagata gttcgaatggc attttatttt 300  
 tagtcctttt gaaagcaata tcataaaata tatatagttc tccatgatgt tcgggtcagt 360  
 cgctccgaag cgtaacctag tataataaat agttcattgc agaaaataac gaaagaaatg 420  
 gtggaatacg atctgttata tctaaactaa agctaactaa cggaataagc aaatacgaat 480  
 cgaccgctaa tttaacaaat atgggttttag caatggaaaag tagagtggca ccggaaattc 540  
 ctgggctcat tcaacctggg aatgtcacgc aagacttgaa gatgatgggc tgtaaattat 600  
 tgaattcccc aaaacctacg aaaacattcc ctggttccca gcctgtgtcc ttccagcatt 660  
 ctgatgtgga agagaagctg cttgcgcgat attactacgt ttgtgagaaa acagatgggc 720  
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 ttgataggga aaataactat tatctgggta atggatttag gtttcccaga ttaccccaaa 840  
 agaagaaaga agagctgcta gagactcttc aagatggcac cttattagat ggtgaacttg 900  
 tcatacaaac taacccaatg acaaaattac aagagtgtcg ttatttaatg ttcgattgtc 960  
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 aagatgatcg gaacaggtgg tattacaatt atgacgttaa gccagttttc agcttatatg 1380

tctggcaagg cggagctgat gtcaattcac gtttaaaaca tttcgaccag cctttcgata 1440  
 ggaaggaatt tgaaatatta gaaagaacat acagaaaatt tgcagagttg agcgtttcag 1500  
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 gcgcaaaaaa ccaagagact ggggcgtggg aaatgttaag attcagggat gataagttaa 1620  
 atggtaatca tacatcgggtg gtccagaaaag ttttgagag tatcaacgat tcagtttcat 1680  
 tggaggacct cgaggaaatt gttggtgata ttaaaagggtg ctgggacgag agaagagcaa 1740  
 atatggctgg tggtagtggg agaccactac cgtctcaaag tcaaaatgcg acattatcta 1800  
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<210> 102

<211> 459

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 102

Met Val Leu Ala Met Glu Ser Arg Val Ala Pro Glu Ile Pro Gly Leu  
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 Ile Gln Pro Gly Asn Val Thr Gln Asp Leu Lys Met Met Val Cys Lys  
 20 25 30  
 Leu Leu Asn Ser Pro Lys Pro Thr Lys Thr Phe Pro Gly Ser Gln Pro  
 35 40 45  
 Val Ser Phe Gln His Ser Asp Val Glu Glu Lys Leu Leu Ala His Asp  
 50 55 60  
 Tyr Tyr Val Cys Glu Lys Thr Asp Gly Leu Arg Val Leu Met Phe Ile  
 65 70 75 80  
 Val Ile Asn Pro Val Thr Gly Glu Gln Gly Cys Phe Met Ile Asp Arg  
 85 90 95  
 Glu Asn Asn Tyr Tyr Leu Val Asn Gly Phe Arg Phe Pro Arg Leu Pro  
 100 105 110  
 Gln Lys Lys Lys Glu Glu Leu Leu Glu Thr Leu Gln Asp Gly Thr Leu  
 115 120 125  
 Leu Asp Gly Glu Leu Val Ile Gln Thr Asn Pro Met Thr Lys Leu Gln  
 130 135 140  
 Glu Leu Arg Tyr Leu Met Phe Asp Cys Leu Ala Ile Asn Gly Arg Cys  
 145 150 155 160  
 Leu Thr Gln Ser Pro Thr Ser Ser Arg Leu Ala His Leu Gly Lys Glu

165

170

175

Phe Phe Lys Pro Tyr Phe Asp Leu Arg Ala Ala Tyr Pro Asn Arg Cys  
180 185 190

Thr Thr Phe Pro Phe Lys Ile Ser Met Lys His Met Asp Phe Ser Tyr  
195 200 205

Gln Leu Val Lys Val Ala Lys Ser Leu Asp Lys Leu Pro His Leu Ser  
210 215 220

Asp Gly Leu Ile Phe Thr Pro Val Lys Ala Pro Tyr Thr Ala Gly Gly  
225 230 235 240

Lys Asp Ser Leu Leu Leu Lys Trp Lys Pro Glu Gln Glu Asn Thr Val  
245 250 255

Asp Phe Lys Leu Ile Leu Asp Ile Pro Met Val Glu Asp Pro Ser Leu  
260 265 270

Pro Lys Asp Asp Arg Asn Arg Trp Tyr Tyr Asn Tyr Asp Val Lys Pro  
275 280 285

Val Phe Ser Leu Tyr Val Trp Gln Gly Gly Ala Asp Val Asn Ser Arg  
290 295 300

Leu Lys His Phe Asp Gln Pro Phe Asp Arg Lys Glu Phe Glu Ile Leu  
305 310 315 320

Glu Arg Thr Tyr Arg Lys Phe Ala Glu Leu Ser Val Ser Asp Glu Glu  
325 330 335

Trp Gln Asn Leu Lys Asn Leu Glu Gln Pro Leu Asn Gly Arg Ile Val  
340 345 350

Glu Cys Ala Lys Asn Gln Glu Thr Gly Ala Trp Glu Met Leu Arg Phe  
355 360 365

Arg Asp Asp Lys Leu Asn Gly Asn His Thr Ser Val Val Gln Lys Val  
370 375 380

Leu Glu Ser Ile Asn Asp Ser Val Ser Leu Glu Asp Leu Glu Glu Ile  
385 390 395 400

Val Gly Asp Ile Lys Arg Cys Trp Asp Glu Arg Arg Ala Asn Met Ala  
405 410 415

Gly Gly Ser Gly Arg Pro Leu Pro Ser Gln Ser Gln Asn Ala Thr Leu

125

420

425

430

Ser Thr Ser Lys Pro Val His Ser Gln Pro Pro Ser Asn Asp Lys Glu  
 435 440 445

Pro Lys Tyr Val Asp Glu Asp Asp Trp Ser Asp  
 450 455

&lt;210&gt; 103

&lt;211&gt; 1076

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 103

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 gaaaaaattg tactgatgct aattttggtg tcgttcttct tttttatttt gtaagactgt 180  
 ttccagaaa tgtttggtt tatttttttaa ttttttgaaa catttttttc atcctttctc 240  
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 caacatcctc ccatcatccc aatattggca tacacacaca tgcagcacag cggaactgcg 360  
 gaggtcagag gcaatgtggc agagacgctg gcgcgcctgt attgtataat agtatatttt 420  
 aactcaatt caattttttg atattaaatt agtgtgtaaa aagcttctga aatcaagaag 480  
 cccgtaccag aagttcaatc atgaaataca tccaaactga acaacaaatc gaagtcccag 540  
 aaggtgtcac tgcagcatc aagtcagaa tcgtcaaggt tgttggtcca agaggtactt 600  
 tgaccaagaa cttgaagcac attgatgtta ccttcaccaa ggtcaacaac caattgatca 660  
 aggttgctgt tcacaacggt ggcagaaagc acgttgctgc tttgagaacc gtcaagtctt 720  
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 aatttttggg cggtatctac gtttctcaca agggttttat tactgaagat ttataa 1076

&lt;210&gt; 104

&lt;211&gt; 191

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 104

Met Lys Tyr Ile Gln Thr Glu Gln Gln Ile Glu Val Pro Glu Gly Val  
 1 5 10 15

Thr Val Ser Ile Lys Ser Arg Ile Val Lys Val Val Gly Pro Arg Gly  
 20 25 30

Thr Leu Thr Lys Asn Leu Lys His Ile Asp Val Thr Phe Thr Lys Val  
 35 40 45  
 Asn Asn Gln Leu Ile Lys Val Ala Val His Asn Gly Gly Arg Lys His  
 50 55 60  
 Val Ala Ala Leu Arg Thr Val Lys Ser Leu Val Asp Asn Met Ile Thr  
 65 70 75 80  
 Gly Val Thr Lys Gly Tyr Lys Tyr Lys Met Arg Tyr Val Tyr Ala His  
 85 90 95  
 Phe Pro Ile Asn Val Asn Ile Val Glu Lys Asp Gly Ala Lys Phe Ile  
 100 105 110  
 Glu Val Arg Asn Phe Leu Gly Asp Lys Lys Ile Arg Asn Val Pro Val  
 115 120 125  
 Arg Asp Gly Val Thr Ile Glu Phe Ser Thr Asn Val Lys Asp Glu Ile  
 130 135 140  
 Val Leu Ser Gly Asn Ser Val Glu Asp Val Ser Gln Asn Ala Ala Asp  
 145 150 155 160  
 Leu Gln Gln Ile Cys Arg Val Arg Asn Lys Asp Ile Arg Lys Phe Leu  
 165 170 175  
 Asp Gly Ile Tyr Val Ser His Lys Gly Phe Ile Thr Glu Asp Leu  
 180 185 190

&lt;210&gt; 105

&lt;211&gt; 1694

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 105

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 aaaactcgga ataccttttg taaaggcgct tgtttggtgt actaacaccg tataaaacat 240  
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 gaaggaaaaa ttaggcgata ttaaaacaaa tctaaaataa agacaagaaa cgaaaaagag 480  
 gttaatcaag tattggaaaa atgtccaaag tgtttattgc cacagcaaag gcaggtaaag 540  
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```

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aacctgggtg ctttgacgtg aagtttttga aaaaagggtg gagatctggt atgggagctg 1620
atttaaataa aagtttatgc tgtgtttgtt tagatagaag catcaggtgg tttagagaag 1680
ctggcggtaa ataa 1694

```

&lt;210&gt; 106

&lt;211&gt; 397

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 106

```

Met Ser Lys Val Phe Ile Ala Thr Ala Asn Ala Gly Lys Ala His Asp
  1             5             10             15

```

```

Ala Asp Ile Phe Ser Val Ser Ala Cys Asn Ser Phe Thr Val Ser Cys
      20             25             30

```

```

Ser Gly Asp Gly Tyr Leu Lys Val Trp Asp Asn Lys Leu Leu Asp Asn
    35             40             45

```

```

Glu Asn Pro Lys Asp Lys Ser Tyr Ser His Phe Val His Lys Ser Gly
    50             55             60

```

```

Leu His His Val Asp Val Leu Gln Ala Ile Glu Arg Asp Ala Phe Glu
    65             70             75             80

```

```

Leu Cys Leu Val Ala Thr Thr Ser Phe Ser Gly Asp Leu Leu Phe Tyr
      85             90             95

```

```

Arg Ile Thr Arg Glu Asp Glu Thr Lys Lys Val Ile Phe Glu Lys Leu
    100            105            110

```

Asp Leu Leu Asp Ser Asp Met Lys Lys His Ser Phe Trp Ala Leu Lys  
115 120 125

Trp Gly Ala Ser Asn Asp Arg Leu Leu Ser His Arg Leu Val Ala Thr  
130 135 140

Asp Val Lys Gly Thr Thr Tyr Ile Trp Lys Phe His Pro Phe Ala Asp  
145 150 155 160

Glu Ser Asn Ser Leu Thr Leu Asn Trp Ser Pro Thr Leu Glu Leu Gln  
165 170 175

Gly Thr Val Glu Ser Pro Met Thr Pro Ser Gln Phe Ala Thr Ser Val  
180 185 190

Asp Ile Ser Glu Arg Gly Leu Ile Ala Thr Gly Phe Asn Asn Gly Thr  
195 200 205

Val Gln Ile Ser Glu Leu Ser Thr Leu Arg Pro Leu Tyr Asn Phe Glu  
210 215 220

Ser Gln His Ser Met Ile Asn Asn Ser Asn Ser Ile Arg Ser Val Lys  
225 230 235 240

Phe Ser Pro Gln Gly Ser Leu Leu Ala Ile Ala His Asp Ser Asn Ser  
245 250 255

Phe Gly Cys Ile Thr Leu Tyr Glu Thr Glu Phe Gly Glu Arg Ile Gly  
260 265 270

Ser Leu Ser Val Pro Thr His Ser Ser Gln Ala Ser Leu Gly Glu Phe  
275 280 285

Ala His Ser Ser Trp Val Met Ser Leu Ser Phe Asn Asp Ser Gly Glu  
290 295 300

Thr Leu Cys Ser Ala Gly Trp Asp Gly Lys Leu Arg Phe Trp Asp Val  
305 310 315 320

Lys Thr Lys Glu Arg Ile Thr Thr Leu Asn Met His Cys Asp Asp Ile  
325 330 335

Glu Ile Glu Glu Asp Ile Leu Ala Val Asp Glu His Gly Asp Ser Leu  
340 345 350

Ala Glu Pro Gly Val Phe Asp Val Lys Phe Leu Lys Lys Gly Trp Arg  
355 360 365

Ser Gly Met Gly Ala Asp Leu Asn Glu Ser Leu Cys Cys Val Cys Leu  
 370 375 380

Asp Arg Ser Ile Arg Trp Phe Arg Glu Ala Gly Gly Lys  
 385 390 395

<210> 107

<211> 1037

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 107

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gcttcgtggg ttcgactgac acggtttcat tcagaaaact catagggaca ggcaacgcat 240
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<210> 108

<211> 178

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 108

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Met Thr Leu Trp Pro His Pro Gly Ser Tyr Lys Ile Lys Ser Ala Thr
  1           5           10           15

Leu Phe Cys Ser Arg Asp Lys Leu Gly Cys Ala Phe Leu Ser Glu Ser
      20           25           30

Ser Leu Cys Met Tyr Phe Leu Tyr Asn Ser Leu Ser Ile Trp Ala Leu
  35           40           45
  
```



Gly Pro His Thr Ala Gly Pro Leu Leu Leu Phe Ser Ile Leu Asn Cys  
 50 55 60  
 Thr Pro Ala Arg Ser Val Thr Leu Pro Ile Ser Pro Ser Arg Ala Ser  
 65 70 75 80  
 Ile Ser Phe Thr Arg Met Pro Leu Pro Thr Pro Pro Ile Glu Gly Leu  
 85 90 95  
 His Glu His Leu Pro Ile Ser Val Asn Asp Gly Val Met Arg Val Val  
 100 105 110  
 Cys Ala Pro Val Leu Asp Asp Ala Ala Ala Ala Ser Gln Pro Ala Cys  
 115 120 125  
 Pro Ala Pro Met Thr Thr Thr Cys Val Leu Val Val Gly Trp Lys Leu  
 130 135 140  
 Val Lys Glu Asp Met Val Asn Arg Leu Leu Arg Thr Cys Lys Gly Asn  
 145 150 155 160  
 Glu Val His Glu Asp Ala Lys Val Val Thr Arg Ser Ile Val Leu Trp  
 165 170 175  
 Gly Val

<210> 109  
 <211> 731  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 109  
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 gcagtagcag cgatggcagc gacaccagcg gcgattgaag ttaatttgac cattgtattt 300  
 gttttgtttt ttagtgctgg tataagctta acaggaaaaga aagaaataaa gatataattt 360  
 caaaagcata cagttgaagc agctctattt ataccggtc ctctatcagt catcactact 420  
 taaacgattc gttaacagat gtcatttag cacctcacat atcctccata tctcatcttt 480  
 cacacaatct cattatcact atggagatgc tcttggttct gaacgaatca tacatctttc 540  
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 gtgggaatgc caattatagg gtgccgaggt gccttataaa acccttttct gtgcctgtga 660  
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cttattgtta a

731

&lt;210&gt; 110

&lt;211&gt; 76

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 110

Met Glu Met Leu Leu Phe Leu Asn Glu Ser Tyr Ile Phe His Arg Leu  
 1 5 10 15

Arg Met Trp Ser Ile Val Leu Trp His Ser Cys Val Phe Val Cys Ala  
 20 25 30

Glu Cys Gly Asn Ala Asn Tyr Arg Val Pro Arg Cys Leu Ile Lys Pro  
 35 40 45

Phe Ser Val Pro Val Thr Phe Pro Phe Ser Val Lys Lys Asn Ile Arg  
 50 55 60

Ile Leu Asp Leu Asp Pro Arg Thr Glu Ala Tyr Cys  
 65 70 75

&lt;210&gt; 111

&lt;211&gt; 1025

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 111

tccttacttt agtctattat caatatctct tccccctcct aaatatgtac tcttttattt 60  
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 gtgtagccta atgtttaatg cctaattttt ttctaaaatg cagcaacata catatgttga 180  
 gtcgtataga catctatata taacaagcac agaaccgtct aattggtatt tttcaggaca 240  
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 caccgccttc tttttatttt tatccgaaga tcttttggaa cccgctctgc gaatagcgaa 360  
 gctaggatac caaattgaaa cttggacata actcatcatt aaagaagtat actgttaaga 420  
 gaggcattca tttcgtgtat tataacgttt agcatcagtt acccttgaaa gcccaacata 480  
 tacaaaaata cgcgtccaag atgtctacta aagcccaaaa ccctatgcgt gatttgaaga 540  
 tcgagaaatt ggtcttgaac atctccgttg gtgaatctgg tgacagatta accagagcct 600  
 ccaaggtttt agaacaatta tctgggtcaa ctccagttca atccaaggcc agatacactg 660  
 tcagaacttt cggatatcaga agaaacgaaa aaattgctgt tcacgttacc gtcagaggtc 720  
 caaaggctga agaaattttg gaaagaggtt tgaagggtcaa ggaataccaa ttgagagaca 780  
 gaaacttctc tgctaccggt aacttcggtt tcggtattga cgaacacatt gacttgggta 840  
 tcaagtatga cccatccatc ggtattttcg gtatggattt ctatgtcgtc atgaacagac 900  
 caggtgctag agtcactaga agaaagagat gtaagggtac tggttgtaac tcccacaaga 960

caactaagga agacaccgtc tcttggttca agcaaaagta cgacgctgat gtgctcgata 1020  
aataa 1025

<210> 112

<211> 174

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 112

Met Ser Thr Lys Ala Gln Asn Pro Met Arg Asp Leu Lys Ile Glu Lys  
1 5 10 15

Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg  
20 25 30

Ala Ser Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser  
35 40 45

Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys  
50 55 60

Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu  
65 70 75 80

Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Asp Arg Asn Phe  
85 90 95

Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu  
100 105 110

Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Phe Gly Met Asp Phe Tyr  
115 120 125

Val Val Met Asn Arg Pro Gly Ala Arg Val Thr Arg Arg Lys Arg Cys  
130 135 140

Lys Gly Thr Val Gly Asn Ser His Lys Thr Thr Lys Glu Asp Thr Val  
145 150 155 160

Ser Trp Phe Lys Gln Lys Tyr Asp Ala Asp Val Leu Asp Lys  
165 170

<210> 113

<211> 1258

<212> DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 113

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taccctatat acaccatac cctattttta aatataaaaa gtaaacttca ttttgaaaga 180
ccactctgca tcagcacgcg ggctctggaa ggaagaaatg acgtttcggc ggaataccct 240
ttcagaaggt ctgctcttgt ggctggttca tgggagacac ccagcggagc tcctcccgag 300
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acaacaggaa ataaacaaag atgggtaaag gtaagccaag aggtttgaac tctgctagaa 540
agctacgtgt ccacagaaga aacaagtatg ttgactatct caaaattaaa aaaaactatc 600
aaccctctat tgtgatatcg ttttaggtga aggaaatgtt gtgagctctg gagtataaaa 660
tttatcaagt aacatatcct ggcgcaaate agtttgagga ggcttaaaat gacacgtcac 720
agtataaaaa agtaatgaat agtgaacggt cagcttcggc cattcttccc aatctatagt 780
gtggaaaata aaccttttct tcccaaaata actcagaaaag tcacaggagg ccgtttttta 840
caacggaatc atttttttac taacagtttt tttttattat tatagccgtt gggccgaaaa 900
caactacaag aagagattgt tgggtactgc cttcaagtct tctccattcg gtggttcttc 960
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```

&lt;210&gt; 114

&lt;211&gt; 145

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 114

```

Met Gly Lys Gly Lys Pro Arg Gly Leu Asn Ser Ala Arg Lys Leu Arg
  1              5              10              15

Val His Arg Arg Asn Asn Arg Trp Ala Glu Asn Asn Tyr Lys Lys Arg
          20              25              30

Leu Leu Gly Thr Ala Phe Lys Ser Ser Pro Phe Gly Gly Ser Ser His
          35              40              45

Ala Lys Gly Ile Val Leu Glu Lys Leu Gly Ile Glu Ser Lys Gln Pro
          50              55              60

Asn Ser Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly
          65              70              75              80

Lys Lys Val Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Val

```

85

90

95

Asp Glu Asn Asp Glu Val Leu Leu Ala Gly Phe Gly Arg Lys Gly Lys  
 100 105 110

Ala Lys Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser  
 115 120 125

Gly Val Ser Leu Leu Ala Leu Trp Lys Glu Lys Lys Glu Lys Pro Arg  
 130 135 140

Ser  
 145

<210> 115

<211> 1733

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 115

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caccgtctgt ggttgtaaag ttactgacac ttttttttct agaaagtcc ggaaaattgc 180
gacactcggg ggagctcgag agttgtatcc agttttcttg ttcggcgata ttccgaacca 240
ggtcggggtt ggctaacagc cgcccaggat ggaagaatta agaatttcac agaagccttc 300
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agcattagaa caatcttttc tcattgacag gtattctcat tgctctatat atattttctt 420
cttcttgaaa gaaatatcag tattacaatc ataacaacaa ccaaaagaaa ataactaata 480
gaccccatia caatatagaa atgttttcca tattcaattc accatgtgtt tttgaacagc 540
tgccatcttt tagtcagccc ctacattcgc gttattttga ttgcagttct ccagtgcgct 600
attatccaga atgtaaaagg aggaaagcaa taaagctaa cctaagagct ccaaaaaaaa 660
gcgatgcaaa ttgttcagaa ctttgagggt atgcacttgc tgaaacacca aatgggtata 720
cattaagctt gtctaagcgg attccatatg aacttttttc aaagtacgtt aatgagaaat 780
taggtgagct aaaggagaac cattacagac caacttacca tgttgtccaa gatttttttg 840
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gattgatgca ggaggaaagc agaaaatcag aacaggaaaa agctgccaag gaagatgaag 1380
aaaggcaaaa gaaagagaag gaagccagat tgaaggcaag gaaagaatct ttgataaata 1440
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ctgagattga ggccagcaat aaaaataata atagcaattc tggttcagca gaaagtata 1560

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135

atgaaagtat aaacagtgat tctgatacga ctttggattt ctctgtgtct ggtaatacac 1620  
taaaaaaaca cgcttcaccc ctattagaag acgttgagga tgaggaagtt gacagataca 1680  
acgagtcctt aagcagatct cccaaggga actctattat tgaggagata taa 1733

&lt;210&gt; 116

&lt;211&gt; 410

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 116

Met Phe Ser Ile Phe Asn Ser Pro Cys Val Phe Glu Gln Leu Pro Ser  
1 5 10 15

Phe Ser Gln Pro Leu His Ser Arg Tyr Phe Asp Cys Ser Ser Pro Val  
20 25 30

Ser Tyr Tyr Pro Glu Cys Lys Arg Arg Lys Ala Ile Lys Ala Asn Leu  
35 40 45

Arg Ala Pro Lys Lys Ser Asp Ala Asn Cys Ser Glu Pro Leu Arg Tyr  
50 55 60

Ala Leu Ala Glu Thr Pro Asn Gly Tyr Thr Leu Ser Leu Ser Lys Arg  
65 70 75 80

Ile Pro Tyr Glu Leu Phe Ser Lys Tyr Val Asn Glu Lys Leu Gly Glu  
85 90 95

Leu Lys Glu Asn His Tyr Arg Pro Thr Tyr His Val Val Gln Asp Phe  
100 105 110

Phe Gly Asn Gln Tyr Tyr Val Glu Asp Glu Ala Asp Glu Asp Ala Leu  
115 120 125

Leu Arg Ser Ala Leu Lys Asp Leu Asp Phe Arg Ala Ile Gly Lys Lys  
130 135 140

Ile Ala Lys Asp Leu Phe Gln Asp Tyr Glu Ile Glu Leu Asn His Arg  
145 150 155 160

Gly Asp Glu Leu Ser Ile Leu Ser Lys Lys Asp Lys Ile Phe Lys Glu  
165 170 175

Phe Ser Leu Asp Gln Val Phe Glu Asp Val Phe Val Ile Gly Cys Gly  
180 185 190

Val Glu Asn Ile Asp Asp Gly Ser Arg Glu Lys Tyr Ala Leu Leu Lys

136

195	200	205
Ile Gly Leu Val Lys His Glu Glu Glu Ile Ser Glu Gly Gly Ile Asn		
210	215	220
Glu Pro Lys Met Pro Ile Ile Glu Ser Lys Ile Asp Glu Ser His Asp		
225	230	235 240
Asp Val Asn Met Ser Glu Ser Leu Lys Glu Glu Glu Ala Glu Lys Ala		
	245	250 255
Lys Glu Pro Leu Thr Lys Glu Asp Gln Ile Lys Lys Trp Ile Glu Glu		
	260	265 270
Glu Arg Leu Met Gln Glu Glu Ser Arg Lys Ser Glu Gln Glu Lys Ala		
	275	280 285
Ala Lys Glu Asp Glu Glu Arg Gln Lys Lys Glu Lys Glu Ala Arg Leu		
	290	295 300
Lys Ala Arg Lys Glu Ser Leu Ile Asn Lys Gln Lys Thr Lys Arg Ser		
	305	310 315 320
Gln Gln Lys Lys Leu Gln Asn Ser Lys Ser Leu Pro Ile Ser Glu Ile		
	325	330 335
Glu Ala Ser Asn Lys Asn Asn Asn Ser Asn Ser Gly Ser Ala Glu Ser		
	340	345 350
Asp Asn Glu Ser Ile Asn Ser Asp Ser Asp Thr Thr Leu Asp Phe Ser		
	355	360 365
Val Ser Gly Asn Thr Leu Lys Lys His Ala Ser Pro Leu Leu Glu Asp		
	370	375 380
Val Glu Asp Glu Glu Val Asp Arg Tyr Asn Glu Ser Leu Ser Arg Ser		
	385	390 395 400
Pro Lys Gly Asn Ser Ile Ile Glu Glu Ile		
	405	410

&lt;210&gt; 117

&lt;211&gt; 890

&lt;212&gt; DNA

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 117

```

caaaaaagtt ttcggatgaa cccgattaat acaagtaaaa tcagcaaaga tatagaagac 60
aaaataagcg tgaaaacaat cataaaccac tcacaacggg ggttttcagc tgttactcct 120
ccatacatat attttgataa agatataatg ttatatattct tttcgtaatt ttgttttact 180
tcggtttgct ctatagattt catcagccgc accgaaaagg gagatcaata aggtaccctt 240
taaaagggat aagaagccta catcacccca ataaatggag taatggccag cattggatga 300
agagaagaat tacgggatac tgggataaca ctgttaaaaa atgcttcgcg acgtgagggg 360
cttcttcata taaattgaac tgccaaatct ctttcacatt atccaggata gtttggaatg 420
tgtgttactg aaggatcaga atcaataaat acaatcaata caaatattta gcgcataaaa 480
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ttgtgagaac tccaaagttt agatatatta tgttagggct ggtgggagct gctgtgttac 600
cgaccgcata catgaggaga ggctatacgg ttcctgcaca tagcttagac aacatcaacg 660
gcgtagacac aactaaggcg tctgttatgg gtacagaaca gagagcagct atgacgaagg 720
gtaagagttt acaagagatg atggatgatg atgaagtaac gtatttgatg ttctctttca 780
atcatgtaag ggaatttgta cttggttccc tgcatttatg ttctttgcat tttgttttcg 840
catttaatca tagtacgaca aacggggaag gggattgtga ttttacataa 890

```

&lt;210&gt; 118

&lt;211&gt; 129

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 118

```

Met Lys Leu Asp Ser Gly Ile Tyr Ser Glu Ala Gln Arg Val Val Arg
1           5           10           15

```

```

Thr Pro Lys Phe Arg Tyr Ile Met Leu Gly Leu Val Gly Ala Ala Val
          20           25           30

```

```

Val Pro Thr Ala Tyr Met Arg Arg Gly Tyr Thr Val Pro Ala His Ser
          35           40           45

```

```

Leu Asp Asn Ile Asn Gly Val Asp Thr Thr Lys Ala Ser Val Met Gly
          50           55           60

```

```

Thr Glu Gln Arg Ala Ala Met Thr Lys Gly Lys Ser Leu Gln Glu Met
          65           70           75           80

```

```

Met Asp Asp Asp Glu Val Thr Tyr Leu Met Phe Leu Phe Asn His Val
          85           90           95

```

```

Arg Glu Phe Val Leu Gly Ser Leu His Leu Cys Ser Leu His Phe Val
          100          105          110

```

```

Phe Ala Phe Asn His Ser Thr Thr Asn Gly Glu Gly Asp Cys Asp Phe
          115          120          125

```



Thr

&lt;210&gt; 119

&lt;211&gt; 1418

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 119

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aatctttgcg attgaattgc tgcacgaaca ttaacattag ttcttttgct aaagtttctc 60
caatatctgg aatatcagaa ttttagcaagg caatcaaagc ggataaagca gggattagcc 120
tgccattctg tttgttcaga gtaaaatcca caacattttt acaaattatg ttgcggccaa 180
taagtatatt gacttgaaat aagtctctgt gcgattcctg taagttgtcc attgtttaa 240
tggatattat gggtgaaacg tgtgacctta tcatttccca gttttctctc tgaaatttaa 300
tgtcttcac cgtatggta gcggtagaca tgctggttt tagccttttt attccttttt 360
aggtttctta ctcaaatgc caaaataaat atcagtgtaa tataattttt caagagtacg 420
taatggaaaa agataaaaa aaggaccgtc ataaaaagag acgtgattaa acctaaaaat 480
ctaaagtaaa gaagtgtta atggttgagg aaaattccag agttttgatt gttcttcctt 540
atacaccgcc tagtgctact ttgcagagga ttatagggca aactattccg ttcttaagag 600
aatgtcaaag tcaactagac atcgtgattg tacctgaatt caaaacctca ttccagttgg 660
attctgcgct aggggaagatg tacagtatta ccagggatgt ccttttgggc tatggaatga 720
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cttcgccaac gtgcactcca caaaaccctt gcgtataa 1418

```

&lt;210&gt; 120

&lt;211&gt; 305

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 120

```

Met Val Glu Glu Asn Ser Arg Val Leu Ile Val Leu Pro Tyr Thr Pro
  1             5             10             15

Pro Ser Ala Thr Leu Gln Arg Ile Ile Gly Gln Thr Ile Pro Phe Leu
          20             25             30

```

```

Arg Glu Cys Gln Ser Gln Leu Asp Ile Val Ile Val Pro Glu Phe Lys
    35                      40                      45

Thr Ser Phe Gln Leu Asp Ser Ala Leu Gly Lys Met Tyr Ser Ile Thr
    50                      55                      60

Arg Asp Val Leu Leu Gly Tyr Gly Met Ile Asn Ser Gly Ile Asn Ile
    65                      70                      75                      80

Ile Phe Asn Asn Ile His Phe Val Glu Ser Asn Leu Gln Trp Lys Val
                85                      90                      95

Val Leu Leu Pro Gln Glu Ser Thr Phe Glu Thr Trp Lys Leu Glu Leu
                100                      105                      110

Gly Gln Gly Gln Tyr His Ser Ile Glu His Tyr Ala Leu His Asp Asn
    115                      120                      125

Ile Met Glu Glu Ile Glu Gly Pro Lys Asp Ala Asn Lys Phe His Val
    130                      135                      140

Thr Ala Leu Gly Gly Thr Phe Asp His Ile His Asp Gly His Lys Ile
    145                      150                      155                      160

Leu Leu Ser Val Ser Thr Phe Ile Thr Ser Gln Arg Leu Ile Cys Gly
                165                      170                      175

Ile Thr Cys Asp Glu Leu Leu Gln Asn Lys Lys Tyr Lys Glu Leu Ile
                180                      185                      190

Glu Pro Tyr Asp Thr Arg Cys Arg His Val His Gln Phe Ile Lys Leu
    195                      200                      205

Leu Lys Pro Asp Leu Ser Val Glu Leu Val Pro Leu Arg Asp Val Cys
    210                      215                      220

Gly Pro Thr Gly Lys Val Pro Glu Ile Glu Cys Leu Val Val Ser Arg
    225                      230                      235                      240

Glu Thr Val Ser Gly Ala Glu Thr Val Asn Lys Thr Arg Ile Glu Lys
                245                      250                      255

Gly Met Ser Pro Leu Ala Val His Val Val Asn Val Leu Gly Gly Arg
                260                      265                      270

Glu Glu Asp Gly Trp Ser Glu Lys Leu Ser Ser Thr Glu Ile Arg Arg
    275                      280                      285

```

Leu Leu Lys Ser Ser Ala Ser Pro Thr Cys Thr Pro Gln Asn Pro Cys  
 290 295 300

Val  
 305

<210> 121  
 <211> 1433  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 121  
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 ccacgattga cgaacaagtt gggttgatcg ttgacagttt gaatgacgaa gagtttagtgt 120  
 ccaccgccga taagatcaag gccaatgctg ctgggtgccaa ggaagttttg aaggaatctg 180  
 caaagactat tgctgattct ggcaaactac catccagctt gttgtcctac ttcgtgtgaa 240  
 taccgtaaga aatggaatag aatatatacg aatgtatacg aatattatag agaacgttct 300  
 cttttatttc tataatgaat aggttcgggt aacgggtccc ttttaggta tttctagaag 360  
 atgagagaag agggaataat gagaaaggcg aaaaataaag gacacctta acgaaagatc 420  
 aaaggtgtcc ttatttactt acaatagctg caattagtag gactcaaaaa aagtgaaaac 480  
 aaaactgaaa ggatagatca atgtcttaca gaggacctat tggaaatttt ggcgggtatgc 540  
 caatgtcatc atcgcaagga ccatactctg gcggtgcaca attcagatca aaccagaacc 600  
 aatccacttc tggcatctta aagcaatgga agcattcttt tgaaaagttt gcctccagaa 660  
 ttgaggggct cactgacaat gcagttgttt ataaattgaa gccttacatt ccaagtttgt 720  
 caagattttt cattgtggcc accttttatg aagattcggt taggatctta tcacaatggg 780  
 cagatcaaat tttttatctg aataagtgga agcattaccc atacttcttt gtcgttgtgt 840  
 ttctagtggg tgttaccggt tccatgttga ttggcgccag tttgttaggt ttaagaaagc 900  
 aaaccaatta tgccaccggt gtgttatgtg cttgcggtat ttctcaagca ttagtttatg 960  
 ggttggtttac gggttcatca tttgtcctaa gaaacttttag tgttattggt ggggttgtaa 1020  
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 acagcaaaaa cgacaaagcg aagggttacc tgttggtttg tggtagaatt ttaattgttt 1140  
 taatgtttat cgctttcact ttcagtaa atcatggtttac tgttggtttg accattatcg 1200  
 gcacaatatg tttcgccatt ggttacaaga caaaattcgc atccattatg ttgggtttga 1260  
 tactaacttt ttacaatatc acgctaaaca actactgggt ttataacaat actaagagag 1320  
 atttcttgaa gtatgagttt taccagaact taagcatcat tgggtgggct ctattagtta 1380  
 ctaatactgg cgctggtgaa ttatccgttg atgaaaagaa gaagatttac tag 1433

<210> 122  
 <211> 310  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 122  
 Met Ser Tyr Arg Gly Pro Ile Gly Asn Phe Gly Gly Met Pro Met Ser

1	5	10	15
Ser Ser Gln Gly Pro Tyr Ser Gly Gly Ala Gln Phe Arg Ser Asn Gln	20	25	30
Asn Gln Ser Thr Ser Gly Ile Leu Lys Gln Trp Lys His Ser Phe Glu	35	40	45
Lys Phe Ala Ser Arg Ile Glu Gly Leu Thr Asp Asn Ala Val Val Tyr	50	55	60
Lys Leu Lys Pro Tyr Ile Pro Ser Leu Ser Arg Phe Phe Ile Val Ala	65	70	80
Thr Phe Tyr Glu Asp Ser Phe Arg Ile Leu Ser Gln Trp Ser Asp Gln	85	90	95
Ile Phe Tyr Leu Asn Lys Trp Lys His Tyr Pro Tyr Phe Phe Val Val	100	105	110
Val Phe Leu Val Val Val Thr Val Ser Met Leu Ile Gly Ala Ser Leu	115	120	125
Leu Val Leu Arg Lys Gln Thr Asn Tyr Ala Thr Gly Val Leu Cys Ala	130	135	140
Cys Val Ile Ser Gln Ala Leu Val Tyr Gly Leu Phe Thr Gly Ser Ser	145	150	155
Phe Val Leu Arg Asn Phe Ser Val Ile Gly Gly Leu Leu Ile Ala Phe	165	170	175
Ser Asp Ser Ile Val Gln Asn Lys Thr Thr Phe Gly Met Leu Pro Glu	180	185	190
Leu Asn Ser Lys Asn Asp Lys Ala Lys Gly Tyr Leu Leu Phe Ala Gly	195	200	205
Arg Ile Leu Ile Val Leu Met Phe Ile Ala Phe Thr Phe Ser Lys Ser	210	215	220
Trp Phe Thr Val Val Leu Thr Ile Ile Gly Thr Ile Cys Phe Ala Ile	225	230	235
Gly Tyr Lys Thr Lys Phe Ala Ser Ile Met Leu Gly Leu Ile Leu Thr	245	250	255
Phe Tyr Asn Ile Thr Leu Asn Asn Tyr Trp Phe Tyr Asn Asn Thr Lys			

<400>	123						
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catttcatta	agaacttgac	taaatatgaa	catttcttaa	aaaaaagggt	gacatataaa	180	
aataatcgaa	tataaacgat	ggaatTTTT	taaaattaaa	cacatatata	tatatatatt	240	
aactataaat	atgtcaaaga	aaccatacaa	tcatagattt	ataactatct	tttggatgac	300	
attaatgaac	ataacgctcc	taatacaaat	gtccaaaaaa	tattaccgc	aaatacgaat	360	
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agagaaaatt	tcataagggt	ttcctaccga	tgcttttata	aaatcttcgt	tttgtctcac	480	
atataccaac	aagagtaacg	atgttttctt	tacctaccct	aacctcagac	atcactggtg	540	
aagtcaacag	ttccgctacc	aaaaccccat	tcgtccgtcg	tcgggtcgaa	ccgggtggta	600	
agttcttttt	gcaacatgct	caaagaactt	tgagaaacca	cacctgggtc	gaatttgaaa	660	
gaattgaagc	tgaaaagaac	gtcaaaaccg	ttgatgaatc	caatgtcgac	ccagatgagt	720	
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aaactgccga	tttgtatgct	gctatgggtt	tgtctaagtt	gcgtttcaga	gctactgaaa	840	
gtcaaatcat	caaggctcac	agaaaacaag	ttgtcaagta	ccatccagac	aagcaatctg	900	
ctgctgggtg	tagtttggac	caagatggct	ttttcaagat	tattcaaaag	gcctttgaaa	960	
ctttgactga	ttccaacaag	agagctcagt	acgactcatg	tgattttgtt	gccgatgttc	1020	
ctcctccaaa	gaagggtacc	gattatgact	tttatgaagc	ttggggcccc	gttttcgaag	1080	
ctgaagctcg	tttttctaag	aagactccta	ttccttctct	aggtaacaaa	gattcttcca	1140	
agaaggaagt	tgaacaattc	tatgctttct	ggcacagatt	tgactcctgg	agaacctttg	1200	
agttcttgga	cgaagatgtc	ccagatgact	cttctaacag	agaccacaag	cgttacattg	1260	
aaagaaagaa	caaggccgca	agagacaaga	agaagactgc	tgataacgct	agattgggtca	1320	
aacttggtga	aagagctgtc	agtgaagatc	cccgtatcaa	aatgttcaaa	gaagaagaga	1380	
agaaggaaaa	ggaaagaaga	aatgggaaa	gagaagccgg	tgccagagct	gaagctgaag	1440	
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ctccgcgaaa	agctgacaaa	aagaaggcta	aggaagctgc	taaggccgcc	aagaaaaaga	1560	
acaagagagc	catccgtaac	tctgctaagg	aagctgacta	ctttggtgat	gctgacaagg	1620	
ccaccacgat	tgacgaacaa	gttggtttga	tcgttgacag	tttgaatgac	gaagagttag	1680	
tgtccaccgc	cgataagatc	aaggccaatg	ctgctgggtc	caaggaagtt	ttgaaggaat	1740	

ctgcaaagac tattgtcgat tctggcaaac taccatccag cttgttgtcc tacttcgtgt 1800  
ga 1802

<210> 124

<211> 433

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 124

Met Phe Ser Leu Pro Thr Leu Thr Ser Asp Ile Thr Val Glu Val Asn  
1 5 10 15

Ser Ser Ala Thr Lys Thr Pro Phe Val Arg Arg Pro Val Glu Pro Val  
20 25 30

Gly Lys Phe Phe Leu Gln His Ala Gln Arg Thr Leu Arg Asn His Thr  
35 40 45

Trp Ser Glu Phe Glu Arg Ile Glu Ala Glu Lys Asn Val Lys Thr Val  
50 55 60

Asp Glu Ser Asn Val Asp Pro Asp Glu Leu Leu Phe Asp Thr Glu Leu  
65 70 75 80

Ala Asp Glu Asp Leu Leu Thr His Asp Ala Arg Asp Trp Lys Thr Ala  
85 90 95

Asp Leu Tyr Ala Ala Met Gly Leu Ser Lys Leu Arg Phe Arg Ala Thr  
100 105 110

Glu Ser Gln Ile Ile Lys Ala His Arg Lys Gln Val Val Lys Tyr His  
115 120 125

Pro Asp Lys Gln Ser Ala Ala Gly Gly Ser Leu Asp Gln Asp Gly Phe  
130 135 140

Phe Lys Ile Ile Gln Lys Ala Phe Glu Thr Leu Thr Asp Ser Asn Lys  
145 150 155 160

Arg Ala Gln Tyr Asp Ser Cys Asp Phe Val Ala Asp Val Pro Pro Pro  
165 170 175

Lys Lys Gly Thr Asp Tyr Asp Phe Tyr Glu Ala Trp Gly Pro Val Phe  
180 185 190

Glu Ala Glu Ala Arg Phe Ser Lys Lys Thr Pro Ile Pro Ser Leu Gly  
195 200 205

144

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Asn Lys Asp Ser Ser Lys Lys Glu Val Glu Gln Phe Tyr Ala Phe Trp
 210                      215                      220

His Arg Phe Asp Ser Trp Arg Thr Phe Glu Phe Leu Asp Glu Asp Val
 225                      230                      235                      240

Pro Asp Asp Ser Ser Asn Arg Asp His Lys Arg Tyr Ile Glu Arg Lys
          245                      250                      255

Asn Lys Ala Ala Arg Asp Lys Lys Lys Thr Ala Asp Asn Ala Arg Leu
          260                      265                      270

Val Lys Leu Val Glu Arg Ala Val Ser Glu Asp Pro Arg Ile Lys Met
          275                      280                      285

Phe Lys Glu Glu Glu Lys Lys Glu Lys Glu Arg Arg Lys Trp Glu Arg
          290                      295                      300

Glu Ala Gly Ala Arg Ala Glu Ala Glu Ala Lys Ala Lys Ala Glu Ala
 305                      310                      315                      320

Glu Ala Lys Ala Lys Ala Glu Ser Glu Ala Lys Ala Asn Ala Ser Ala
          325                      330                      335

Lys Ala Asp Lys Lys Lys Ala Lys Glu Ala Ala Lys Ala Ala Lys Lys
          340                      345                      350

Lys Asn Lys Arg Ala Ile Arg Asn Ser Ala Lys Glu Ala Asp Tyr Phe
          355                      360                      365

Gly Asp Ala Asp Lys Ala Thr Thr Ile Asp Glu Gln Val Gly Leu Ile
          370                      375                      380

Val Asp Ser Leu Asn Asp Glu Glu Leu Val Ser Thr Ala Asp Lys Ile
          385                      390                      395                      400

Lys Ala Asn Ala Ala Gly Ala Lys Glu Val Leu Lys Glu Ser Ala Lys
          405                      410                      415

Thr Ile Val Asp Ser Gly Lys Leu Pro Ser Ser Leu Leu Ser Tyr Phe
          420                      425                      430

Val

```

<210> 125  
 <211> 1472  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 125  
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 aagggcctcg aaagacgtta atgcatccgt acacctacat ctttacattt tttgctgttg 120  
 cacctacact gttttttttt ttttcacctt atgagtcctg tatttcttga aagagccgat 180  
 aacaatatc caggtggagt cccgaggcag aatcaaggct gcggagagaa gttcctctca 240  
 aactaatggg agtgatccgc tcagttctcc catcacgaca gaactgtctg agacaaagtc 300  
 tttccagcag agtccgccta cgctcttgct gcagagattc gcccgaaggc aggtttcctg 360  
 aaattctttt cactagtaaa gtgttcggtc atgtaaaaca tactgccgta gttttgagct 420  
 aaaattaaag atatattaga tttttagaat ttcttagata gtctcaacgt gttaaaacaa 480  
 aagcataacc aaagaaaaaa atggctaagt tcttgaaagc tggtaaagtt ggtacgtatc 540  
 attttcagtt tttggacatc aacaaaaaac cgtgcaactg tggattaga aatccaagtt 600  
 attagcagtt gatgttgat aatttgagtt tgaattcgag tattgtatct tcatatggga 660  
 gtagggagga aaaagcgtgg agatgttaga tctgggaaaa aaccttttaa tttgaatgat 720  
 agcttattaa tagaaatatt ggacaaaaag atgaatgatt taggagcgaa actaacgatt 780  
 attcatattc attgagctat acgaggcagt ggaagggtta tcaaaaagtt gtaattttaa 840  
 agaaaaaagc atcaatagcc accaaataag atggtgaaag ttccgcgata tttttgctaa 900  
 gaccataggc acatgtacgc aggcgaccag ggccttttat ttactgtagt tctttccatg 960  
 ccctattaaa aattcgtggg cctatgataa tttttctctc cctagtattg aagaacaaaa 1020  
 ttgagaattc gccaaacttt aagaagggtt cacatttact aactatttct tttccttctt 1080  
 ttttttacac agctgtcgtt gtccgtgggc gttacgccgg taagaagggtt gttatcgtaa 1140  
 aaccacatga tgaagggttc aagtctcacc catttggtca cgctttgggt gccgggtattg 1200  
 aaagataccc attgaaggtc accaagaagc acggtgccaa gaagggtgct aagagaacca 1260  
 agatcaagcc tttcatcaag gtcgtcaact acaaccattt attgccaacc agatacactt 1320  
 tagatgttga agctttcaaa tccgttgttt ctactgaaac tttcgaacaa ccttcccaac 1380  
 gtgaagaagc taagaaagtc gtcaagaagg ctttcgaaga aagacaccaa gctggtaaga 1440  
 accaatgggt cttctctaag ttgagatttt aa 1472

<210> 126  
 <211> 136  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 126  
 Met Ala Lys Phe Leu Lys Ala Gly Lys Val Ala Val Val Val Arg Gly  
 1 5 10 15  
 Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly  
 20 25 30  
 Ser Lys Ser His Pro Phe Gly His Ala Leu Val Ala Gly Ile Glu Arg  
 35 40 45



Tyr Pro Leu Lys Val Thr Lys Lys His Gly Ala Lys Lys Val Ala Lys  
 50 55 60  
 Arg Thr Lys Ile Lys Pro Phe Ile Lys Val Val Asn Tyr Asn His Leu  
 65 70 75 80  
 Leu Pro Thr Arg Tyr Thr Leu Asp Val Glu Ala Phe Lys Ser Val Val  
 85 90 95  
 Ser Thr Glu Thr Phe Glu Gln Pro Ser Gln Arg Glu Glu Ala Lys Lys  
 100 105 110  
 Val Val Lys Lys Ala Phe Glu Glu Arg His Gln Ala Gly Lys Asn Gln  
 115 120 125  
 Trp Phe Phe Ser Lys Leu Arg Phe  
 130 135

&lt;210&gt; 127

&lt;211&gt; 1299

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 127

ttacttacgt ctattataac cttccgcgta aaaaagaaat attgacatcc tttcttgtat 60  
 ttagcccata cattttcacc catgcacccat tggattataa agaaaaaaat ttaataaaaa 120  
 tctgccgggg aaatttcaga agaaaaaagg aagggtgtgtt cgcatttaac acggggccacc 180  
 ataaactttt gtttgccacc catctagacg ggatccgccc cgccaaggc tctcttcctc 240  
 tagctaggca atgtggctct cggaaaggaa actcccacca ggacgtggtg ggaaatgcag 300  
 caattcccct ctgcttcccg ctgacctttc ttgggcccag tttagtaagt atgctctcat 360  
 ctttcatgtg tgctgtaact tgcaagtcac taacactatc tataattgat attagacggt 420  
 aaaagttcta tatagcattt gcttttattt agagaatacg aaaacacacc agataattag 480  
 tgcataatata ttagatcaat atggtatgtg aaagagatat taaacataag atgtgaagga 540  
 aacagaagag aacaatattt gaggaatgaa ttcggatgaa attctagtag aagaaaaaag 600  
 cctaaaataa aaagaaagaa aggaaaataa agcagtaatc aacctctgac atttgatagg 660  
 agtatgcgtt tccgcaaaat caacaaatca tgcattaaac tggtaacgga gacttttaag 720  
 acgtgcaaag aaagcaatta atttttagat agggaattga aaggctctgt atagcagaaa 780  
 atttgagatc tactgtggag ataagcatat ggtgttgagt tatgggtaat ctaacaataa 840  
 tagaaactta tagcagttga agatggcgga tcatgatgcc ggatactgct gggtaatgat 900  
 ttatccttct ttttttgag cacaaatgct cactttttcc tgtctcctct aacttttctg 960  
 atgtatccta cccaacccta cagttttcaa attactaaca tcaatttttt tgtgaaacga 1020  
 ctttcgtttt cgtttctatt tatttcatta cagggttttag ttcaagattt gttgcaccca 1080  
 actgctgctt ctgaagccag aaagcacaag ttaaagactt tggttcaagg cccaagatcc 1140  
 tacttcttgg atgtcaaatg cccaggttgt ttgaacatca ccactgtttt ttctcatgct 1200  
 caaactgctg tcacttgtga atcatgctct actgtcttat gtactccaac cgggtggttaag 1260  
 gccaaattat ctgaaggtag ttctttcaga agaaagtaa 1299

<210> 128  
 <211> 82  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 128  
 Met Val Leu Val Gln Asp Leu Leu His Pro Thr Ala Ala Ser Glu Ala  
           1                  5                  10                  15  
 Arg Lys His Lys Leu Lys Thr Leu Val Gln Gly Pro Arg Ser Tyr Phe  
                   20                  25                  30  
 Leu Asp Val Lys Cys Pro Gly Cys Leu Asn Ile Thr Thr Val Phe Ser  
                   35                  40                  45  
 His Ala Gln Thr Ala Val Thr Cys Glu Ser Cys Ser Thr Val Leu Cys  
                   50                  55                  60  
 Thr Pro Thr Gly Gly Lys Ala Lys Leu Ser Glu Gly Thr Ser Phe Arg  
                   65                  70                  75                  80  
 Arg Lys

<210> 129  
 <211> 1262  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 129  
 taaaacatgg catttttaaat agtactgccaa aaattttaatg caatggcaat tagttggcta 60  
 tgttgctaca tattatatttc catagcattc tctgtcacaa acttcaaaat aaaagacagt 120  
 gacatccgaa catccgatac acccatatcat catgaaaata aatcctgaca ttggaagaag 180  
 tcttgataca aaaaaagatc gctgtcaaaa atgcgggccag actgccgctg catcgtacca 240  
 acagtgcgta tgttcagacg gagagacgac ctctagagag acgtccgctg gtgcggcaac 300  
 gctgacgggt tagttgttcg acgggatgat gggttccgcc agggggaggg aaggctttcc 360  
 accaagagag gtaaaattat tcgtcgaaat gaactcagag atacatccat attgttgaca 420  
 atgtatatct taattgatgt ggtattttca ctgttttaac gtaaattgaa ggagattaag 480  
 caaaaaaaca atcagtaata atgggtatgt ggacgattag gaatagacaa accatgttat 540  
 ttatctccat tagggcgtga gagtgttaatt agtacacagg tactactaga atgctaaaga 600  
 acttttttaa atatcctgaa tcgtagggca aatccatgtc aagcaagaaa ctaatagtta 660  
 ttaaacttca ttacttttg agctagttaa atattttcat catttcctaa agtactgaac 720  
 acctgaatga tactttttatt ggccctttta ataagaactc tggttagaaa atatattgag 780  
 gatatcatta gtaatactca ttagatatatt gtgaatttag ccgtttcccc attacagaaa 840

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aaagatacaa ctaattacat gtgcagtcaa attacttttt ttttaagatc aattactaac 900
aatcaactat catgctaaat ttgctgtgat atcattttga accagttaac gtcccaaaga 960
ccagaaagac ctactgtaag ggtaagacct gtcgtaagca cactcaacac aaggttactc 1020
aatacaaaagc tggtaaggct tccttggtcg ctcaaggtaa gagacggtat gaccgtaaac 1080
aatctgggttt cgggtgggtcaa accaagcctg ttttccacaa gaaagctaag actaccaaga 1140
aggttggttt gagattggaa tgtgtcaa at gtaagactag agcccaatta accttgaaga 1200
gatgtaagca cttcgaattg ggtggtgaaa agaagcaaaa gggtaagct ttgcaattct 1260
ga 1262

```

&lt;210&gt; 130

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 130

```

Met Val Asn Val Pro Lys Thr Arg Lys Thr Tyr Cys Lys Gly Lys Thr
  1             5             10             15

```

```

Cys Arg Lys His Thr Gln His Lys Val Thr Gln Tyr Lys Ala Gly Lys
      20             25             30

```

```

Ala Ser Leu Phe Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser
    35             40             45

```

```

Gly Phe Gly Gly Gln Thr Lys Pro Val Phe His Lys Lys Ala Lys Thr
    50             55             60

```

```

Thr Lys Lys Val Val Leu Arg Leu Glu Cys Val Lys Cys Lys Thr Arg
    65             70             75             80

```

```

Ala Gln Leu Thr Leu Lys Arg Cys Lys His Phe Glu Leu Gly Gly Glu
      85             90             95

```

```

Lys Lys Gln Lys Gly Gln Ala Leu Gln Phe
    100             105

```

&lt;210&gt; 131

&lt;211&gt; 962

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 131

```

catcgcttga tttccggcct gcaaaaataa agtagtcggt acgtactttc gttttcaatt 60
tccatgggtgc acagtatctt aactatctgc ttagtcgagg agaaccagga ttctgttcgt 120
tgetcagccg cttcgtggat attctcttgg atactttaaa catggaccta cgttccgctc 180

```

```

tcgaaaagac caatataata aaaagttata aattacattt ccttattagg tatacgacct 240
cgcgcttcga agtagaggag cccttttttg cgtacctaca tatggcgcgat cagacagaca 300
aacttcccc aaaaatgtat taccccgcg aataagaaaa cagaccatt caccacgac 360
gtatcaagtt acttccttg tgcaatgtcc cactataaaa aaattccttg acgctagatc 420
gttggaactaa aatctgcgtc acaatcgct aaacaggaaa tattgcctat tttcgtacaa 480
ggttacttcc tagatgctat atgtccctac ggccttgct aacaccatcc agcatgcaat 540
acagtgcacat atatatacac acaccacacc cacaccacaca cccacaccca cacacacca 600
cacacacaca cccacacaca cccacaccca caccacacc acaccacac acaccacacc 660
cacacaccac acccacaccc acaccacacc acaccacac accacacacc accctatcta 720
acctgtctct taacctaccc tcacattacc ctacctccc actcgttacc ctgccccact 780
caaccatacc actcccaacc accatccatc tctctactta ctactaccat ccaccgcca 840
tcataaccgt taccctccaa ttaccatata ccaactccac taccattacc ctgctattac 900
cctaccatcc accatgtcct actcactgta ctgttggtct accctccata ttgaaacggt 960
aa 962

```

&lt;210&gt; 132

&lt;211&gt; 153

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 132

```

Met Ser Leu Arg Pro Cys Leu Thr Pro Ser Ser Met Gln Tyr Ser Asp
  1              5              10              15

```

```

Ile Tyr Ile His Thr Pro His Pro His Pro His Pro His Pro His Thr
      20              25              30

```

```

Pro Thr His Thr His Pro His Thr Pro Thr Pro Thr Pro His Pro His
      35              40              45

```

```

Pro His Thr Pro His Pro His Thr Thr Pro Thr Pro Thr Pro His His
      50              55              60

```

```

Thr His Thr Pro His Thr Thr Leu Ser Asn Leu Ser Leu Asn Leu Pro
      65              70              75              80

```

```

Ser His Tyr Pro Thr Ser Pro Leu Val Thr Leu Pro His Ser Thr Ile
      85              90              95

```

```

Pro Leu Pro Thr Thr Ile His Leu Ser Thr Tyr Tyr Tyr His Pro Pro
      100              105              110

```

```

Pro Ile Ile Thr Val Thr Leu Gln Leu Pro Ile Ser Asn Ser Thr Thr
      115              120              125

```

```

Ile Thr Leu Leu Leu Pro Tyr His Pro Pro Cys Pro Thr His Cys Thr
      130              135              140

```

150

Val Val Leu Pro Ser Ile Leu Lys Arg  
145 150

<210> 133

<211> 3752

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 133

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ttccataggg cttattttcc agttgatgga atgggagggt gctcttaacg cgaagactaa 60
cgtgcaagcc aacagttata gaaaagtacc gtgagagaga aaaaaaaaaa agatatagca 120
ttcaatgagg ctttattgag gggcacgatg ctcttttttt cttctgtact ttataaataa 180
ttccgtattt cttcgctttg tttcatgctc tgttctgagc ttttagtttc tcttattgag 240
agccttttcc aatcaaggc tcaggaagtg actcgtcctt agaagaacaa ggtttggatt 300
tggtagggtt cttgtacgaa gttctcaata taatttgcgc atttactgta cggttcatac 360
tagtttattc cgggtaacaa gttttcttgt gatgctaaat caatgtgtat attgagaaaa 420
ctatgtagta agttacacaa agcaacaaag gatattatta tatgtgacag agaagaattg 480
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&lt;210&gt; 134

&lt;211&gt; 1083

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 134

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Ser Lys Gln Glu Thr Ser Glu Glu Glu Asp Thr Ala Gly Lys His Glu
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Gln Arg Glu Thr Leu Ser Glu Glu Val Ser Asp Lys Phe Pro Glu Asn
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Val Ala Ser Phe Arg Ser Gln Thr Thr Ser Val His Gln Ala Thr Gln

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Ala Ser Ser His Glu Gly Glu Val Asn Gly Asp Ser Arg Pro Asp Asp	100	105	110
Val Pro Glu Thr Asn Glu Lys Ile Ser Gln Ala Ile Arg Ala Lys Ile	115	120	125
Ser Ser Ser Ser Ser Ser Pro Asn Val Arg Asn Val Asp Ile Gln Asn	130	135	140
His Gln Pro Phe Ser Arg Asp Gln Leu Arg Ala Met Leu Lys Glu Pro	145	150	155
Lys Arg Lys Thr Val Asp Asp Phe Ile Glu Glu Glu Gly Leu Gly Ala	165	170	175
Val Glu Glu Glu Asp Leu Ser Asp Glu Val Leu Glu Lys Asn Thr Thr	180	185	190
Glu Pro Glu Asn Val Glu Lys Asp Ile Glu Tyr Ser Asp Ser Asp Lys	195	200	205
Asp Thr Asp Asp Val Gly Ser Asp Asp Pro Thr Ala Pro Asn Ser Pro	210	215	220
Ile Lys Leu Gly Arg Arg Lys Leu Val Arg Gly Asp Gln Leu Asp Ala	225	230	235
Thr Thr Ser Ser Met Phe Asn Asn Glu Ser Asp Ser Glu Leu Ser Asp	245	250	255
Ile Asp Asp Ser Lys Asn Ile Ala Leu Ser Ser Ser Leu Phe Arg Gly	260	265	270
Gly Ser Ser Pro Val Lys Glu Thr Asn Asn Asn Leu Ser Asn Met Asn	275	280	285
Ser Ser Pro Ala Gln Asn Pro Lys Arg Gly Ser Val Ser Arg Ser Asn	290	295	300
Asp Ser Asn Lys Ser Ser His Ile Ala Val Ser Lys Arg Pro Lys Gln	305	310	315
Lys Lys Gly Ile Tyr Arg Asp Ser Gly Gly Arg Thr Arg Leu Gln Ile			

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Ala Cys Asp Lys Gly Lys Tyr Asp Val Val Lys Lys Met Ile Glu Glu		
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Gly Gly Tyr Asp Ile Asn Asp Gln Asp Asn Ala Gly Asn Thr Ala Leu		
355	360	365
His Glu Ala Ala Leu Gln Gly His Ile Glu Ile Val Glu Leu Leu Ile		
370	375	380
Glu Asn Gly Ala Asp Val Asn Ile Lys Ser Ile Glu Met Phe Gly Asp		
385	390	400
Thr Pro Leu Ile Asp Ala Ser Ala Asn Gly His Leu Asp Val Val Lys		
405	410	415
Tyr Leu Leu Lys Asn Gly Ala Asp Pro Thr Ile Arg Asn Ala Lys Gly		
420	425	430
Leu Thr Ala Phe Glu Ser Val Asp Asp Glu Ser Glu Phe Asp Asp Glu		
435	440	445
Glu Asp Gln Lys Ile Leu Arg Glu Ile Lys Lys Arg Leu Ser Ile Ala		
450	455	460
Ala Lys Lys Trp Thr Asn Arg Ala Gly Ile His Asn Asp Lys Ser Lys		
465	470	475
Asn Gly Asn Asn Ala His Thr Ile Asp Gln Pro Pro Phe Asp Asn Thr		
485	490	495
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Asn Ile Asp Glu Lys Ala Pro Glu Glu Glu Phe Tyr Trp Thr Asp Val		
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Thr Ser Arg Ala Gly Lys Glu Lys Leu Phe Lys Ala Ser Lys Glu Gly		
530	535	540
His Leu Pro Tyr Val Gly Thr Tyr Val Glu Asn Gly Gly Lys Ile Asp		
545	550	555
Leu Arg Ser Phe Phe Glu Ser Val Lys Cys Gly His Glu Asp Ile Thr		
565	570	575
Ser Ile Phe Leu Ala Phe Gly Phe Pro Val Asn Gln Thr Ser Arg Asp		



580

585

590

Asn Lys Thr Ser Ala Leu Met Val Ala Val Gly Arg Gly His Leu Gly  
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Thr Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Pro Thr Lys Arg Asp  
610 615 620

Lys Lys Gly Arg Thr Ala Leu Tyr Tyr Ala Lys Asn Ser Ile Met Gly  
625 630 635 640

Ile Thr Asn Ser Glu Glu Ile Gln Leu Ile Glu Asn Ala Ile Asn Asn  
645 650 655

Tyr Leu Lys Lys His Ser Glu Asp Asn Asn Asp Asp Asp Asp Asp Asp  
660 665 670

Asp Asn Asn Asn Glu Thr Tyr Lys His Glu Lys Lys Arg Glu Lys Thr  
675 680 685

Gln Ser Pro Ile Leu Ala Ser Arg Arg Ser Ala Thr Pro Arg Ile Glu  
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725 730 735

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Leu Gly Leu Lys Ile Ile Asn Phe Asn Asp Lys Leu Asp Tyr Lys Arg				
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Phe Leu Pro Leu Tyr Tyr Phe Val Asp Glu Lys Asn Asp Lys Phe Val				
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Lys Asp Asn Gln Pro Thr Ser Glu Lys Ile Pro Val Asp Pro Ser His				
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Leu Thr Pro Leu Trp Asn Met Leu Lys Phe Ile Phe Leu Tyr Gly Gly				
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Ser Tyr Asp Asp Lys Lys Asn Asn Met Glu Asn Lys Arg Tyr Val Val				
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Asn Phe Asp Gly Val Asp Leu Asp Thr Lys Ile Gly Tyr Glu Leu Leu				
	980	985	990	
Glu Tyr Lys Lys Phe Val Ser Leu Pro Met Ala Trp Ile Lys Trp Asp				
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Asn Val Val Ile Glu Asn His Ala Lys Arg Lys Glu Ile Glu Gly Asn				
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Met Ile Gln Ile Ser Ile Asn Glu Phe Ala Arg Trp Arg Asn Asp Lys				
	1025	1030	1035	1040
Leu Asn Lys Ala Gln Gln Pro Thr Arg Lys Gln Arg Ser Leu Lys Ile				
	1045	1050	1055	
Pro Arg Glu Leu Pro Val Lys Phe Gln His Arg Met Ser Ile Ser Ser				
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<211> 4883  
<212> DNA  
<213> *Saccharomyces cerevisiae*

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<212> PRT

<213> *Saccharomyces cerevisiae*

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Lys Leu Pro Phe Ala Ser Leu Gln Asn Leu Asp Ile Ser Asn Ser Lys  
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Ser Leu Phe Val Ala Ala Ser Gly Ser Lys Ala Val Val Gly Glu Leu  
 50 55 60

Gln Leu Leu Arg Asp His Ile Thr Ser Asp Ser Thr Pro Leu Thr Phe  
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Lys Trp Glu Lys Glu Ile Pro Asp Val Ile Phe Val Cys Phe His Gly  
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Asp Gln Val Leu Val Ser Thr Arg Asn Ala Leu Tyr Ser Leu Asp Leu  
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Glu Glu Leu Ser Glu Phe Arg Thr Val Thr Ser Phe Glu Lys Pro Val  
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Asn Asp Leu Ser Ala Leu Asp Leu Arg Thr Lys Ser Thr Lys Gln Leu  
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Ala Gln Asn Val Thr Ser Phe Asp Val Thr Asn Ser Gln Leu Ala Val  
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Met Glu Lys Gln Phe Glu Phe Ser Leu Pro Ser Glu Leu Glu Glu Leu  
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Pro Val Glu Glu Tyr Ser Pro Leu Ser Val Thr Ile Leu Ser Pro Gln  
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Val Ser Tyr Asp Gln Lys Met Tyr Ile Ile Lys His Ile Asp Gly Ser  
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Ala Ser Phe Gln Glu Thr Phe Asp Ile Thr Pro Pro Phe Gly Gln Ile  
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Val Arg Phe Pro Tyr Met Tyr Lys Val Thr Leu Ser Gly Leu Ile Glu  
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Pro Asp Ala Asn Val Asn Val Leu Ala Ser Ser Cys Ser Ser Glu Val  
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Ser Ile Trp Asp Ser Lys Gln Val Ile Glu Pro Ser Gln Asp Ser Glu  
 305 310 315 320

Arg Ala Val Leu Pro Ile Ser Glu Glu Thr Asp Lys Asp Thr Asn Pro  
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 340 345 350

Cys Ser Gly Val Asp Thr Ile Glu Arg Leu Pro Leu Val Tyr Ile Leu  
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Ile Lys Ser Gly His Tyr Ser Ile Asn Leu Glu Ser Leu Glu His Glu  
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Gln Glu Glu Lys Lys Lys Asn Asn Glu Ser Ser Lys Ala Leu Ser Glu  
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Gly Ala Pro Ser Phe Gly Ser Ser Ala Phe Lys Ile Asp Leu Pro Ser  
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Asp Pro Ala Ser Ala Lys Pro Val Phe Gly Lys Pro Ala Phe Gly Ala  
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Phe Gly Ala Pro Ser Phe Gly Ser Gly Lys Ser Ser Val Glu Ser Pro
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Ala Ser Gly Ser Ala Phe Gly Lys Pro Ser Phe Gly Thr Pro Ser Phe
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Gly Ser Gly Asn Ser Ser Val Glu Pro Pro Ala Ser Gly Ser Ala Phe
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Gly Lys Pro Ser Phe Gly Thr Pro Ser Phe Gly Ser Gly Asn Ser Ser
    580                      585                      590

Ala Glu Pro Pro Ala Ser Gly Ser Ala Phe Gly Lys Pro Ser Phe Gly
    595                      600                      605

Thr Ser Ala Phe Gly Thr Ala Ser Ser Asn Glu Thr Asn Ser Gly Ser
    610                      615                      620

Ile Phe Gly Lys Ala Ala Phe Gly Ser Ser Ser Phe Ala Pro Ala Asn
    625                      630                      635                      640

Asn Glu Leu Phe Gly Ser Asn Phe Thr Ile Ser Lys Pro Thr Val Asp
                      645                      650                      655

Ser Pro Lys Glu Val Asp Ser Thr Ser Pro Phe Pro Ser Ser Gly Asp
                      660                      665                      670

Gln Ser Glu Asp Glu Ser Lys Ser Asp Val Asp Ser Ser Ser Thr Pro
    675                      680                      685

Phe Gly Thr Lys Pro Asn Thr Ser Thr Lys Pro Lys Thr Asn Ala Phe
    690                      695                      700

Asp Phe Gly Ser Ser Ser Phe Gly Ser Gly Phe Ser Lys Ala Leu Glu
    705                      710                      715                      720

Ser Val Gly Ser Asp Thr Thr Phe Lys Phe Gly Thr Gln Ala Ser Pro
                      725                      730                      735

Phe Ser Ser Gln Leu Gly Asn Lys Ser Pro Phe Ser Ser Phe Thr Lys
                      740                      745                      750

Asp Asp Thr Glu Asn Gly Ser Leu Ser Lys Gly Ser Thr Ser Glu Ile
    755                      760                      765

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Asn Asp Asp Asn Glu Glu His Glu Ser Asn Gly Pro Asn Val Ser Gly  
 770 775 780

Asn Asp Leu Thr Asp Ser Thr Val Glu Gln Thr Ser Ser Thr Arg Leu  
 785 790 795 800

Pro Glu Thr Pro Ser Asp Glu Asp Gly Glu Val Val Glu Glu Glu Ala  
 805 810 815

Gln Lys Ser Pro Ile Gly Lys Leu Thr Glu Thr Ile Lys Lys Ser Ala  
 820 825 830

Asn Ile Asp Met Ala Gly Leu Lys Asn Pro Val Phe Gly Asn His Val  
 835 840 845

Lys Ala Lys Ser Glu Ser Pro Phe Ser Ala Phe Ala Thr Asn Ile Thr  
 850 855 860

Lys Pro Ser Ser Thr Thr Pro Ala Phe Ser Phe Gly Asn Ser Thr Met  
 865 870 875 880

Asn Lys Ser Asn Thr Ser Thr Val Ser Pro Met Glu Glu Ala Asp Thr  
 885 890 895

Lys Glu Thr Ser Glu Lys Gly Pro Ile Thr Leu Lys Ser Val Glu Asn  
 900 905 910

Pro Phe Leu Pro Ala Lys Glu Glu Arg Thr Gly Glu Ser Ser Lys Lys  
 915 920 925

Asp His Asn Asp Asp Pro Lys Asp Gly Tyr Val Ser Gly Ser Glu Ile  
 930 935 940

Ser Val Arg Thr Ser Glu Ser Ala Phe Asp Thr Thr Ala Asn Glu Glu  
 945 950 955 960

Ile Pro Lys Ser Gln Asp Val Asn Asn His Glu Lys Ser Glu Thr Asp  
 965 970 975

Pro Lys Tyr Ser Gln His Ala Val Val Asp His Asp Asn Lys Ser Lys  
 980 985 990

Glu Met Asn Glu Thr Ser Lys Asn Asn Glu Arg Ser Gly Gln Pro Asn  
 995 1000 1005

His Gly Val Gln Gly Asp Gly Ile Ala Leu Lys Lys Asp Asn Glu Lys  
 1010 1015 1020



Glu Asn Phe Asp Ser Asn Met Ala Ile Lys Gln Phe Glu Asp His Gln  
 1025 1030 1035 1040  
 Ser Ser Glu Glu Asp Ala Ser Glu Lys Asp Ser Arg Gln Ser Ser Glu  
 1045 1050 1055  
 Val Lys Glu Ser Asp Asp Asn Met Ser Leu Asn Ser Asp Arg Asp Glu  
 1060 1065 1070  
 Ser Ile Ser Glu Ser Tyr Asp Lys Leu Glu Asp Ile Asn Thr Asp Glu  
 1075 1080 1085  
 Leu Pro His Gly Gly Glu Ala Phe Lys Ala Arg Glu Val Ser Ala Ser  
 1090 1095 1100  
 Ala Asp Phe Asp Val Gln Thr Ser Leu Glu Asp Asn Tyr Ala Glu Ser  
 1105 1110 1115 1120  
 Gly Ile Gln Thr Asp Leu Ser Glu Ser Ser Lys Glu Asn Glu Val Gln  
 1125 1130 1135  
 Thr Asp Ala Ile Pro Val Lys His Asn Ser Thr Gln Thr Val Lys Lys  
 1140 1145 1150  
 Glu Ala Val Asp Asn Gly Leu Gln Thr Glu Pro Val Glu Thr Cys Asn  
 1155 1160 1165  
 Phe Ser Val Gln Thr Phe Glu Gly Asp Glu Asn Tyr Leu Ala Glu Gln  
 1170 1175 1180  
 Cys Lys Pro Lys Gln Leu Lys Glu Tyr Tyr Thr Ser Ala Lys Val Ser  
 1185 1190 1195 1200  
 Asn Ile Pro Phe Val Ser Gln Asn Ser Thr Leu Arg Leu Ile Glu Ser  
 1205 1210 1215  
 Thr Phe Gln Thr Val Glu Ala Glu Phe Thr Val Leu Met Glu Asn Ile  
 1220 1225 1230  
 Arg Asn Met Asp Thr Phe Phe Thr Asp Gln Ser Ser Ile Pro Leu Val  
 1235 1240 1245  
 Lys Arg Thr Val Arg Ser Ile Asn Asn Leu Tyr Thr Trp Arg Ile Pro  
 1250 1255 1260  
 Glu Ala Glu Ile Leu Leu Asn Ile Gln Asn Asn Ile Lys Cys Glu Gln  
 1265 1270 1275 1280

Met Gln Ile Thr Asn Ala Asn Ile Gln Asp Leu Lys Glu Lys Val Thr  
1285 1290 1295

Asp Tyr Val Arg Lys Asp Ile Ala Gln Ile Thr Glu Asp Val Ala Asn  
1300 1305 1310

Ala Lys Glu Glu Tyr Leu Phe Leu Met His Phe Asp Asp Ala Ser Ser  
1315 1320 1325

Gly Tyr Val Lys Asp Leu Ser Thr His Gln Phe Arg Met Gln Lys Thr  
1330 1335 1340

Leu Arg Gln Lys Leu Phe Asp Val Ser Ala Lys Ile Asn His Thr Glu  
1345 1350 1355 1360

Glu Leu Leu Asn Ile Leu Lys Leu Phe Thr Val Lys Asn Lys Arg Leu  
1365 1370 1375

Asp Asp Asn Pro Leu Val Ala Lys Leu Ala Lys Glu Ser Leu Ala Arg  
1380 1385 1390

Asp Gly Leu Leu Lys Glu Ile Lys Leu Leu Arg Glu Gln Val Ser Arg  
1395 1400 1405

Leu Gln Leu Glu Glu Lys Gly Lys Lys Ala Ser Ser Phe Asp Ala Ser  
1410 1415 1420

Ser Ser Ile Thr Lys Asp Met Lys Gly Phe Lys Val Val Glu Val Gly  
1425 1430 1435 1440

Leu Ala Met Asn Thr Lys Lys Gln Ile Gly Asp Phe Phe Lys Asn Leu  
1445 1450 1455

Asn Met Ala Lys  
1460

<210> 137  
<211> 1321  
<212> DNA  
<213> *Saccharomyces cerevisiae*

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ttgactgcaa tttgagttta ttacatccgt acattactaa gatgtatggt ttttctattt 180

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agtcttgaga ttgagaggtg gtatcattga accatctttg aaagcttttg cttccaagta 1200
caactgtgac aaatctgttt gccgtaagtg ttatgctaga ttgccaccaa gagctaccaa 1260
ctgtagaaag agaaagtgtg gtcacaccaa ccaattgcgt ccaaagaaga agttaaagt 1320
a 1321

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&lt;210&gt; 138

&lt;211&gt; 128

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 138

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Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
  1             5             10             15

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Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
      20             25             30

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Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
      35             40             45

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Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
      50             55             60

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Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ile Ile Glu Pro
      65             70             75             80

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Ser Leu Lys Ala Leu Ala Ser Lys Tyr Asn Cys Asp Lys Ser Val Cys
      85             90             95

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Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr Asn Cys Arg Lys
      100            105            110

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Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys Lys Lys Leu Lys  
 115 120 125

<210> 139  
 <211> 2216  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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 attgagagcg gtacatcttc tgatccagac accaaaaagg ttaaagagag tccagcaaat 180  
 gatcaagctt ccaacgagtg atgtaatat aaacaatgta attatataaa tatgaaacat 240  
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 ccgtactagt agttaagtat gaacaaattt tgggtttatt tgccattttt tttcacgcgg 360  
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 ccatacgaaga taaaggaacg taagtttgtc aattcaacct cacattttca acgcacatta 480  
 agcacttggg tcgtggagaa atgaatgatc ctctgtaaatt ttagcgggt gatccgtaca 540  
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 ccataacgga ctttcagcat acactagatg tttatatctt cgggaaaaag ggtgtagaaa 1260  
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 ggagaccctc agggcgagga aattttatca aatccttcaa ccttcgaatt agtcatgact 1380  
 tcaaatgtat cctggagata ggttcaagta gagatttagg ttggtgtccc atagtgaata 1440  
 aaaagactca caaaaaatgt ggctctccca ttaacatatc tcttcataag tgttgcgatt 1500  
 accatagaga agtgcaattt cgtggaacaa gtgctaaaag aattgaatta aatgggtgggt 1560  
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 aatttcagaa tccagatatg ctggcaaac tagacaataa aagaaggaaa ataatagaaa 1800  
 ctaagaaatc gacagactg agccgcgaac taggcaaaat tatgagaagg agggaaatcca 1860  
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aagtactcaa gtcttctgta tcaggagcg aacctaagaa caacttactc ggtaaaaaaa 2040  
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<210> 140

<211> 571

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 140

Met Asn Asp Pro Arg Glu Ile Leu Ala Val Asp Pro Tyr Asn Asn Ile  
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Thr Ser Asp Glu Glu Asp Glu Gln Ala Ile Ala Arg Glu Leu Glu Phe  
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Met Glu Arg Lys Arg Gln Ala Leu Val Glu Arg Leu Lys Arg Lys Gln  
 35 40 45

Glu Phe Lys Lys Pro Gln Asp Pro Asn Phe Glu Ala Ile Glu Val Pro  
 50 55 60

Gln Ser Pro Thr Lys Asn Arg Val Lys Val Gly Ser His Asn Ala Thr  
 65 70 75 80

Gln Gln Gly Thr Lys Phe Glu Gly Ser Asn Ile Asn Glu Val Arg Leu  
 85 90 95

Ser Gln Leu Gln Gln Gln Pro Lys Pro Pro Ala Ser Thr Thr Thr Tyr  
 100 105 110

Phe Met Glu Lys Phe Gln Asn Ala Lys Lys Asn Glu Asp Lys Gln Ile  
 115 120 125

Ala Lys Phe Glu Ser Met Met Asn Ala Arg Val His Thr Phe Ser Thr  
 130 135 140

Asp Glu Lys Lys Tyr Val Pro Ile Ile Thr Asn Glu Leu Glu Ser Phe  
 145 150 155 160

Ser Asn Leu Trp Val Lys Lys Arg Tyr Ile Pro Glu Asp Asp Leu Lys  
 165 170 175

Arg Ala Leu His Glu Ile Lys Ile Leu Arg Leu Gly Lys Leu Phe Ala  
 180 185 190

Lys Ile Arg Pro Pro Lys Phe Gln Glu Pro Glu Tyr Ala Asn Trp Ala  
 195 200 205  
 Thr Val Gly Leu Ile Ser His Lys Ser Asp Ile Lys Phe Thr Ser Ser  
 210 215 220  
 Glu Lys Pro Val Lys Phe Phe Met Phe Thr Ile Thr Asp Phe Gln His  
 225 230 235 240  
 Thr Leu Asp Val Tyr Ile Phe Gly Lys Lys Gly Val Glu Arg Tyr Tyr  
 245 250 255  
 Asn Leu Arg Leu Gly Asp Val Ile Ala Ile Leu Asn Pro Glu Val Leu  
 260 265 270  
 Pro Trp Arg Pro Ser Gly Arg Gly Asn Phe Ile Lys Ser Phe Asn Leu  
 275 280 285  
 Arg Ile Ser His Asp Phe Lys Cys Ile Leu Glu Ile Gly Ser Ser Arg  
 290 295 300  
 Asp Leu Gly Trp Cys Pro Ile Val Asn Lys Lys Thr His Lys Lys Cys  
 305 310 315 320  
 Gly Ser Pro Ile Asn Ile Ser Leu His Lys Cys Cys Asp Tyr His Arg  
 325 330 335  
 Glu Val Gln Phe Arg Gly Thr Ser Ala Lys Arg Ile Glu Leu Asn Gly  
 340 345 350  
 Gly Tyr Ala Leu Gly Ala Pro Thr Lys Val Asp Ser Gln Pro Ser Leu  
 355 360 365  
 Tyr Lys Ala Lys Gly Glu Asn Gly Phe Asn Ile Ile Lys Gly Thr Arg  
 370 375 380  
 Lys Arg Leu Ser Glu Glu Glu Glu Arg Leu Lys Lys Ser Ser His Asn  
 385 390 395 400  
 Phe Thr Asn Ser Asn Ser Ala Lys Ala Phe Phe Asp Glu Lys Phe Gln  
 405 410 415  
 Asn Pro Asp Met Leu Ala Asn Leu Asp Asn Lys Arg Arg Lys Ile Ile  
 420 425 430  
 Glu Thr Lys Lys Ser Thr Ala Leu Ser Arg Glu Leu Gly Lys Ile Met  
 435 440 445

Arg Arg Arg Glu Ser S r Gly Leu Glu Asp Lys Ser Val Gly Glu Arg  
 450 455 460  
 Gln Lys Met Lys Arg Thr Thr Glu Ser Ala Leu Gln Thr Gly Leu Ile  
 465 470 475 480  
 Gln Arg Leu Gly Phe Asp Pro Thr His Gly Lys Ile Ser Gln Val Leu  
 485 490 495  
 Lys Ser Ser Val Ser Gly Ser Glu Pro Lys Asn Asn Leu Leu Gly Lys  
 500 505 510  
 Lys Lys Thr Val Ile Asn Asp Leu Leu His Tyr Lys Lys Glu Lys Val  
 515 520 525  
 Ile Leu Ala Pro Ser Lys Asn Glu Trp Phe Lys Lys Arg Ser His Arg  
 530 535 540  
 Glu Glu Val Trp Gln Lys His Phe Gly Ser Lys Glu Thr Lys Glu Thr  
 545 550 555 560  
 Ser Asp Gly Ser Ala Ser Asp Leu Glu Ile Ile  
 565 570

&lt;210&gt; 141

&lt;211&gt; 1133

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 141

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 aaatgactta ctatgaaaag acacctttga ttcgtcaatt tttgaacaat ggtaagacaa 180  
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 gaatcgggca tttgataagg aagagtaatg aagaagcgt aagcgagggt tctgggaagc 300  
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 aaaaaggtag tccagttact cttgaaaaat tgacaagtgt tgcaacttct ttggcctccc 840  
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<210> 142

<211> 210

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 142

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Phe Asp Asn Glu Thr Ile Trp Glu Gly His Ser Thr Ile Val Asp Glu  
 20 25 30

Ile Ile Glu Gln Leu Lys Glu Asn Asp Ile Ser Leu Pro Arg Val Lys  
 35 40 45

Ala Leu Val Cys Ser Val Gly Gly Gly Gly Leu Phe Ser Gly Ile Ile  
 50 55 60

Lys Gly Leu Asp Arg Asn Gln Leu Ala Glu Lys Ile Pro Val Val Ala  
 65 70 75 80

Val Glu Thr Ala Gly Cys Asp Val Leu Asn Lys Ser Leu Lys Lys Gly  
 85 90 95

Ser Pro Val Thr Leu Glu Lys Leu Thr Ser Val Ala Thr Ser Leu Ala  
 100 105 110

Ser Pro Tyr Ile Ala Ser Phe Ala Phe Glu Ser Phe Asn Lys Tyr Gly  
 115 120 125

Cys Lys Ser Val Val Leu Ser Asp Gln Asp Val Leu Ala Thr Cys Leu  
 130 135 140

Arg Tyr Ala Asp Asp Tyr Asn Phe Ile Val Glu Pro Ala Cys Gly Ala  
 145 150 155 160

Ser Leu His Leu Cys Tyr His Pro Glu Ile Leu Glu Asp Ile Leu Glu  
 165 170 175

Gln Lys Ile Tyr Glu Asp Asp Ile Val Ile Ile Ile Ala Cys Gly Gly  
 180 185 190

Ser Cys Met Thr Tyr Glu Asp Leu Val Lys Ala Ser Ser Thr Leu Asn



195

200

205

Val Ser  
210

&lt;210&gt; 143

&lt;211&gt; 2549

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 143

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<210> 144

<211> 682

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 144

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Val Val Leu Tyr Ala Leu Phe Val Val Ile Leu Pro Leu Gln Asn Ser  
 20 25 30

Phe His Ser Ser Asn Val Leu Val Arg Gly Ala Asp Asp Val Glu Asn  
 35 40 45

Tyr Gly Thr Val Ile Gly Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val  
 50 55 60

Ala Val Met Lys Asn Gly Lys Thr Glu Ile Leu Ala Asn Glu Gln Gly  
 65 70 75 80

Asn Arg Ile Thr Pro Ser Tyr Val Ala Phe Thr Asp Asp Glu Arg Leu  
 85 90 95

Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Ala Asn Pro Gln Asn Thr  
 100 105 110

Ile Phe Asp Ile Lys Arg Leu Ile Gly Leu Lys Tyr Asn Asp Arg Ser  
 115 120 125

Val Gln Lys Asp Ile Lys His Leu Pro Phe Asn Val Val Asn Lys Asp  
 130 135 140

Gly Lys Pro Ala Val Glu Val Ser Val Lys Gly Glu Lys Lys Val Phe  
 145 150 155 160

Thr Pro Glu Glu Ile Ser Gly Met Ile Leu Gly Lys Met Lys Gln Ile  
 165 170 175

Ala Glu Asp Tyr Leu Gly Thr Lys Val Thr His Ala Val Val Thr Val  
180 185 190

Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly  
195 200 205

Thr Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr Ala  
210 215 220

Ala Ala Ile Ala Tyr Gly Leu Asp Lys Ser Asp Lys Glu His Gln Ile  
225 230 235 240

Ile Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Ser  
245 250 255

Ile Glu Asn Gly Val Phe Glu Val Gln Ala Thr Ser Gly Asp Thr His  
260 265 270

Leu Gly Gly Glu Asp Phe Asp Tyr Lys Ile Val Arg Gln Leu Ile Lys  
275 280 285

Ala Phe Lys Lys Lys His Gly Ile Asp Val Ser Asp Asn Asn Lys Ala  
290 295 300

Leu Ala Lys Leu Lys Arg Glu Ala Glu Lys Ala Lys Arg Ala Leu Ser  
305 310 315 320

Ser Gln Met Ser Thr Arg Ile Glu Ile Asp Ser Phe Val Asp Gly Ile  
325 330 335

Asp Leu Ser Glu Thr Leu Thr Arg Ala Lys Phe Glu Glu Leu Asn Leu  
340 345 350

Asp Leu Phe Lys Lys Thr Leu Lys Pro Val Glu Lys Val Leu Gln Asp  
355 360 365

Ser Gly Leu Glu Lys Lys Asp Val Asp Asp Ile Val Leu Val Gly Gly  
370 375 380

Ser Thr Arg Ile Pro Lys Val Gln Gln Leu Leu Glu Ser Tyr Phe Asp  
385 390 395 400

Gly Lys Lys Ala Ser Lys Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr  
405 410 415

Gly Ala Ala Val Gln Ala Gly Val Leu Ser Gly Glu Glu Gly Val Glu  
420 425 430

Asp Ile Val Leu Leu Asp Val Asn Ala Leu Thr Leu Gly Ile Glu Thr  
435 440 445

Thr Gly Gly Val Met Thr Pro Leu Ile Lys Arg Asn Thr Ala Ile Pro  
450 455 460

Thr Lys Lys Ser Gln Ile Phe Ser Thr Ala Val Asp Asn Gln Pro Thr  
465 470 475 480

Val Met Ile Lys Val Tyr Glu Gly Glu Arg Ala Met Ser Lys Asp Asn  
485 490 495

Asn Leu Leu Gly Lys Phe Glu Leu Thr Gly Ile Pro Pro Ala Pro Arg  
500 505 510

Gly Val Pro Gln Ile Glu Val Thr Phe Ala Leu Asp Ala Asn Gly Ile  
515 520 525

Leu Lys Val Ser Ala Thr Asp Lys Gly Thr Gly Lys Ser Glu Ser Ile  
530 535 540

Thr Ile Thr Asn Asp Lys Gly Arg Leu Thr Gln Glu Glu Ile Asp Arg  
545 550 555 560

Met Val Glu Glu Ala Glu Lys Phe Ala Ser Glu Asp Ala Ser Ile Lys  
565 570 575

Ala Lys Val Glu Ser Arg Asn Lys Leu Glu Asn Tyr Ala His Ser Leu  
580 585 590

Lys Asn Gln Val Asn Gly Asp Leu Gly Glu Lys Leu Glu Glu Glu Asp  
595 600 605

Lys Glu Thr Leu Leu Asp Ala Ala Asn Asp Val Leu Glu Trp Leu Asp  
610 615 620

Asp Asn Phe Glu Thr Ala Ile Ala Glu Asp Phe Asp Glu Lys Phe Glu  
625 630 635 640

Ser Leu Ser Lys Val Ala Tyr Pro Ile Thr Ser Lys Leu Tyr Gly Gly  
645 650 655

Ala Asp Gly Ser Gly Ala Ala Asp Tyr Asp Asp Glu Asp Glu Asp Asp  
660 665 670

Asp Gly Asp Tyr Phe Glu His Asp Glu Leu  
675 680

<210> 145  
 <211> 1253  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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<210> 146  
 <211> 250  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 146  
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 Pro Thr Gly Gln Val Met Ala Tyr Gly Met Asn Asp Thr Asn Lys Ser  
 35 40 45  
 Leu Thr Gly Val Ala His Ala Glu Phe Met Gly Ile Asp Gln Ile Lys

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Ala Met Leu Gly Ser Arg Gly Val Val Asp Val Phe Lys Asp Ile Thr		
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Leu Tyr Val Thr Val Glu Pro Cys Ile Met Cys Ala Ser Ala Leu Lys		
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Gln Leu Asp Ile Gly Lys Val Val Phe Gly Cys Gly Asn Glu Arg Phe		
100	105	110
Gly Gly Asn Gly Thr Val Leu Ser Val Asn His Asp Thr Cys Thr Leu		
115	120	125
Val Pro Lys Asn Asn Ser Ala Ala Gly Tyr Glu Ser Ile Pro Gly Ile		
130	135	140
Leu Arg Lys Glu Ala Ile Met Leu Leu Arg Tyr Phe Tyr Val Arg Gln		
145	150	155 160
Asn Glu Arg Ala Pro Lys Pro Arg Ser Lys Ser Asp Arg Val Leu Asp		
	165	170 175
Lys Asn Thr Phe Pro Pro Met Glu Trp Ser Lys Tyr Leu Asn Glu Glu		
	180	185 190
Ala Phe Ile Glu Thr Phe Gly Asp Asp Tyr Arg Thr Cys Phe Ala Asn		
195	200	205
Lys Val Asp Leu Ser Ser Asn Ser Val Asp Trp Asp Leu Ile Asp Ser		
210	215	220
His Gln Asp Asn Ile Ile Gln Glu Leu Glu Glu Gln Cys Lys Met Phe		
225	230	235 240
Lys Phe Asn Val His Lys Lys Ser Lys Val		
	245	250

&lt;210&gt; 147

&lt;211&gt; 3167

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 147

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<210> 148

<211> 888

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 148

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 20 25 30

Leu Ser Glu Asn Asp Gly Asp Val Ser Pro Ser Val Leu Lys Gln Lys  
 35 40 45

Glu Ile Ser Val Asp Asp Met Asp Met Ile Ser Leu Pro Thr Glu Phe  
 50 55 60

Asp Arg Gln Met Val Leu Gly Ser Pro Met Phe Phe Asp Leu Glu Asp  
 65 70 75 80

Glu Glu Asn Lys Ile Asp Pro Leu Pro Ser Val Ser His His Tyr Gly  
 85 90 95

Asn Gly Glu Ser Asp Ser Phe Val Ser Ser Tyr Thr Pro Ser Asn Leu  
 100 105 110

Lys Thr Gly Glu Glu Thr Lys Asp Leu Phe Ile Asn Pro Phe Glu Leu  
 115 120 125

Val Ser Gln Met Arg Lys Arg Tyr Ile Ala Ala Ser Lys Gln Asp Gly  
 130 135 140

Ile Ser Asn Ile Lys Asn Asp Thr Glu Lys Trp Phe Leu Tyr Pro Lys  
 145 150 155 160

Pro Leu Pro Lys Phe Trp Arg Phe Glu Asp Asp Lys Arg Phe Gln Asp  
 165 170 175

Pro Ser Asp Ser Asp Leu Asn Asp Asp Gly Asp Ser Thr Gly Thr Gly  
 180 185 190

Ala Ala Thr Pro His Arg His Gly Tyr Tyr Tyr Pro Ser Tyr Phe Thr



~~179~~

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 Trp Asn Ile Gln Ile Ala Arg Ile Phe Pro Lys Leu Phe Lys Glu Asn  
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 Val Val Ser Asn Phe Gln Glu Phe Leu Asp Leu Ile Phe Asn Pro Leu  
                     530                      535                      540  
 Phe Thr Leu Glu Lys Glu Gln Leu Pro Ile Asp Ser Ser Val Asn Thr  
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 Asp Ile Ile Gly Leu Gln Phe Phe Leu Ser Asn Val Cys Ser Met Asp  
                     565                      570                      575  
 Leu Val Ile Lys Glu Ser Asp Glu Tyr Tyr Trp Lys Glu Phe Thr Asp  
                     580                      585                      590  
 Met Asn Cys Lys Pro Lys Phe Trp Thr Ala Gln Gly Asp Asn Pro Thr  
                     595                      600                      605  
 Val Ala His Tyr Met Tyr Tyr Ile Tyr Lys Ser Leu Ala Lys Val Asn  
                     610                      615                      620  
 Phe Leu Arg Ser Gln Asn Leu Gln Asn Thr Ile Thr Leu Arg Asn Tyr  
 625                      630                      635                      640  
 Cys Ser Pro Leu Ser Ser Arg Thr Ser Gln Phe Gly Val Asp Leu Tyr  
                     645                      650                      655  
 Phe Thr Asp Gln Val Glu Ser Leu Val Cys Asn Leu Leu Leu Cys Asn  
                     660                      665                      670  
 Gly Gly Leu Leu Gln Val Glu Pro Leu Trp Asp Thr Ala Thr Met Ile  
                     675                      680                      685  
 Gln Tyr Leu Phe Tyr Leu Phe Gln Ile Pro Ile Leu Ala Ala Pro Leu  
                     690                      695                      700  
 Ser Ser Val Ser Leu Leu Asn Ser Gln Lys Ser Thr Phe Leu Lys Asn

705		710		715		720
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	725		730		735	
Lys Ile Asn Pro Ser Arg Asp Ile Thr Val Gly Glu Gln Arg Ser Tyr						
	740		745		750	
Glu Thr Asn Pro Phe Met Lys Met Phe Lys Met Gly Leu Lys Ile Ser						
	755		760		765	
Leu Ser Ser Lys Ser Ile Leu Tyr Asn Ser Ser Tyr Thr Leu Glu Pro						
	770		775		780	
Leu Ile Glu Glu Tyr Ser Val Ala Ala Ser Ile Tyr Leu Leu Asn Pro						
	785		790		795	800
Thr Asp Leu Cys Glu Leu Ser Arg Thr Ser Val Leu Ser Ser Gly Tyr						
	805		810		815	
Glu Gly Trp Tyr Lys Ala His Trp Ile Gly Val Gly Val Lys Lys Ala						
	820		825		830	
Pro Tyr Phe Glu Glu Asn Val Gly Gly Ile Asp Asn Trp Tyr Asp Thr						
	835		840		845	
Ala Lys Asp Thr Ser Ile Lys His Asn Val Pro Met Ile Arg Arg Arg						
	850		855		860	
Tyr Arg Lys Glu Thr Leu Asp Gln Glu Trp Asn Phe Val Arg Asp His						
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Phe Gly Val Ile Asn Ser Ile Trp						
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&lt;210&gt; 149

&lt;211&gt; 3146

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 149

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&lt;210&gt; 150

&lt;211&gt; 881

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 150

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His Asn Lys Phe Arg Ala Leu His Val Asp Thr Ala Pro Leu Thr Trp  
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Ser Asp Thr Leu Ala Thr Tyr Ala Gln Asn Tyr Ala Asp Gln Tyr Asp  
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Cys Ser Gly Val Leu Thr His Ser Asp Gly Pro Tyr Gly Glu Asn Leu  
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Ala Leu Gly Tyr Thr Asp Thr Gly Ala Val Asp Ala Trp Tyr Gly Glu  
 85 90 95

Ile Ser Lys Tyr Asn Tyr Ser Asn Pro Gly Phe Ser Glu Ser Thr Gly  
 100 105 110

His Phe Thr Gln Val Val Trp Lys Ser Thr Ala Glu Ile Gly Cys Gly  
 115 120 125

Tyr Lys Tyr Cys Gly Thr Thr Trp Asn Asn Tyr Ile Val Cys Ser Tyr  
 130 135 140

Asn Pro Pro Gly Asn Tyr Leu Gly Glu Phe Ala Glu Glu Val Glu Pro  
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Leu Ile Ser Thr Val Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser  
 165 170 175

Thr Thr Ser Asp Thr Val Ser Thr Ile Ser Ser Ser Ile Met Pro Ala  
 180 185 190

Val Ala Gln Gly Tyr Thr Thr Thr Val Ser Ser Ala Ala Ser Ser Ser  
 195 200 205

Ser Leu Lys Ser Thr Thr Ile Asn Pro Ala Lys Thr Ala Thr Leu Thr

210	215	220
Ala Ser Ser Ser Thr Val Ile Thr Ser Ser Thr Glu Ser Val Gly Ser		
225	230	235 240
Ser Thr Val Ser Ser Ala Ser Ser Ser Ser Val Thr Thr Ser Tyr Ala		
	245	250 255
Thr Ser Ser Ser Thr Val Val Ser Ser Asp Ala Thr Ser Ser Thr Thr		
	260	265 270
Thr Thr Ser Ser Val Ala Thr Ser Ser Ser Thr Thr Ser Ser Asp Pro		
	275	280 285
Thr Ser Ser Thr Ala Ala Ala Ser Ser Ser Asp Pro Ala Ser Ser Ser		
	290	295 300
Ala Ala Ala Ser Ser Ser Ala Ser Thr Glu Asn Ala Ala Ser Ser Ser		
305	310	315 320
Ser Ala Ile Ser Ser Ser Ser Ser Met Val Ser Ala Pro Leu Ser Ser		
	325	330 335
Thr Leu Thr Thr Ser Thr Ala Ser Ser Arg Ser Val Thr Ser Asn Ser		
	340	345 350
Val Asn Ser Val Lys Phe Ala Asn Thr Thr Val Phe Ser Ala Gln Thr		
	355	360 365
Thr Ser Ser Val Ser Ala Ser Leu Ser Ser Ser Val Ala Ala Asp Asp		
	370	375 380
Ile Gln Gly Ser Thr Ser Lys Glu Ala Thr Ser Ser Val Ser Glu His		
385	390	395 400
Thr Ser Ile Val Thr Ser Ala Thr Asn Ala Ala Gln Tyr Ala Thr Arg		
	405	410 415
Leu Gly Ser Ser Ser Arg Ser Ser Ser Gly Ala Val Ser Ser Ser Ala		
	420	425 430
Val Ser Gln Ser Val Leu Asn Ser Val Ile Ala Val Asn Thr Asp Val		
	435	440 445
Ser Val Thr Ser Val Ser Ser Thr Ala His Thr Thr Lys Asp Thr Ala		
	450	455 460
Thr Thr Ser Val Thr Ala Ser Glu Ser Ile Thr Ser Glu Thr Ala Gln		

465	470	475	480
Ala Ser Ser Ser Thr Glu Lys Asn Ile Ser Asn Ser Ala Ala Thr Ser			
485	490	495	
Ser Ser Ile Tyr Ser Asn Ser Ala Ser Val Ser Gly His Gly Val Thr			
500	505	510	
Tyr Ala Ala Glu Tyr Ala Ile Thr Ser Glu Gln Ser Ser Ala Leu Ala			
515	520	525	
Thr Ser Val Pro Ala Thr Asn Cys Ser Ser Ile Val Lys Thr Thr Thr			
530	535	540	
Leu Glu Asn Ser Ser Thr Thr Thr Ile Thr Ala Ile Thr Lys Ser Thr			
545	550	555	560
Thr Thr Leu Ala Thr Thr Ala Asn Asn Ser Thr Arg Ala Ala Thr Ala			
565	570	575	
Val Thr Ile Asp Pro Thr Leu Asp Pro Thr Asp Asn Ser Ala Ser Pro			
580	585	590	
Thr Asp Asn Ala Lys His Thr Ser Thr Tyr Gly Ser Ser Ser Thr Gly			
595	600	605	
Ala Ser Leu Asp Ser Leu Arg Thr Thr Thr Ser Ile Ser Val Ser Ser			
610	615	620	
Asn Thr Thr Gln Leu Val Ser Thr Cys Thr Ser Glu Ser Asp Tyr Ser			
625	630	635	640
Asp Ser Pro Ser Phe Ala Ile Ser Thr Ala Thr Thr Thr Glu Ser Asn			
645	650	655	
Leu Ile Thr Asn Thr Ile Thr Ala Ser Cys Ser Thr Asp Ser Asn Phe			
660	665	670	
Pro Thr Ser Ala Ala Ser Ser Thr Asp Glu Thr Ala Phe Thr Arg Thr			
675	680	685	
Ile Ser Thr Ser Cys Ser Thr Leu Asn Gly Ala Ser Thr Gln Thr Ser			
690	695	700	
Glu Leu Thr Thr Ser Pro Met Lys Thr Asn Thr Val Val Pro Ala Ser			
705	710	715	720
Ser Phe Pro Ser Thr Thr Thr Thr Cys Leu Glu Asn Asp Asp Thr Ala			

725

730

735

Phe Ser Ser Ile Tyr Thr Glu Val Asn Ala Ala Thr Ile Ile Asn Pro  
 740 745 750

Gly Glu Thr Ser Ser Leu Ala Ser Asp Phe Ala Thr Ser Glu Lys Pro  
 755 760 765

Asn Glu Pro Thr Ser Val Lys Ser Thr Ser Asn Glu Gly Thr Ser Ser  
 770 775 780

Thr Thr Thr Thr Tyr Gln Gln Thr Val Ala Thr Leu Tyr Ala Lys Pro  
 785 790 795 800

Ser Ser Thr Ser Leu Gly Ala Arg Thr Thr Thr Gly Ser Asn Gly Arg  
 805 810 815

Ser Thr Thr Ser Gln Gln Asp Gly Ser Ala Met His Gln Pro Thr Ser  
 820 825 830

Ser Ile Tyr Thr Gln Leu Lys Glu Gly Thr Ser Thr Thr Ala Lys Leu  
 835 840 845

Ser Ala Tyr Glu Gly Ala Ala Thr Pro Leu Ser Ile Phe Gln Cys Asn  
 850 855 860

Ser Leu Ala Gly Thr Ile Ala Ala Phe Val Val Ala Val Leu Phe Ala  
 865 870 875 880

Phe

&lt;210&gt; 151

&lt;211&gt; 830

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 151

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 gtgaagtgtt gctcaatcta tttgtttccg taggagtgtt attctcaatc gtgttgtctg 180  
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 caatgaagca tcccttcctt aatgatggca gcattccgta ttctcttttg tagggtttcg 300  
 tttgccttca agtggtttgt tcttatttag ctttttcctt taccttaatt tttttctttt 360  
 ctctgaagaa aatgaatgag tttaaagata tagcaattaa aaagtaacag tgaagaaatt 420  
 tctcagatga gcagatggga attaaagaac tatctacaga gctctttact aaattgaatc 480



aataatacat acttacaaac atgtcacaga tagcacaaga aatgacagtg agcttaagaa 540  
acgccaggac acaattggat atgggtcaatc agcagctagc atatttggac agacaagaaa 600  
agcttgctga attgacaaag aaagaactag agtcttatcc aacggacaaa gtatggagat 660  
cttgcggtaa atcgtttatc ttacaggata aatccaaata cgttaatgat ttatcacatg 720  
ccgaaactgt tcttctggat caaagaaaaa cattaagat aaagaagaac tatttagaaa 780  
ctactgttga aaaaacaata gacaatctaa aggcattgat gaagaattaa 830

<210> 152

<211> 109

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 152

Met Ser Gln Ile Ala Gln Glu Met Thr Val Ser Leu Arg Asn Ala Arg  
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Thr Gln Leu Asp Met Val Asn Gln Gln Leu Ala Tyr Leu Asp Arg Gln  
20 25 30

Glu Lys Leu Ala Glu Leu Thr Lys Lys Glu Leu Glu Ser Tyr Pro Thr  
35 40 45

Asp Lys Val Trp Arg Ser Cys Gly Lys Ser Phe Ile Leu Gln Asp Lys  
50 55 60

Ser Lys Tyr Val Asn Asp Leu Ser His Ala Glu Thr Val Leu Leu Asp  
65 70 75 80

Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Glu Thr Thr Val  
85 90 95

Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn  
100 105

<210> 153

<211> 1478

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 153

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atactttgtc cgttgataa gactctagtt ctttcttgt caattcagca agcttttctt 180  
gtctgtccaa atatgctagc tgctgattga ccatatccaa ttgtgtcctg gcgtttctta 240  
agctcactgt catttcttgt gctatctgtg acatgtttgt aagtatgtat tattgattca 300

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atttagtaaa gagctctgta gatagttctt taattcccat ctgctcatct gagaaatttc 360
ttcactgtta ctttttaatt gctatatctt taaactcatt cattttcttc agagaaaaga 420
aaaaaattaa ggtaaaggaa aaggctaaat aagaacaaaa cacttgaagg caaacgaaac 480
cctacaaaag agaatacgga atgctgccat cattaaggaa gggatgcttc attgtgaatt 540
ccataagatt gaaactgccc cgattctact cattaatgc ccagccactg gggacagaca 600
acacgattga gaataacact cctacggaaa caaatagatt gagcaaaact tcacagaagt 660
tttgggaaaa ggtgtcacta aatagggatg ttgagaaagg aaagattgct ctacaattag 720
atggcaggac tataaaaact cctctaggaa atggaattat agttgataat gcaaagtctc 780
tcttagcata cctattaaaa ctggagtggg cgtccctatc cagtctttcc atcaaaaactc 840
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ctggctgtga ccctcaatta gttgcaaaga ttggaggcaa cagtgatgtt ataaaaaatc 960
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aaggaagatt acgcaatgcg caaatgagt tatatatacc catcatcaaa ggaatggaag 1080
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<210> 154

<211> 325

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 154

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Met Leu Pro Ser Leu Arg Lys Gly Cys Phe Ile Val Asn Ser Ile Arg
  1                      5                      10                      15

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Leu Lys Leu Pro Arg Phe Tyr Ser Leu Asn Ala Gln Pro Leu Gly Thr
          20                      25                      30

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Asp Asn Thr Ile Glu Asn Asn Thr Pro Thr Glu Thr Asn Arg Leu Ser
          35                      40                      45

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Lys Thr Ser Gln Lys Phe Trp Glu Lys Val Ser Leu Asn Arg Asp Val
          50                      55                      60

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Glu Lys Gly Lys Ile Ala Leu Gln Leu Asp Gly Arg Thr Ile Lys Thr
          65                      70                      75                      80

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Pro Leu Gly Asn Gly Ile Ile Val Asp Asn Ala Lys Ser Leu Leu Ala
          85                      90                      95

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Tyr Leu Leu Lys Leu Glu Trp Ser Ser Leu Ser Ser Leu Ser Ile Lys
          100                      105                      110

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Thr His Ser Leu Pro Leu Thr Ser Leu Val Ala Arg Cys Ile Asp Leu  
 115 120 125  
 Gln Met Thr Asn Glu Pro Gly Cys Asp Pro Gln Leu Val Ala Lys Ile  
 130 135 140  
 Gly Gly Asn Ser Asp Val Ile Lys Asn Gln Leu Leu Arg Tyr Leu Asp  
 145 150 155 160  
 Thr Asp Thr Leu Leu Val Phe Ser Pro Met Asn Glu Phe Glu Gly Arg  
 165 170 175  
 Leu Arg Asn Ala Gln Asn Glu Leu Tyr Ile Pro Ile Ile Lys Gly Met  
 180 185 190  
 Glu Glu Phe Leu Arg Asn Phe Ser Ser Glu Ser Asn Ile Arg Leu Gln  
 195 200 205  
 Ile Leu Asp Ala Asp Ile His Gly Leu Arg Gly Asn Gln Gln Ser Asp  
 210 215 220  
 Ile Val Lys Asn Ala Ala Lys Lys Tyr Met Ser Ser Leu Ser Pro Trp  
 225 230 235 240  
 Asp Leu Ala Ile Leu Glu Lys Thr Val Leu Thr Thr Lys Ser Phe Ile  
 245 250 255  
 Cys Gly Val Leu Leu Leu Glu Asn Lys Lys Asp Thr Ala Asn Leu Ile  
 260 265 270  
 Pro Ala Leu Lys Thr Asp Met Asp Asn Ile Val Arg Ala Ala Thr Leu  
 275 280 285  
 Glu Thr Ile Phe Gln Val Glu Lys Trp Gly Glu Val Glu Asp Thr His  
 290 295 300  
 Asp Val Asp Lys Arg Asp Ile Arg Arg Lys Ile His Thr Ala Ala Ile  
 305 310 315 320  
 Ala Ala Phe Lys Gln  
 325

<210> 155  
 <211> 2336  
 <212> DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 155

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ggcgaatgttt accattataa tgaaggggac ttggctgcct cttcaaggg atgtagatca 120
agaggtagct gtgctagtga aatagggtcac atgtaccaga aaatcaagaa atcttagatg 180
tgtgtaatat tgcaatttag tttcaaacaa gatccttgta tttatataaa caaagatata 240
atTTTTAAAA aaaaattaga aaaagcaaata ataattcagg tcccacttgg aataatggca 300
ctgtattgat gcattttcct tatgcttagt gacgcgtttt cgcgcgtag tttcaagttt 360
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cgatagaagg tataatatat gcctgtgagg tgtatgacct tgtaccccg cttttacata 600
aaagcaaaac aaagatcatt aatgctgcta aattaattat agaaacgcat ctttcatatt 660
atacaatact caataacatt tcagatatac aagcctatct ttctacttgg cttagggatc 720
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ttttttcaag ctacgattat gctttcgggg ttgcatacaa cttgttaaata tgctctgaat 960
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&lt;210&gt; 156

&lt;211&gt; 611

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 156

Met Glu Ile Phe Lys Glu Glu Glu Glu Glu Ala Phe Ser Ala Ile Glu  
 1 5 10 15

Gly Ile Il Tyr Ala Cys Glu Val Tyr Asp Pro Val Pro Arg His Leu  
 20 25 30

His Lys Ser Lys Thr Lys Ile Ile Asn Ala Ala Lys Leu Ile Ile Glu  
 35 40 45

Thr His Leu Ser Tyr Tyr Thr Ile Leu Asn Asn Ile Ser Asp Ile Gln  
 50 55 60

Ala Tyr Leu Ser Thr Trp Leu Arg Asp Leu Gly Thr Thr Gly Pro Tyr  
 65 70 75 80

Gln Thr Ile Leu Ser Glu Ser Ile Ser Leu Met Phe Asp Arg Thr Val  
 85 90 95

Ser Ile Phe Arg Lys Cys Thr Ile Glu Gly Gly Phe Pro His Leu Ile  
 100 105 110

Ala Arg Leu Tyr Leu Arg Leu Lys Ser Tyr Gln Lys Leu Leu Asn Asp  
 115 120 125

Ala Gly Leu Lys Asn Phe Phe Ser Ser Tyr Asp Tyr Ala Phe Gly Val  
 130 135 140

Ala Tyr Asn Leu Val Asn Cys Ser Glu Tyr Arg Tyr Asp Glu Val His  
 145 150 155 160

Tyr Ile Ser Asn Gly Thr Tyr Ser Leu Val Ala Ser Met Lys Ile Asp  
 165 170 175

Pro Ala Glu Val Ile Lys Arg Glu His Phe Arg Leu Thr Ile Pro Lys  
 180 185 190

Phe Asn Ile Ser Asn Ile Leu Ile Glu Ile Phe His Leu Leu Asp Gly  
 195 200 205

Leu Ala Phe Phe Lys Val Asn Pro Asp Ser Leu Ser Ile Ser Thr Ala  
 210 215 220

Ser Ala Glu Thr Ile Phe Arg Ser Ile Ser Glu Gly Asn His Gln Val  
 225 230 235 240

Leu Glu Leu Gly Arg Ser Leu Met Phe Pro Leu Leu Arg Thr Gly Asp

245

250

255

Phe Glu Ile Cys Arg Ile Asp Asp Ala Gly Ala Val Ile Thr Phe Thr  
 260 265 270

Glu Ala Lys Asp Val Lys Leu Glu Ile Ile Ser Leu Asp Glu Val Ser  
 275 280 285

Trp Val Met Gln Trp Lys Ser Cys Leu Gln Asn Tyr Glu Arg Arg Ala  
 290 295 300

Ala Asn Asp Ser Ser Phe Ile Lys Thr His Leu Gln Phe Lys Lys Ala  
 305 310 315 320

Asn Asn Phe Asn Glu Asp Asn Asn Gly Leu Gly Leu Ile Val Asp Arg  
 325 330 335

Asn Ile Pro Thr Asp Asp Phe Thr Leu Ala Ser Thr Asn Arg Gln Ser  
 340 345 350

Pro Pro Pro Ser Asn Thr Gly Cys Ser Leu His Arg Ser Lys Pro Leu  
 355 360 365

His Ile Pro Leu Ser Ser Val Ile Arg Glu Asp Phe Tyr Asp Ser Ser  
 370 375 380

Leu Asn Glu Arg Ile Ser Lys Asp Gly Asp Ser Ser Cys Glu Ser Phe  
 385 390 395 400

Ser Gly Ala Glu Ser Ile Leu Ser Asp Tyr Asp Phe His Asp Asn Glu  
 405 410 415

Phe Phe Asn Asn Gln Ser Pro His Tyr Phe Ser Glu His Ile Asp Asn  
 420 425 430

Asn Ser Arg Glu Val Val Ile Thr Asp Glu Asn Thr Ile Ile Ser Leu  
 435 440 445

Glu Asn Thr Gln Val Ser Arg Trp Ser Asn Tyr Ser Trp Gln Lys Ile  
 450 455 460

Ser Pro His Gln Leu Gln Val Ser Ile Ile Gln Leu Arg Met Gly Asn  
 465 470 475 480

Phe Ile Val Ala Tyr Asp Ser Asp Tyr Asn Leu His Gln Phe Lys Ile  
 485 490 495

Arg Leu Cys Asp Asp Ile Lys Cys Ile Gln Ser Thr Glu Gln Asp Ile

500                      505                      510  
 Gln Ile Arg Val Pro Leu Gly Ala Ile Met Cys Ser Val Thr Gly Ile  
     515                      520                      525  
 Leu Asn Ile Arg Thr Lys Asp Ala Asp Lys Leu Leu Arg Val Leu Ser  
     530                      535                      540  
 Phe Tyr Thr Thr Asp His Thr Glu Ala Val Ser His Ser Asn Asn Gln  
     545                      550                      555                      560  
 Asp Ala Thr Ala Ser Pro Leu Ser Ser Val Ser Ser Ala Met Asp Leu  
                     565                      570                      575  
 Lys His Ser Leu Gln Lys Cys Ser Ser Thr Ile Met Pro Gln Glu Leu  
                     580                      585                      590  
 Thr Gln Asp Val Ile Gly Ser Lys Ser Asp Leu Ile Ser Asn Ile Arg  
                     595                      600                      605  
 Gln Lys Ile  
     610

&lt;210&gt; 157

&lt;211&gt; 2960

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 157

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agccaaaatt ttttatatga 2960

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&lt;210&gt; 158

&lt;211&gt; 819

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 158

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Met Ser Ser Leu Asp Glu Asp Glu Glu Asp Phe Glu Met Leu Asp Thr
  1                      5                      10                      15

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Glu Asn Leu Gln Phe Met Gly Lys Lys Met Phe Gly Lys Gln Ala Gly
          20                      25                      30

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Glu Asp Glu Ser Asp Asp Phe Ala Ile Gly Gly Ser Thr Pro Thr Asn

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35	40	45
Lys Leu Lys Phe Tyr Pro Tyr Ser Asn Asn Lys Leu Thr Arg Ser Thr		
50	55	60
Gly Thr Leu Asn Leu Ser Leu Ser Asn Thr Ala Leu Ser Glu Ala Asn		
65	70	75
Ser Lys Phe Leu Gly Lys Ile Glu Glu Glu Glu Glu Glu Glu Glu		
85	90	95
Gly Lys Asp Glu Glu Ser Val Asp Ser Arg Ile Lys Arg Trp Ser Pro		
100	105	110
Phe His Glu Asn Glu Ser Val Thr Thr Pro Ile Thr Lys Arg Ser Ala		
115	120	125
Glu Lys Thr Asn Ser Pro Ile Ser Leu Lys Gln Trp Asn Gln Arg Trp		
130	135	140
Phe Pro Lys Asn Asp Ala Arg Thr Glu Asn Thr Ser Ser Ser Ser Ser		
145	150	155
Tyr Ser Val Ala Lys Pro Asn Gln Ser Ala Phe Thr Ser Ser Gly Leu		
165	170	175
Val Ser Lys Met Ser Met Asp Thr Ser Leu Tyr Pro Ala Lys Leu Arg		
180	185	190
Ile Pro Glu Thr Pro Val Lys Lys Ser Pro Leu Val Glu Gly Arg Asp		
195	200	205
His Lys His Val His Leu Ser Ser Ser Lys Asn Ala Ser Ser Ser Leu		
210	215	220
Ser Val Ser Pro Leu Asn Phe Val Glu Asp Asn Asn Leu Gln Glu Asp		
225	230	235
Leu Leu Phe Ser Asp Ser Pro Ser Ser Lys Ala Leu Pro Ser Ile His		
245	250	255
Val Pro Thr Ile Asp Ser Ser Pro Leu Ser Glu Ala Lys Tyr His Ala		
260	265	270
His Asp Arg His Asn Asn Gln Thr Asn Ile Leu Ser Pro Thr Asn Ser		
275	280	285
Leu Val Thr Asn Ser Ser Pro Gln Thr Leu His Ser Asn Lys Phe Lys		

195

290 295 300

Lys Ile Lys Arg Ala Arg Asn Ser Val Ile Leu Lys Asn Arg Glu Leu  
305 310 315 320

Thr Asn Ser Leu Gln Gln Phe Lys Asp Asp Leu Tyr Gly Thr Asp Glu  
325 330 335

Asn Phe Pro Pro Pro Ile Ile Ile Ser Ser His His Ser Thr Arg Lys  
340 345 350

Asn Pro Gln Pro Tyr Gln Phe Arg Gly Arg Tyr Asp Asn Asp Thr Asp  
355 360 365

Glu Glu Ile Ser Thr Pro Thr Arg Arg Lys Ser Ile Ile Gly Ala Thr  
370 375 380

Ser Gln Thr His Arg Glu Ser Arg Pro Leu Ser Leu Ser Ser Ala Ile  
385 390 395 400

Val Thr Asn Thr Thr Ser Ala Glu Thr His Ser Ile Ser Ser Thr Asp  
405 410 415

Ser Ser Pro Leu Asn Ser Lys Arg Arg Leu Ile Ser Ser Asn Lys Leu  
420 425 430

Ser Ala Asn Pro Asp Ser His Leu Phe Glu Lys Phe Thr Asn Val His  
435 440 445

Ser Ile Gly Lys Gly Gln Phe Ser Thr Val Tyr Gln Val Thr Phe Ala  
450 455 460

Gln Thr Asn Lys Lys Tyr Ala Ile Lys Ala Ile Lys Pro Asn Lys Tyr  
465 470 475 480

Asn Ser Leu Lys Arg Ile Leu Leu Glu Ile Lys Ile Leu Asn Glu Val  
485 490 495

Thr Asn Gln Ile Thr Met Asp Gln Glu Gly Lys Glu Tyr Ile Ile Asp  
500 505 510

Tyr Ile Ser Ser Trp Lys Phe Gln Asn Ser Tyr Tyr Ile Met Thr Glu  
515 520 525

Leu Cys Glu Asn Gly Asn Leu Asp Gly Phe Leu Gln Glu Gln Val Ile  
530 535 540

Ala Lys Lys Lys Arg Leu Glu Asp Trp Arg Ile Trp Lys Ile Ile Val

545	550	555	560
Glu Leu Ser Leu Ala Leu Arg Phe Ile His Asp Ser Cys His Ile Val			
565	570	575	
His Leu Asp Leu Lys Pro Ala Asn Val Met Ile Thr Phe Glu Gly Asn			
580	585	590	
Leu Lys Leu Gly Asp Phe Gly Met Ala Thr His Leu Pro Leu Glu Asp			
595	600	605	
Lys Ser Phe Glu Asn Glu Gly Asp Arg Glu Tyr Ile Ala Pro Glu Ile			
610	615	620	
Ile Ser Asp Cys Thr Tyr Asp Tyr Lys Ala Asp Ile Phe Ser Leu Gly			
625	630	635	640
Leu Met Ile Val Glu Ile Ala Ala Asn Val Val Leu Pro Asp Asn Gly			
645	650	655	
Asn Ala Trp His Lys Leu Arg Ser Gly Asp Leu Ser Asp Ala Gly Arg			
660	665	670	
Leu Ser Ser Thr Asp Ile His Ser Glu Ser Leu Phe Ser Asp Ile Thr			
675	680	685	
Lys Val Asp Thr Asn Asp Leu Phe Asp Phe Glu Arg Asp Asn Ile Ser			
690	695	700	
Gly Asn Ser Asn Asn Ala Gly Thr Ser Thr Val His Asn Asn Ser Asn			
705	710	715	720
Ile Asn Asn Pro Asn Met Asn Asn Gly Asn Asp Asn Asn Asn Val Asn			
725	730	735	
Thr Ala Ala Thr Lys Asn Arg Leu Ile Leu His Lys Ser Ser Lys Ile			
740	745	750	
Pro Ala Trp Val Pro Lys Phe Leu Ile Asp Gly Glu Ser Leu Glu Arg			
755	760	765	
Ile Val Arg Trp Met Ile Glu Pro Asn Tyr Glu Arg Arg Pro Thr Ala			
770	775	780	
Asn Gln Ile Leu Gln Thr Glu Glu Cys Leu Tyr Val Glu Met Thr Arg			
785	790	795	800
Asn Ala Gly Ala Ile Ile Gln Glu Asp Asp Phe Gly Pro Lys Pro Lys			

Phe Phe Ile

<210> 159

<211> 809

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 159

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ggaatgcctg tatgtagaaa tgacacgcaa tgcaggtgct attatccagg aagacgactt 180
tggacctaag ccaaaatttt ttatatgata aatggaacaa aaaaccttgt tttatttaca 240
tacttttttc ccacacgtgc ttatgggccc cattgtataa ataatccaat aacgaaaaag 300
agtgttaatt cagtccggta gtaataccat gtaaaacctt agatgagttt attttaagta 360
cagccgcttc aagcattttt atttttattt tacagatgta gcagataaca accgttaaata 420
tatattatat atatatatat atatatatca aatcacgact attacatata tattgagaat 480
aaggggaagga tggaagacaa atgacaaaaa gtttgaagca taaatatggt cttcgcttag 540
atgttcatct tggttcttct ccagtttctt ctcttagcgt tgtaacggat agtggtgttg 600
gttctcaatc tgatccattg tggcaatggt ctgttttgct tcttagcctt agccattttt 660
tgcttgattc tgaaagactt ttgagcctaa ttaaaaggga aacatatcgt gcacatacga 720
agtgtacaat tgtaaaaaat gttagtaaca atgttcaaac tcatcaatat gatgcattca 780
cggatccaag gcaataccac ctgacataa 809
    
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<210> 160

<211> 102

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 160

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Met Thr Lys Ser Leu Lys His Lys Tyr Val Leu Arg Leu Asp Val His
  1             5             10             15

Leu Gly Ser Ser Pro Val Ser Ser Leu Ser Val Val Thr Asp Ser Val
          20             25             30

Val Gly Ser Gln Ser Asp Pro Leu Trp Gln Trp Ser Val Leu Leu Leu
          35             40             45

Ser Leu Ser His Phe Leu Leu Asp Ser Glu Arg Leu Leu Ser Leu Ile
          50             55             60

Lys Arg Glu Thr Tyr Arg Ala His Thr Lys Cys Thr Ile Val Lys Asn
    
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65

70

75

80

Val Ser Asn Asn Val Gln Thr His Gln Tyr Asp Ala Phe Thr Asp Pro  
 85 90 95

Arg Gln Tyr His Leu Thr  
 100

&lt;210&gt; 161

&lt;211&gt; 1042

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 161

tattcaagaa ttatttcaca tcttccagcg agtaaacaatg ccgctggtaa tcgcgcgtcc 60  
 tcaatatttg agtttttcaa atagtggagt gtggatgtat agaggaatta cacactttta 120  
 agtatgtgat gtatgggagc acagtaccaa ttttaactttt tttttttttc atttttttagc 180  
 ttgattttca aaaaacttat gggcgtttta ggctccggtt caaactacca ccaccacgcg 240  
 gcaggccgag gcaaacagta cgcttggcg gggacgcga agcgactcct tctgttccaa 300  
 gctcaatggt ccttgcggtt acgctcgcg gtgggctaac taacgcaatt cggttttgg 360  
 gctgtcgaga accgagaatt attcttcgcc ttgatagata ctttaaaact tctacttaat 420  
 atactttcta caatttttgg tacattcata ttatactgaa aattcgaaaa agacaagcaa 480  
 ataaacacag atagatcaac atggctgtat gttagaaaga tattataaat ccaggttaga 540  
 tgctgaactg atcaatagca aattataaac cacatccatc taaatgacct taccacctac 600  
 aatttggtt tgaaatagaa gcaatgtgta aaatataggg aaaggattag gagtggttaac 660  
 cataactaaa tttttcttat ccgaaacaga aatctaaagt cgccactacg cagattaaaa 720  
 tatggtcata aactgcttat tctgagaact tttggtggtc cagcgtggtt tatgtcaggt 780  
 ggtattgcct tggatccgtg aatgcatcat attgatgagt ttgaacattg ttactaacat 840  
 tttttacaat tgtacacttc gtatgtgcac gatatgtttc ctttttaatt aggctcaaaa 900  
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 atggatcaga ttgagaacca acaacactat ccgttacaac gctaagagaa gaaactggag 1020  
 aagaaccaag atgaacatct aa 1042

&lt;210&gt; 162

&lt;211&gt; 51

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 162

Met Ala Ala Gln Lys Ser Phe Arg Ile Lys Gln Lys Met Ala Lys Ala  
 1 5 10 15

Lys Lys Gln Asn Arg Pro Leu Pro Gln Trp Ile Arg Leu Arg Thr Asn  
 20 25 30

Asn Thr Ile Arg Tyr Asn Ala Lys Arg Arg Asn Trp Arg Arg Thr Lys  
 35 40 45

Met Asn Ile  
 50

<210> 163  
 <211> 893  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 163  
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 accattgagc ttggaacaga aggagtcgct tcggcggtccc cgccaaggcg tactgtttgc 120  
 ctccgctgc cgcgtggtgg tggtagtttg agccggagcc taaaacgccc ataagttttt 180  
 tgaaaatcaa gctaaaaaat gaaaaaaaaa aaaagttaaa ttggtactgt gcgccatac 240  
 atcacatact taaaagtgtg taattcctct atacatccac acctcactat ttgaaaaact 300  
 caaatattga ggacgcgcga ttaccagcgg catgtttact cgctggaaga tgtgaaataa 360  
 ttcttgaata tgggtttgca gttagtcaat ttcaatctaa ataattctaa tcgactattc 420  
 aattcttaaa ttgtaaggtt ttttaatggc ctttcagttc tagtattttt tataaaacaa 480  
 gaccaacata catatccaag atgaccagat cttccgtttt agctgatgct ttgaatgcca 540  
 ttaacaacgc tgaaaagacc ggtaagcgtc aagttttaat cagaccatcc tccaagggtca 600  
 ttatcaagtt tttgcaagtt atgcaaaagc acggttacat tggatgaatt gaatacatcg 660  
 atgaccacag atctggttaag attgttggtc aattgaacgg tagattgaac aagtgtggtg 720  
 ttatttcccc aagattcaac gttaagattg gtgacattga aaaatggact gccaaacttg 780  
 tgccagccag acaattcggc tacgtcatct tgaccacctc tgctgggtatc atggaccatg 840  
 aagaagccag aagaaagcac gtttctggtg agattttggg tttcgtttac taa 893

<210> 164  
 <211> 130  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 164  
 Met Thr Arg Ser Ser Val Leu Ala Asp Ala Leu Asn Ala Ile Asn Asn  
 1 5 10 15  
 Ala Glu Lys Thr Gly Lys Arg Gln Val Leu Ile Arg Pro Ser Ser Lys  
 20 25 30  
 Val Ile Ile Lys Phe Leu Gln Val Met Gln Lys His Gly Tyr Ile Gly  
 35 40 45  
 Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln  
 50 55 60

Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asn  
65 70 75 80

Val Lys Ile Gly Asp Ile Glu Lys Trp Thr Ala Asn Leu Leu Pro Ala  
85 90 95

Arg Gln Phe Gly Tyr Val Ile Leu Thr Thr Ser Ala Gly Ile Met Asp  
100 105 110

His Glu Glu Ala Arg Arg Lys His Val Ser Gly Lys Ile Leu Gly Phe  
115 120 125

Val Tyr  
130

<210> 165

<211> 4265

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 165

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cttcttcggg gttccccaat gtcactgcc a tctctaaagt agatagaaag ggcgatcgct 60
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gtgtcattac tctaggttat ggtatcatgg catctgttgt caagggtaac gcaacctctg 180
cgtaagagat acgtctacga tagcatgtaa cagcgtatat ataatctata tgtattcgat 240
taatccaaca cttctgttgt gtagtcta a gtctgaaaaa aaggtagcgt tccctgttat 300
aatcaggtat atttcgttat tcttataagc taaaagatta aaaatttttc cactttcctt 360
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agatgggatt actggaaaaa taaaggaggg aaaatcctgc agaacgttgt tgtttcaatc 480
gaaggtttct tcattcgaaa atgggttctt cagatgtttc aagtcgtgaa tgttcattgg 540
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acttgatgaa tgttctagat gacaaggatg aaataaagca agagtctgtc ccagtctcag 660
atcgtgaaat tgaggatacg gaatccgatg cttccgctgt ttcttcattt gctagcgcta 720
atgagttaat agctgagcca cacgctgcaa gtgaaactaa tcttggaact aatggtcaag 780
atggaagaaa tgtcttagaa caacaaagag acgtgggttg tagactaata gaagaaaaca 840
aggaaacgca aaaagagggt gataaagtct gtattgtccc caaggtttgg tacgataaat 900
ttttcgaccc cgatgttacc gatcctgaag atataggccc tattaatata cgcattgatt 960
gcagagactt tgaaaatttt gtgcttgagg attacaatag atgtccgtat ctgtctattg 1020
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tggttaactaa tttggttatc aaccaaacca caggggagtt agagacagaa tacaataaat 1140
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aaaagagtat gaatctgttt tttgagaaag ctgatcatct agacgtgaat gcggtggatt 1320
ttaaaatttg gtttgtgtca gagggatctg atattgccac agatagcaat gttagtactt 1380
ttttgaattc ttcatatgaa ataactccgc ttcaatttct cgaactaccg ataaagaaac 1440

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tactaatacc agacatgttt gaaaaccgtt tagacaagat aacttcaaāt ccgagtgacc 1500  
ttgtcataga aattaaacct atagaaggga atcaccattg gccttcaaac tattttgctt 1560  
ataataaaact cgaaccagca tcaggtacta ctggtttggt caatttggga aatacatgtt 1620  
acatgaattc tgcgttgcaa tgcctggtac acattccgca gttgcgtgat tatttccttt 1680  
atgatgggta tgaagacgaa atcaatgaag aaaatcctct tgggtaccac ggctatgtgg 1740  
ctagggcatt tagtgacttg gttcagaagt tgtttcaaaa caggatgagc ataatgcaaa 1800  
gaaatgctgc tttccccct tcaatgttca aatccactat cgggcacttt aattcgatgt 1860  
tttctgggta tatgcaacag gattctcaag aatttttagc cttcctgtta gacagtttac 1920  
atgaagattt gaacaggata ataaagaaag aatacacaga aaaaccatca ttatctcctg 1980  
gtgatgacgt gaatgattgg aatgtagtca agaaactggc agacgatact tgggagatgc 2040  
atttaaagag aaattgttcc gttataacgg atttatttgt cgggatgtac aaatcaacgc 2100  
tatattgtcc cgaatgtcaa aatgtttcta taacgtttga cccgtataat gatgttacat 2160  
tgccgcttcc ggttgatata gtgtgggata aaactataaa aatttttccc atgaactctc 2220  
caccacttct tcttgaagtt gagttaagca aatcgccac ttatatggac ttgaagaatt 2280  
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aattgatcaa acctgctgat gacgttattt tttatgaatt accagtaaca aatgacaatg 2460  
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gcaatggatt aggagctct aaactacagg aaataatcca aaagtcacgc cagggatatg 3900  
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gccagaaaa cgaagtcgct gatttgaatt taaaaaatgg tgtgacacta gaatcgccag 4260  
aataa 4265



&lt;210&gt; 166

&lt;211&gt; 1254

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 166

Met Gly Ser Ser Asp Val Ser Ser Arg Glu Cys Ser Leu Val Tyr Asn  
 1 5 10 15

Glu Asp Pro Asp Phe Thr Asp Gly Thr Thr Pro Cys Asp Arg Leu Gly  
 20 25 30

Val Asp Leu Met Asn Val Leu Asp Asp Lys Asp Glu Ile Lys Gln Glu  
 35 40 45

Ser Val Pro Val Ser Asp Arg Glu Ile Glu Asp Thr Glu Ser Asp Ala  
 50 55 60

Ser Ala Val Ser Ser Phe Ala Ser Ala Asn Glu Leu Ile Ala Glu Pro  
 65 70 75 80

His Ala Ala Ser Glu Thr Asn Leu Gly Thr Asn Gly Gln Asp Gly Arg  
 85 90 95

Asn Val Leu Glu Gln Gln Arg Asp Val Val Ala Arg Leu Ile Glu Glu  
 100 105 110

Asn Lys Glu Thr Gln Lys Glu Gly Asp Lys Val Cys Ile Val Pro Lys  
 115 120 125

Val Trp Tyr Asp Lys Phe Phe Asp Pro Asp Val Thr Asp Pro Glu Asp  
 130 135 140

Ile Gly Pro Ile Asn Thr Arg Met Ile Cys Arg Asp Phe Glu Asn Phe  
 145 150 155 160

Val Leu Glu Asp Tyr Asn Arg Cys Pro Tyr Leu Ser Ile Ala Glu Pro  
 165 170 175

Val Phe Asn Phe Leu Ser Glu Ile Tyr Gly Met Thr Ser Gly Ser Tyr  
 180 185 190

Pro Val Val Thr Asn Leu Val Ile Asn Gln Thr Thr Gly Glu Leu Glu  
 195 200 205

Thr Glu Tyr Asn Lys Trp Phe Phe Arg Leu His Tyr Leu Thr Glu Lys

210		215		220
Gln Asp Gly Arg Lys Arg Arg His Gly Gln Asp Asp Ser Ile Met Tyr				
225		230		240
Leu Ser Met Ser Ala Leu Asn Leu Val Arg Asp Leu Val Glu Lys Ser				
	245		250	255
Met Asn Leu Phe Phe Glu Lys Ala Asp His Leu Asp Val Asn Ala Val				
	260		265	270
Asp Phe Lys Ile Trp Phe Val Ser Glu Gly Ser Asp Ile Ala Thr Asp				
	275		280	285
Ser Asn Val Ser Thr Phe Leu Asn Ser Ser Tyr Glu Ile Thr Pro Leu				
	290		295	300
Gln Phe Leu Glu Leu Pro Ile Lys Lys Leu Leu Ile Pro Asp Met Phe				
	305		310	315
Glu Asn Arg Leu Asp Lys Ile Thr Ser Asn Pro Ser Asp Leu Val Ile				
	325		330	335
Glu Ile Lys Pro Ile Glu Gly Asn His His Trp Pro Ser Asn Tyr Phe				
	340		345	350
Ala Tyr Asn Lys Leu Glu Pro Ala Ser Gly Thr Thr Gly Leu Val Asn				
	355		360	365
Leu Gly Asn Thr Cys Tyr Met Asn Ser Ala Leu Gln Cys Leu Val His				
	370		375	380
Ile Pro Gln Leu Arg Asp Tyr Phe Leu Tyr Asp Gly Tyr Glu Asp Glu				
	385		390	395
Ile Asn Glu Glu Asn Pro Leu Gly Tyr His Gly Tyr Val Ala Arg Ala				
	405		410	415
Phe Ser Asp Leu Val Gln Lys Leu Phe Gln Asn Arg Met Ser Ile Met				
	420		425	430
Gln Arg Asn Ala Ala Phe Pro Pro Ser Met Phe Lys Ser Thr Ile Gly				
	435		440	445
His Phe Asn Ser Met Phe Ser Gly Tyr Met Gln Gln Asp Ser Gln Glu				
	450		455	460
Phe Leu Ala Phe Leu Leu Asp Ser Leu His Glu Asp Leu Asn Arg Ile				

465	470	475	480
Ile Lys Lys Glu Tyr Thr Glu Lys Pro Ser Leu Ser Pro Gly Asp Asp			
485	490	495	
Val Asn Asp Trp Asn Val Val Lys Lys Leu Ala Asp Asp Thr Trp Glu			
500	505	510	
Met His Leu Lys Arg Asn Cys Ser Val Ile Thr Asp Leu Phe Val Gly			
515	520	525	
Met Tyr Lys Ser Thr Leu Tyr Cys Pro Glu Cys Gln Asn Val Ser Ile			
530	535	540	
Thr Phe Asp Pro Tyr Asn Asp Val Thr Leu Pro Leu Pro Val Asp Thr			
545	550	555	560
Val Trp Asp Lys Thr Ile Lys Ile Phe Pro Met Asn Ser Pro Pro Leu			
565	570	575	
Leu Leu Glu Val Glu Leu Ser Lys Ser Ser Thr Tyr Met Asp Leu Lys			
580	585	590	
Asn Tyr Val Gly Lys Met Ser Gly Leu Asp Pro Asn Thr Leu Phe Gly			
595	600	605	
Cys Glu Ile Phe Ser Asn Gln Ile Tyr Val Asn Tyr Glu Ser Thr Glu			
610	615	620	
Ser Asn Ala Gln Phe Leu Thr Leu Gln Glu Leu Ile Lys Pro Ala Asp			
625	630	635	640
Asp Val Ile Phe Tyr Glu Leu Pro Val Thr Asn Asp Asn Glu Val Ile			
645	650	655	
Val Pro Val Leu Asn Thr Arg Ile Glu Lys Gly Tyr Lys Asn Ala Met			
660	665	670	
Leu Phe Gly Val Pro Phe Phe Ile Thr Leu Lys Glu Asp Glu Leu Asn			
675	680	685	
Asn Pro Gly Ala Ile Arg Met Lys Leu Gln Asn Arg Phe Val His Leu			
690	695	700	
Ser Gly Gly Tyr Ile Pro Phe Pro Glu Pro Val Gly Asn Arg Thr Asp			
705	710	715	720
Phe Ala Asp Ala Phe Pro Leu Leu Val Glu Lys Tyr Pro Asp Val Glu			

~~206~~

980 985 990

Gln Ala Thr Lys Gln Ile Gln Leu Trp Asn Thr Pro Asp Ile Leu Leu  
995 1000 1005

Ile His Leu Lys Arg Phe Glu Ser Gln Arg Ser Phe Ser Asp Lys Ile  
1010 1015 1020

Asp Ala Thr Val Asn Phe Pro Ile Thr Asp Leu Asp Leu Ser Arg Tyr  
1025 1030 1035 1040

Val Val Tyr Lys Asp Asp Pro Arg Gly Leu Ile Tyr Asp Leu Tyr Ala  
1045 1050 1055

Val Asp Asn His Tyr Gly Gly Leu Gly Gly Gly His Tyr Thr Ala Tyr  
1060 1065 1070

Val Lys Asn Phe Ala Asp Asn Lys Trp Tyr Tyr Phe Asp Asp Ser Arg  
1075 1080 1085

Val Thr Glu Thr Ala Pro Glu Asn Ser Ile Ala Gly Ser Ala Tyr Leu  
1090 1095 1100

Leu Phe Tyr Ile Arg Arg His Lys Asp Gly Asn Gly Leu Gly Ser Ser  
1105 1110 1115 1120

Lys Leu Gln Glu Ile Ile Gln Lys Ser Arg His Gly Tyr Asp Glu Arg  
1125 1130 1135

Ile Lys Lys Ile Tyr Asp Glu Gln Met Lys Leu Tyr Glu Phe Asn Lys  
1140 1145 1150

Thr Asp Glu Glu Glu Asp Val Ser Asp Asp Met Ile Glu Cys Asn Glu  
1155 1160 1165

Asp Val Gln Ala Pro Glu Tyr Ser Asn Arg Ser Leu Glu Val Gly His  
1170 1175 1180

Ile Glu Thr Gln Asp Cys Asn Asp Glu Asp Asp Asn Asp Asp Gly Glu  
1185 1190 1195 1200

Arg Thr Asn Ser Gly Arg Arg Lys Leu Arg Leu Leu Lys Lys Val Tyr  
1205 1210 1215

Lys Asn Asn Ser Gly Leu Gly Ser Ser Ser Thr Ser Glu Ile Ser Glu  
1220 1225 1230

Gly Cys Pro Glu Asn Glu Val Ala Asp Leu Asn Leu Lys Asn Gly Val

1235

1240

1245

Thr Leu Glu Ser Pro Glu  
1250

&lt;210&gt; 167

&lt;211&gt; 3146

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 167

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&lt;210&gt; 168

&lt;211&gt; 881

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 168

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Met Arg Phe Ser His Phe Leu Lys Tyr Asn Ala Val Pro Glu Trp Gln
 1             5             10            15

Asn His Tyr Met Asp Tyr Ser Glu Leu Lys Asn Leu Ile Tyr Thr Leu
      20             25            30

Gln Thr Asp Glu Leu Gln Val Gly Asp Asn Glu Glu Gly Phe Gly Ala
      35             40            45

Gly Lys Ser Ser Asn Ile Thr Asp Arg Phe Lys Asn Lys Phe Ser Phe
      50             55            60

Lys Asn Ala Lys Glu Asp Thr Ser Ser Gly Met Asn Lys Asp Ala Gly
      65             70            75            80

Ile Val Glu Glu Thr Ile Glu Leu Arg Glu Leu Pro Thr Ala Gln Thr
      85             90            95

Val Ala Ala Lys Pro Ser Pro Phe Arg Arg Met Lys Glu Lys Ile Phe
      100            105            110

Tyr Lys Arg Arg Ser Ser Ser Ala Ser Ser Val Ser Ser Thr Ala Asn

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115	120	125
Glu Asn Leu Gln Leu Asp Thr Tyr Asp Thr Phe Val Gly Asp Leu Thr		
130	135	140
Ala Glu Lys Gln Lys Val Asp Asp Phe Tyr Lys Arg Thr Glu Ala Lys		
145	150	155 160
Phe Tyr Asp Lys Phe Asp Ala Leu Val Lys Asp Leu Lys Lys Ile Gly		
	165 170	175
Val Ile Glu Tyr Asp Ile Asp Asp Asp Thr Leu Phe Asn Glu Pro Ile		
	180 185	190
Ala Ser Thr Asn Asp Glu Val Pro Pro Leu Asp Leu Asp Asp Asp Glu		
	195 200	205
Asp Asp Asp Glu Phe Tyr Asp Asp Gln Ser Asn Ile Glu Asp Asn Thr		
	210 215	220
Ala Leu Leu His His Ser Gln Tyr Asn Ile Lys Ser Gln Lys Lys Ser		
225	230	235 240
Leu Leu Lys Lys Ser Ile Val Asn Leu Tyr Ile Asp Leu Cys Gln Leu		
	245	250 255
Lys Ser Phe Ile Glu Leu Asn Arg Ile Gly Phe Ala Lys Ile Thr Lys		
	260 265	270
Lys Ser Asp Lys Val Leu His Leu Asn Thr Arg Thr Glu Leu Ile Glu		
	275 280	285
Ser Glu Gln Phe Phe Lys Asp Thr Tyr Ala Phe Gln Ala Glu Thr Ile		
	290 295	300
Glu Leu Leu Asn Ser Lys Ile Ser Gln Leu Val Thr Phe Tyr Ala Arg		
305	310	315 320
Ile Thr Asp Arg Pro His Asn Ile Ser His Ser Lys Gln Glu Leu Lys		
	325 330	335
Ser Tyr Leu His Asp His Ile Val Trp Glu Arg Ser Asn Thr Trp Lys		
	340 345	350
Asp Met Leu Gly Leu Leu Ser Gln Ala Asp Glu Leu Thr Pro Lys Glu		
	355 360	365
Thr Glu Tyr Asn Ala Asn Lys Leu Val Gly Lys Leu Asp Leu Glu Tyr		



370	375	380
Tyr Arg Trp Pro Leu Pro Arg Pro Ile Asn Leu Lys Phe Thr Ser Ile		
385	390	395 400
Asn Asn Val Ala Leu Pro Lys Leu Phe Phe Thr Lys Lys Ala Tyr Lys		
405	410	415
Ile Tyr Phe Ile Ile Leu Val Thr Gly Leu Leu Leu Gly Ile Lys Thr		
420	425	430
Phe Asn Asp Ala Ala Gln His Arg Cys Met Ala Leu Val Glu Cys Val		
435	440	445
Ala Phe Leu Trp Ala Ser Glu Ala Ile Pro Leu His Ile Thr Ala Phe		
450	455	460
Leu Val Pro Leu Leu Val Val Leu Phe Lys Val Leu Lys Thr Ser Asp		
465	470	475 480
Gly Ala Ile Met Ser Ala Ala Ser Ala Ser Ser Glu Ile Leu Ala Ala		
485	490	495
Met Trp Ser Ser Thr Ile Met Ile Leu Leu Ala Gly Phe Thr Leu Gly		
500	505	510
Glu Val Leu Ala Gln Tyr Asn Ile Ala Lys Val Leu Ala Ser Trp Leu		
515	520	525
Leu Ala Phe Ala Gly Cys Lys Pro Arg Asn Val Leu Leu Met Ala Met		
530	535	540
Cys Val Val Phe Phe Leu Ser Met Trp Ile Ser Asn Val Ala Ala Pro		
545	550	555 560
Val Leu Thr Tyr Ser Leu Leu Ser Pro Leu Leu Asp Ala Met Asp Ala		
565	570	575
Asp Ser Pro Phe Ala Gln Ala Leu Val Leu Gly Val Ala Leu Ala Ala		
580	585	590
Asn Ile Gly Gly Met Ser Ser Pro Ile Ser Ser Pro Gln Asn Ile Ile		
595	600	605
Ser Met Ser Tyr Leu Lys Pro Tyr Gly Ile Gly Trp Gly Gln Phe Phe		
610	615	620
Ala Val Ala Leu Pro Ser Gly Ile Leu Ala Met Leu Leu Val Trp Ile		

625		630		635		640
Leu Leu Phe Thr Thr Phe Lys Met Asn Lys Thr Lys Leu Glu Lys Phe						
	645			650		655
Lys Pro Ile Lys Thr Lys Phe Thr Val Lys Gln Tyr Tyr Ile Ile Thr						
	660			665		670
Val Thr Val Ala Thr Ile Leu Leu Trp Cys Val Glu Ser Gln Ile Glu						
	675			680		685
Gly Ala Phe Gly Ser Ser Gly Gln Ile Ala Ile Ile Pro Ile Val Leu						
	690			695		700
Phe Phe Gly Thr Gly Leu Leu Ser Thr Gln Asp Leu Asn Ala Phe Pro						
	705			710		715
Trp Ser Ile Val Ile Leu Ala Met Gly Gly Ile Ala Leu Gly Lys Ala						
	725			730		735
Val Ser Ser Ser Gly Leu Leu Ser Thr Ile Ala Lys Ala Leu Gln Lys						
	740			745		750
Lys Ile Glu Asn Asp Gly Val Phe Ala Ile Leu Cys Ile Phe Gly Ile						
	755			760		765
Leu Met Leu Val Val Gly Thr Phe Val Ser His Thr Val Ser Ala Ile						
	770			775		780
Ile Ile Ile Pro Leu Val Gln Glu Val Gly Asp Lys Leu Gly Asn Pro						
	785			790		795
Lys Ala Ala Pro Ile Leu Val Phe Gly Cys Ala Leu Leu Ser Ser Cys						
	805			810		815
Gly Met Gly Leu Ala Ser Ser Gly Phe Pro Asn Val Thr Ala Ile Ser						
	820			825		830
Lys Val Asp Arg Lys Gly Asp Arg Tyr Leu Ser Val Met Thr Phe Leu						
	835			840		845
Thr Arg Gly Val Pro Ala Ser Ile Leu Ala Phe Leu Cys Val Ile Thr						
	850			855		860
Leu Gly Tyr Gly Ile Met Ala Ser Val Val Lys Gly Asn Ala Thr Ser						
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						880
Ala						

&lt;210&gt; 169

&lt;211&gt; 2093

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 169

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&lt;210&gt; 170

&lt;211&gt; 530

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 170

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Glu Asp Gly Arg Asn Asp His His Asn Asn Asn Asn Asn Leu Met Lys  
 20 25 30

Lys Ala Met Met Asn Asn Glu Gln Ile Asp Arg Thr Gln Asp Ile Asp  
 35 40 45

Asn Ala Lys Glu Met Leu Arg Lys Ile Ser Ser Glu Ser Ser Ser Arg  
 50 55 60

Arg Ser Ser Leu Leu Asn Lys Asp Ser Ser Leu Val Asn Gly Asn Ala  
 65 70 75 80

Asn Ser Gly Gly Gly Thr Ser Ile Asn Gly Thr Arg Gly Ser Ser Lys  
 85 90 95

Ser Ser Asn Thr His Phe Gln Tyr Ala Ser Thr Ala Tyr Gly Val Arg  
 100 105 110

Met Leu Ser Lys Asp Ile Ser Asn Thr Lys Val Glu Leu Asp Val Glu  
 115 120 125

Asn Leu Met Ile Val Thr Lys Leu Asn Asp Val Ser Leu Tyr Phe Leu  
 130 135 140

Thr Arg Glu Leu Val Glu Trp Val Leu Val His Phe Pro Arg Val Thr  
 145 150 155 160

Val Tyr Val Asp Ser Glu Leu Lys Asn Ser Lys Lys Phe Ala Ala Gly  
 165 170 175

Glu Leu Cys Glu Asp Ser Lys Cys Arg Glu Ser Arg Ile Lys Tyr Trp  
 180 185 190

Thr Lys Asp Phe Ile Arg Glu His Asp Val Phe Phe Asp Leu Val Val  
 195 200 205

Thr Leu Gly Gly Asp Gly Thr Val Leu Phe Val Ser Ser Ile Phe Gln  
 210 215 220

Arg His Val Pro Pro Val Met Ser Phe Ser Leu Gly Ser Leu Gly Phe

~~215~~

485

490

495

Asn Gly Ser Asp Asp Glu Ser Asp Asp Glu Ser Val Asn Cys Glu Ala  
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Cys Lys Leu Lys Pro Ser Ser Val Pro Lys Pro Ser Gln Ala Arg Phe  
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Ser Val  
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<210> 171  
 <211> 1255  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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<210> 172  
 <211> 128  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 172

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
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Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp  
 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ile Ile Glu Pro  
 65 70 75 80

Ser Leu Lys Ala Leu Ala Ser Lys Tyr Asn Cys Asp Lys Ser Val Cys  
 85 90 95

Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr Asn Cys Arg Lys  
 100 105 110

Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys Lys Lys Leu Lys  
 115 120 125

&lt;210&gt; 173

&lt;211&gt; 1175

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 173

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 cctgaaaata ttgcgtatca atgatatttg ctccctcttt ctccctcatt aaaaatattc 540  
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 ttttaaacga tttcgacacc gcttttccac agtatacctc atacatgatg caaaaccatt 720  
 taaccctacc tcaacctgtt gctgactact actatcacat ggttgatttg gcttcaacag 780

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&lt;210&gt; 174

&lt;211&gt; 224

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 174

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Met Ile Phe Ala Pro Ser Phe Ser Leu Ile Lys Asn Ile Leu Leu Val
  1             5             10             15

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Ser Phe Leu Ile Ser His Ser Phe Ala Ala Lys Thr Leu Thr Ser Ser
          20             25             30

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Ser Asn Asp Asp Thr Leu Ala Arg Ser Ala Ala Ala Asp Ala Asp Met
      35             40             45

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Ala Phe Phe Met Glu Phe Leu Asn Asp Phe Asp Thr Ala Phe Pro Gln
      50             55             60

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Tyr Thr Ser Tyr Met Met Gln Asn His Leu Thr Leu Pro Gln Pro Val
      65             70             75             80

```

```

Ala Asp Tyr Tyr Tyr His Met Val Asp Leu Ala Ser Thr Ala Asp Leu
          85             90             95

```

```

Gln Ser Asp Ile Ala Gln Ser Phe Pro Phe Thr Gln Phe Gln Thr Phe
      100             105             110

```

```

Ile Thr Ala Phe Pro Trp Tyr Thr Ser Leu Leu Asn Lys Ala Ser Ala
      115             120             125

```

```

Thr Thr Ile Tyr Leu Pro Gln His Phe Ile Thr Gly Glu Thr Glu Ala
      130             135             140

```

```

Thr Met Thr Asn Ser Ser Tyr Ala Ser Gln Lys Asn Ser Val Ser Asn
      145             150             155             160

```

```

Ser Val Pro Phe Ser Thr Ala Asn Ala Gly Gln Ser Met Ile Ser Met
          165             170             175

```



Ala Asn Glu Glu Asn Ser Thr Thr Ala Leu Ile Ser Ala Ser Asn Ser  
 180 185 190

Ser Ser Thr Ser Arg Thr Ser Gln Ser Gln Asn Gly Ala His Ala Lys  
 195 200 205

Ser Leu Tyr Phe Pro Met Ala Leu Phe Gly Ile Phe Ala Val Ala Leu  
 210 215 220

<210> 175  
 <211> 1618  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 175  
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 tacctatttc ttaaaggcct ttgtcacttc tttatgggaa tggcgctact ttaattttcc 180  
 gcctactttg aaaaatttac caaggcgaaa ttgagtgcgc taggcggaag ttccagggca 240  
 cggtcaccga acctttgtgc tgtttcgaac gaggggtccg ctggagggtg acggacgcgg 300  
 .gaggagctgg aaagatggaa tggaggact gcaacactca gtaagaagg tctgtgtagg 360  
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 aaaaatcgcg agttattaag tgtgtaattt agaataccga aatagcaca gaagagataa 480  
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 cccaactttt gttggccgct aacaccatt taggtgctag aaacgttcaa gtatgtacac 600  
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 gggtttagaa gagttagaat ttcacttctt agtgagggtg aggagaagaa actcaataag 780  
 aatatacatc ctgactgtg tcaaagatta tgaactccga tgaaacagta aaacgtcaaa 840  
 aaattccacg ggatataatt cggactctta ttggatatgg aagaaaacat tatatatgca 900  
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 tgaagaagct gctgccgctg aagaaggtga agaagaagaa gttaaggaag aagtcactga 1560  
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&lt;210&gt; 176

&lt;211&gt; 252

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 176

```

Met Ser Leu Pro Ala Thr Phe Asp Leu Thr Pro Glu Asp Ala Gln Leu
  1              5              10              15

Leu Leu Ala Ala Asn Thr His Leu Gly Ala Arg Asn Val Gln Val His
      20              25              30

Gln Glu Pro Tyr Val Phe Asn Ala Arg Pro Asp Gly Val His Val Ile
      35              40              45

Asn Val Gly Lys Thr Trp Glu Lys Leu Val Leu Ala Ala Arg Ile Ile
      50              55              60

Ala Ala Ile Pro Asn Pro Glu Asp Val Val Ala Ile Ser Ser Arg Thr
      65              70              75              80

Tyr Gly Gln Arg Ala Val Leu Lys Phe Ala Ala His Thr Gly Ala Thr
      85              90              95

Pro Ile Ala Gly Arg Phe Thr Pro Gly Ser Phe Thr Asn Tyr Ile Thr
      100             105             110

Arg Ser Phe Lys Glu Pro Arg Leu Val Ile Val Thr Asp Pro Arg Leu
      115             120             125

Asp Ala Gln Ala Ile Lys Glu Ala Ser Tyr Val Asn Ile Pro Val Ile
      130             135             140

Ala Leu Thr Asp Leu Asp Ser Pro Ser Glu Phe Val Asp Val Ala Ile
      145             150             155             160

Pro Cys Asn Asn Arg Gly Lys His Ser Ile Gly Leu Ile Trp Tyr Leu
      165             170             175

Leu Ala Arg Glu Val Leu Arg Leu Arg Gly Ala Leu Val Asp Arg Thr
      180             185             190

Gln Pro Trp Ser Ile Met Pro Asp Leu Tyr Phe Tyr Arg Asn Pro Glu
      195             200             205

Glu Val Glu Gln Val Ala Glu Glu Ala Ala Ala Ala Glu Glu Gly Glu
      210             215             220

```

220

Glu Glu Glu Val Lys Glu Glu Val Thr Glu Gly Gln Ala Glu Ala Thr  
 225 230 235 240

Glu Trp Ala Glu Glu Asn Ala Asp Asn Val Glu Trp  
 245 250

<210> 177

<211> 2345

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 177

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tccatgcttg ctaacttatt accgtcaata gaagacttga gtcaggtggc tttaatgagt 180
actattcttt ttttttttcc aaagagcact atgttgataa taccgcagta attttttttg 240
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tgatcggcac attggcattt cctatgacat ttgtgaagac cattgttgaa agttctagcg 1980

```

```

aacatgaggt gacaactcaa tcctctaacc caataaaaaac tgagccgaaa gatgagatag 2040
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taaaaaattt agtactatta attttgacaa atccatttat ttcaataacc ttattcggac 2160
tattttttga tgatgaattt catggatttg atataataaa caaactgggt tcagcatggt 2220
tggatttgaa atgttggagt tggtttgtac tttgtatagg ttggcttcca tgttggctat 2280
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gttag                                           2345

```

&lt;210&gt; 178

&lt;211&gt; 614

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 178

```

Met Ala Leu Leu Glu Lys Leu His Arg Arg Ile Val Asp Met Gly Leu
  1              5              10              15

```

```

Val Pro Arg Ile Ile Ala Leu Leu Pro Val Ile Ser Met Leu Cys Ala
              20              25              30

```

```

Leu Phe Gly Phe Ile Ser Ile Ala Ile Leu Pro Met Asp Gly Gln Tyr
      35              40              45

```

```

Arg Arg Thr Tyr Ile Ser Glu Asn Ala Leu Met Pro Ser Gln Ala Tyr
      50              55              60

```

```

Ser Tyr Phe Arg Glu Ser Glu Trp Asn Ile Leu Arg Gly Tyr Arg Ser
      65              70              75              80

```

```

Gln Ile Lys Glu Met Val Asn Met Thr Ser Met Glu Arg Asn Asn Leu
              85              90              95

```

```

Met Gly Ser Trp Leu Gln Glu Phe Gly Thr Lys Thr Ala Ile Tyr Glu
      100              105              110

```

```

Asn Glu Gln Tyr Gly Glu Thr Leu Tyr Gly Val Met His Ala Pro Arg
      115              120              125

```

```

Gly Asp Gly Thr Glu Ala Met Val Leu Ala Val Pro Trp Phe Asn Ser
      130              135              140

```

```

Asp Asp Glu Phe Asn Ile Gly Gly Ala Ala Leu Gly Val Ser Leu Ala
      145              150              155              160

```

```

Arg Phe Phe Ser Arg Trp Pro Val Trp Ser Lys Asn Ile Ile Val Val
              165              170              175

```

Phe Ser Glu Asn Pro Arg Ala Ala Leu Arg Ser Trp Val Glu Ala Tyr  
180 185 190

His Thr Ser Leu Asp Leu Thr Gly Gly Ser Ile Glu Ala Ala Val Val  
195 200 205

Leu Asp Tyr Ser Ser Thr Glu Asp Phe Phe Glu Tyr Val Glu Ile Ser  
210 215 220

Tyr Asp Gly Leu Asn Gly Glu Leu Pro Asn Leu Asp Leu Val Asn Ile  
225 230 235 240

Ala Ile Ser Ile Thr Glu His Glu Gly Met Lys Val Ser Leu His Gly  
245 250 255

Leu Pro Ser Asp Gln Leu Thr Asn Asn Asn Phe Trp Ser Arg Leu Lys  
260 265 270

Ile Leu Cys Leu Gly Ile Arg Asp Trp Ala Leu Ser Gly Val Lys Lys  
275 280 285

Pro His Gly Asn Glu Ala Phe Ser Gly Trp Arg Ile Gln Ser Val Thr  
290 295 300

Leu Lys Ala His Gly Asn Ser Gly His Asp Ile Thr Thr Phe Gly Arg  
305 310 315 320

Ile Pro Glu Ala Met Phe Arg Ser Ile Asn Asn Leu Leu Glu Lys Phe  
325 330 335

His Gln Ser Phe Phe Phe Tyr Leu Leu Leu Ala Pro Arg Gln Phe Val  
340 345 350

Ser Ile Ser Ser Tyr Leu Pro Ser Ala Val Ala Leu Ser Ile Ala Phe  
355 360 365

Ala Ile Ser Ser Leu Asn Ala Phe Ile Asn Asn Ala Tyr Ala Asn Ile  
370 375 380

Ser Leu Phe Ser Glu Tyr Asn Leu Val Ala Leu Leu Val Trp Phe Val  
385 390 395 400

Ser Leu Val Ile Ser Phe Val Val Ser Gln Ala Phe Leu Leu Ile Pro  
405 410 415

Ser Ser Gly Leu Leu Met Thr Ile Ser Met Ala Ser Cys Phe Leu Pro  
420 425 430

Leu Ile Leu Ser Arg Lys Ile His Ile Ser Glu Pro Leu Ser Tyr Arg  
 435 440 445  
 Leu Lys Asn Val Ala Phe Leu Tyr Phe Ser Leu Val Ser Thr Ser Leu  
 450 455 460  
 Leu Met Ile Asn Phe Ala Met Ala Leu Leu Ile Gly Thr Leu Ala Phe  
 465 470 475 480  
 Pro Met Thr Phe Val Lys Thr Ile Val Glu Ser Ser Ser Glu His Glu  
 485 490 495  
 Val Thr Thr Gln Ser Ser Asn Pro Ile Lys Thr Glu Pro Lys Asp Glu  
 500 505 510  
 Ile Glu Leu Val Glu Asn His Met Asp Thr Thr Pro Ala Thr Pro Gln  
 515 520 525  
 Gln Gln Lys Gln Lys Leu Lys Asn Leu Val Leu Leu Ile Leu Thr Asn  
 530 535 540  
 Pro Phe Ile Ser Ile Thr Leu Phe Gly Leu Phe Phe Asp Asp Glu Phe  
 545 550 555 560  
 His Gly Phe Asp Ile Ile Asn Lys Leu Val Ser Ala Trp Leu Asp Leu  
 565 570 575  
 Lys Cys Trp Ser Trp Phe Val Leu Cys Ile Gly Trp Leu Pro Cys Trp  
 580 585 590  
 Leu Leu Ile Leu Ala Ser Ser Phe Glu Ser Lys Ser Val Val Val Arg  
 595 600 605  
 Ser Lys Glu Lys Gln Ser  
 610

&lt;210&gt; 179

&lt;211&gt; 845

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 179

tccgtcccaa agatagcttg atcatcctaa gcgggtcgca ttttactatc cccagttccg 60  
 aagaataaca aggctcaatg catatgctgt ttatcgtgct cacaaggcgg tatgacgttt 120  
 ttagcaatgt aattatatta aaaagatctt cagtcactat gagggttgga ttgccccata 180  
 gagagctata agccgacgtg aaagctgctg gttccagctt ggctcatgct gtcaccagtc 240

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actagtcact tggtcgcatt cattgctact catctgcgag tgagcatatt tgagatctga 300
cttgccaagg gattagaatc acgtaagact cttgatcctt agaagatatt tctgacaaag 360
aaccacctaa gccatgcaag tttttttttt catttggtgg cgaaacaaag gtgatgaaag 420
tttcttcttg tacaaacgcc aagcccgcata ggtgagacaa ttcttgaagt aatggacctc 480
tgagtaagca tatcagtcga atgaagttcc aatatgcgtt ggccaaggaa cagctaggca 540
gcaactcgcg cagtggcgtc aaaaaactaa taagtaaaca ccactggctt ccggaatact 600
atttctctga tctctcattt tctgttgtag agcagtggga cagtagagcc attgaaaaaa 660
ctacaatcat atcttgtagt cggcccgcga accaagagat ttatcctttg agacattgtg 720
agaccctccg ttcgcaaccg tgctctctgt tttcatcact atatgcacgc tctttccaaa 780
gtcctctgcac tttgcacgtg gcggagccat cgcccggctt ccatatgtac ggctgccaca 840
cctaa 845

```

&lt;210&gt; 180

&lt;211&gt; 114

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 180

```

Met Lys Phe Gln Tyr Ala Leu Ala Lys Glu Gln Leu Gly Ser Asn Ser
  1                      5                      10                     15

```

```

Arg Ser Gly Val Lys Lys Leu Ile Ser Lys His His Trp Leu Pro Glu
          20                      25                     30

```

```

Tyr Tyr Phe Ser Asp Leu Ser Phe Ser Val Val Gln Gln Trp Asp Ser
          35                      40                     45

```

```

Arg Ala Ile Glu Lys Thr Thr Ile Ile Ser Cys Met Arg Pro Ala Asn
          50                      55                     60

```

```

Gln Glu Ile Tyr Pro Leu Arg His Cys Glu Thr Leu Arg Ser Gln Pro
          65                      70                     75                     80

```

```

Cys Ser Leu Phe Ser Ser Leu Tyr Ala Arg Ser Phe Gln Ser Ser Cys
          85                      90                     95

```

```

Thr Leu His Val Ala Glu Pro Ser Pro Gly Phe His Met Tyr Gly Cys
          100                     105                    110

```

His Thr

&lt;210&gt; 181

&lt;211&gt; 959

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

<400> 181

```
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gaaattaaac ttggttgggg ttaattattt gatgggtata ttaatttgca accgcaaggt 120
atcgataata aatattctac aaaaccttta tcaatagtgg tgaagtcttt agtgcgatct 180
acctgggggtt aatgaacgag aagttcttga gatattcttc ctgtttacct ccgtgcatcc 240
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tattaaatgg tttaaataatt ttgagatgtt cgttatatca gaaacttcct tacttctatc 420
ttttattcca atacaaagaa gtcacaagat tacttggtaa gaaagaagca gttaattttt 480
aattttgccg acaagccaag atgcaaattt tcgtcaagac tttaaccggt aagactatta 540
ccctggaagt tgaatcttct gacactattg acaatgtcaa gtccaagatc caagacaagg 600
aaggatttcc acctgaccaa caagattga tctttgctgg taagcaattg gaagatggta 660
gaactttgtc cgactacaac atccaaaagg aatctactct acacttggtc ttgagattga 720
gaggtggtgg taagaagaga aagaagaagg tctacaccac cccaaagaag atcaagcaca 780
agcacaagaa ggtcaagttg gctgtcttgt cctactacaa ggtcgatgct gaaggtaagg 840
ttaccaaatt gagaagagaa tgtagcaacc caacttggtg tgctgggtgt ttcttggcta 900
accacaagga cagattgtac tgtggtaagt gtcattccgt ctacaagggt aacgcttaa 959
```

<210> 182

<211> 152

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 182

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Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
  1              5              10              15

Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
      20              25              30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
      35              40              45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
      50              55              60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Gly Lys Lys Arg
      65              70              75              80

Lys Lys Lys Val Tyr Thr Thr Pro Lys Lys Ile Lys His Lys His Lys
      85              90              95

Lys Val Lys Leu Ala Val Leu Ser Tyr Tyr Lys Val Asp Ala Glu Gly
      100              105              110
```



Lys Val Thr Lys Leu Arg Arg Glu Cys Ser Asn Pro Thr Cys Gly Ala  
 115 120 125

Gly Val Phe Leu Ala Asn His Lys Asp Arg Leu Tyr Cys Gly Lys Cys  
 130 135 140

His Ser Val Tyr Lys Val Asn Ala  
 145 150

<210> 183  
 <211> 848  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 183  
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 caaccaatat gtcgggggaat tgggtgggcaa atgaggtgat tcggccaata tcgaaatatt 180  
 gcccgcgtgta atactgaaca cctgacaaac agaccagcgc caattcatct tgatttacct 240  
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 aatagtctga tggaaaggag cccttttcaa aaaggatctt gaatcttttc tcagtagggt 420  
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 aagaattccc gcataagtac gtcacaggct tatcgtcgga cgatagtcct atggatttaa 720  
 atgtagggat gttgaattca tccctcagag attccggata ttctccgtct aattccaaag 780  
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 cgtattga 848

<210> 184  
 <211> 115  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 184  
 Met Gly Ala Ser Ser Gly Arg Ile Gly Lys Ser Met Leu Thr Gln Gly  
 1 5 10 15

Thr Phe Pro Leu Ala Ser Ser Gly Cys Leu Lys Cys Asp Ser Thr Ala  
 20 25 30

Gln Ser Leu His Ala Ser Ser Ser Ala Leu Ile Glu Phe Leu Val Asp  
 35 40 45

Phe Gly Ile Lys Pro Lys Glu Phe Pro His Lys Tyr Val Thr Gly Leu  
 50 55 60  
 Ser Ser Asp Asp Ser Pro Met Asp Leu Asn Val Gly Met Leu Asn Ser  
 65 70 75 80  
 Ser Leu Arg Asp Ser Gly Tyr Ser Pro Ser Asn Ser Lys Ala Phe Ser  
 85 90 95  
 Ile Ile Thr Ser Leu Phe Leu Phe Ser Thr Glu Tyr Leu Gly Leu Ile  
 100 105 110  
 Cys Thr Tyr  
 115

<210> 185  
 <211> 2600  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 185  
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 atgaaatcat agttctttac atacatgtag ccggaatccc ttgaagttga tctgcctcct 180  
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 aaaagcgatg ccctctttat tgacagttac taattcgcca aactgctttt ttttatcaat 360  
 gtgattttcg cgttcacgcc attatccaat gtcaaaaagg ataatggaaa tgttaacatg 420  
 cctgtatgat ccgaccgttt ttagcaaaact tatcagggga aaaagtatat tccattaaat 480  
 gacacatgcc accatagata atggataatg aagaagttaa cgaagaatgt atgagattat 540  
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 aaaatgcata tatcacgttc agatgcttcc tggatggaat acatcgcaaa tctactaggt 660  
 ttctcgaaga gctacttttg aaacaagaaa atatgtacca taataacaat tacgaacgca 720  
 taaatgattc cgtgatacca ttggttctga aacttttatg gcttcaaatt cacgaacctt 780  
 cactccaatg gtttgagcac tggttccatg atatcatgcg actaagtaac agaagaaagt 840  
 tcagagtttt tagaattttt caaaaaaaaaa tgattcaatt tttcaaaatt acacacaggt 900  
 attactatga catcatcgaa cacctatgcg caaagtacga tatgaattcc gttatttcaa 960  
 atgctctctt cgcgaagttg aatttaatgc aatacacaga tggactttca actcatgaga 1020  
 aaattatctt aaacacgagt aatccactga cgttttccat tgtaatctca ctacaaagat 1080  
 gcgatgattaa tctaggttcc acacattttt ataaaacact actaaacaag ccgtctaaca 1140  
 aaccaagag tgtggaaggt tttgagaagt ctattaggta cttgaatatt gcctcactct 1200  
 atctcccagc cgttggagat acttattttc aacgagcgaa aatttacttg atcactggga 1260  
 aattctcact gtatttcttt gaattagtaa gaggagcatt ggtaaggatt ccgtctaaat 1320  
 gtgcgttaaa caatttgaaa gatttcattt tgactcctga tttccggaa agaagacgtc 1380  
 tgatgaaaaa attggcaatt cttgtgtcaa aagatctcaa aggtgagaaa tcattctttg 1440

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&lt;210&gt; 186

&lt;211&gt; 699

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 186

```

Met Asp Asn Glu Glu Val Asn Glu Glu Cys Met Arg Leu Phe Phe Lys
  1                      5                      10                      15

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```

Asn Ala Arg Ala His Leu Asp Lys His Leu Thr Ser Arg Leu Thr Cys
                20                      25                      30

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Asp Glu Asn Ala Tyr Ile Thr Phe Arg Cys Phe Leu Asp Gly Ile His
                35                      40                      45

```

```

Arg Lys Ser Thr Arg Phe Leu Glu Glu Leu Leu Leu Lys Gln Glu Asn
  50                      55                      60

```

```

Met Tyr His Asn Asn Asn Tyr Glu Arg Ile Asn Asp Ser Val Ile Pro
  65                      70                      75                      80

```

```

Leu Val Leu Lys Leu Leu Trp Leu Gln Ile His Glu Pro Thr Leu Gln
                85                      90                      95

```

```

Trp Phe Glu His Trp Phe His Asp Ile Met Arg Leu Ser Asn Arg Arg
                100                      105                      110

```

Lys Phe Arg Val Phe Arg Ile Phe Gln Lys Lys Met Ile Gln Phe Phe  
115 120 125

Lys Ile Thr His Arg Tyr Tyr Tyr Asp Ile Ile Glu His Leu Cys Ala  
130 135 140

Lys Tyr Asp Met Asn Ser Val Ile Ser Asn Ala Leu Phe Ala Lys Leu  
145 150 155 160

Asn Leu Met Gln Tyr Thr Asp Gly Leu Ser Thr His Glu Lys Ile Ile  
165 170 175

Leu Asn Thr Ser Asn Pro Leu Thr Phe Ser Ile Val Ile Ser Leu Gln  
180 185 190

Arg Cys Val Ile Asn Leu Gly Ser Thr His Phe Tyr Lys Thr Leu Leu  
195 200 205

Asn Lys Pro Ser Asn Lys Pro Lys Ser Val Glu Gly Phe Glu Lys Ser  
210 215 220

Ile Arg Tyr Leu Asn Ile Ala Ser Leu Tyr Leu Pro Ala Val Gly Asp  
225 230 235 240

Thr Tyr Phe Gln Arg Ala Lys Ile Tyr Leu Ile Thr Gly Lys Phe Ser  
245 250 255

Leu Tyr Phe Phe Glu Leu Val Arg Gly Ala Leu Val Arg Ile Pro Ser  
260 265 270

Lys Cys Ala Leu Asn Asn Leu Lys Asp Phe Ile Leu Thr Pro Asp Phe  
275 280 285

Pro Glu Arg Arg Arg Leu Met Lys Lys Leu Ala Ile Leu Val Ser Lys  
290 295 300

Asp Leu Lys Gly Glu Lys Ser Phe Phe Glu Gly Gln Ile Val Leu Gln  
305 310 315 320

Phe Leu Ser Ile Val Glu His Thr Leu Val Pro Gln Ser Trp Asn Ala  
325 330 335

Ser Arg Ala Ser Asn Cys Trp Leu Leu Lys Glu His Leu Gln Met Ala  
340 345 350

Ala Leu Lys Tyr His Ser Gly Asn Ile Asn Val Ile Leu Glu Asn Leu  
355 360 365

Ala Ala Thr Met Gly Ser Phe Asp Leu Met Phe Thr Thr Arg Lys Ser  
 370 375 380

Lys Glu Gln Lys Asn Lys Leu Lys Tyr Ala Asp Leu Ser Glu Arg Gln  
 385 390 395 400

Val Phe Phe Leu Asp Leu Ser Phe Asp Phe Ile Ala Asn Ile Ile Asp  
 405 410 415

Val Val Ile Lys Pro Ser Trp Gln Lys Asn Met Glu Asp Phe Arg Tyr  
 420 425 430

Leu Ala Ile Ile Arg Leu Leu Met Cys Trp Ile Lys Ser Tyr Arg Ser  
 435 440 445

Ile Leu Gln Tyr Thr His Arg His Arg Lys Phe Cys Thr Ser Phe Ala  
 450 455 460

Leu Leu Leu Asn Asp Leu Ile Asn Ser Pro Leu Asn Cys Ser Gly Asn  
 465 470 475 480

Ile Tyr Ser His Arg Pro Lys Arg Ser Tyr Leu Phe Arg Glu Asp Ile  
 485 490 495

Ile Phe Arg Glu Phe Ser Cys Ile Asn Phe Ala Leu Thr Asp Phe Asn  
 500 505 510

Asp Asp Tyr Val Tyr Asp Ser Pro Asp Met Ile Asn Asn Ile Ile Gly  
 515 520 525

Cys Pro Thr Leu Thr Lys Val Leu Ser Pro Lys Glu Glu Cys Val Leu  
 530 535 540

Arg Ile Arg Ser Ile Ile Phe Ser Gly Met Lys Phe Leu Glu Lys Asn  
 545 550 555 560

Asp Thr Gly Val Ile Trp Asn Ala Ser Lys Tyr Lys Phe Asp Leu Ile  
 565 570 575

Ser Pro Asn Ile Lys Ile Lys Arg Gln Ile Ala Leu Ser Glu Ile Ser  
 580 585 590

Ser Lys Ile Asn Val Lys Thr Gln Gln Glu Arg Val Val Ser Ser Arg  
 595 600 605

Lys Val Glu Ala Lys Arg Asp Glu Gln Gln Arg Lys Arg Ala Gly Lys  
 610 615 620

Ile Ala Val Thr Glu Leu Glu Lys Gln Phe Ala Asn Val Arg Arg Thr  
 625 630 635 640

Lys Lys Leu Ser Pro Leu Pro Glu Lys Asp Gly Val Ser Ser Glu Leu  
 645 650 655

Val Lys His Ala Ala Ser Arg Gly Arg Lys Thr Ile Thr Gly Pro Leu  
 660 665 670

Ser Ser Asp Phe Leu Ser Tyr Pro Asp Glu Ala Ile Asp Ala Asp Glu  
 675 680 685

Asp Ile Thr Val Gln Val Pro Asp Thr Pro Thr  
 690 695

<210> 187  
 <211> 2471  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 187  
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 tgcgcacgag cgttcttgaa aaataatctc atacattctt cgtaaacttc ttcattatcc 240  
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 caataaagag ggcacgcgtt ttgaaagcac cttcgtctgt gcgctcgctt cagctacgta 480  
 aaggtgtatt atagacaata atgaaagtgc tatgtgtcgc agagaaaaat tctatagcga 540  
 aggcagtttc acagatccta ggaggaggca gatcaacttc aagggattcc ggctacatgt 600  
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&lt;210&gt; 188

&lt;211&gt; 656

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 188

```

Met Lys Val Leu Cys Val Ala Glu Lys Asn Ser Ile Ala Lys Ala Val
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Ser Gln Ile Leu Gly Gly Gly Arg Ser Thr Ser Arg Asp Ser Gly Tyr
          20             25             30

Met Tyr Val Lys Asn Tyr Asp Phe Met Phe Ser Gly Phe Pro Phe Ala
          35             40             45

Arg Asn Gly Ala Asn Cys Glu Val Thr Met Thr Ser Val Ala Gly His
          50             55             60

Leu Thr Gly Ile Asp Phe Ser His Asp Ser His Gly Trp Gly Lys Cys
          65             70             75             80

Ala Ile Gln Glu Leu Phe Asp Ala Pro Leu Asn Glu Ile Met Asn Asn
          85             90             95

Asn Gln Lys Lys Ile Ala Ser Asn Ile Lys Arg Glu Ala Arg Asn Ala
          100            105            110

Asp Tyr Leu Met Ile Trp Thr Asp Cys Asp Arg Glu Gly Glu Tyr Ile

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115		120		125
Gly Trp Glu Ile Trp Gln Glu Ala Lys Arg Gly Asn Arg Leu Ile Gln				
130		135		140
Asn Asp Gln Val Tyr Arg Ala Val Phe Ser His Leu Glu Arg Gln His				
145		150		155 160
Ile Leu Asn Ala Ala Arg Asn Pro Ser Arg Leu Asp Met Lys Ser Val				
	165		170	175
His Ala Val Gly Thr Arg Ile Glu Ile Asp Leu Arg Ala Gly Val Thr				
	180		185	190
Phe Thr Arg Leu Leu Thr Glu Thr Leu Arg Asn Lys Leu Arg Asn Gln				
	195		200	205
Ala Thr Met Thr Lys Asp Gly Ala Lys His Arg Gly Gly Asn Lys Asn				
	210		215	220
Asp Ser Gln Val Val Ser Tyr Gly Thr Cys Gln Phe Pro Thr Leu Gly				
	225		230 235	240
Phe Val Val Asp Arg Phe Glu Arg Ile Arg Asn Phe Val Pro Glu Glu				
	245		250	255
Phe Trp Tyr Ile Gln Leu Val Val Glu Asn Lys Asp Asn Gly Gly Thr				
	260		265	270
Thr Thr Phe Gln Trp Asp Arg Gly His Leu Phe Asp Arg Leu Ser Val				
	275		280	285
Leu Thr Phe Tyr Glu Thr Cys Ile Glu Thr Ala Gly Asn Val Ala Gln				
	290		295	300
Val Val Asp Leu Lys Ser Lys Pro Thr Thr Lys Tyr Arg Pro Leu Pro				
	305		310 315	320
Leu Thr Thr Val Glu Leu Gln Lys Asn Cys Ala Arg Tyr Leu Arg Leu				
	325		330	335
Asn Ala Lys Gln Ser Leu Asp Ala Ala Glu Lys Leu Tyr Gln Lys Gly				
	340		345	350
Phe Ile Ser Tyr Pro Arg Thr Glu Thr Asp Thr Phe Pro His Ala Met				
	355		360	365
Asp Leu Lys Ser Leu Val Glu Lys Gln Ala Gln Leu Asp Gln Leu Ala				



370	375	380
Ala Gly Gly Arg Thr Ala Trp Ala Ser Tyr Ala Ala Ser Leu Leu Gln		
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Pro Glu Asn Thr Ser Asn Asn Asn Lys Phe Lys Phe Pro Arg Ser Gly		
405	410	415
Ser His Asp Asp Lys Ala His Pro Pro Ile His Pro Ile Val Ser Leu		
420	425	430
Gly Pro Glu Ala Asn Val Ser Pro Val Glu Arg Arg Val Tyr Glu Tyr		
435	440	445
Val Ala Arg His Phe Leu Ala Cys Cys Ser Glu Asp Ala Lys Gly Gln		
450	455	460
Ser Met Thr Leu Val Leu Asp Trp Ala Val Glu Arg Phe Ser Ala Ser		
465	470	475 480
Gly Leu Val Val Leu Glu Arg Asn Phe Leu Asp Val Tyr Pro Trp Ala		
485	490	495
Arg Trp Glu Thr Thr Lys Gln Leu Pro Arg Leu Glu Met Asn Ala Leu		
500	505	510
Val Asp Ile Ala Lys Ala Glu Met Lys Ala Gly Thr Thr Ala Pro Pro		
515	520	525
Lys Pro Met Thr Glu Ser Glu Leu Ile Leu Leu Met Asp Thr Asn Gly		
530	535	540
Ile Gly Thr Asp Ala Thr Ile Ala Glu His Ile Asp Lys Ile Gln Val		
545	550	555 560
Arg Asn Tyr Val Arg Ser Glu Lys Val Gly Lys Glu Thr Tyr Leu Gln		
565	570	575
Pro Thr Thr Leu Gly Val Ser Leu Val His Gly Phe Glu Ala Ile Gly		
580	585	590
Leu Glu Asp Ser Phe Ala Lys Pro Phe Gln Arg Arg Glu Met Glu Gln		
595	600	605
Asp Leu Lys Lys Ile Cys Glu Gly His Ala Ser Lys Thr Asp Val Val		
610	615	620
Lys Asp Ile Val Glu Lys Tyr Arg Lys Tyr Trp His Lys Thr Asn Ala		

625

630

635

640

Cys Lys Asn Thr Leu Leu Gln Val Tyr Asp Arg Val Lys Ala Ser Met  
 645 650 655

&lt;210&gt; 189

&lt;211&gt; 1937

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 189

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tcctttcccc caactag

1937

&lt;210&gt; 190

&lt;211&gt; 478

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 190

Met Thr Gly Pro Gly Pro Glu Ile Asn Lys Glu Glu His Pro Ser Ser  
 1 5 10 15

Pro Gly Lys Lys Gln Ile Thr Tyr Asn Ser Ile Pro Lys Asn Ala Asn  
 20 25 30

Leu Ile Asp Gly Ser Thr Asn Ser Ser Lys Arg Pro Ile Glu Lys Tyr  
 35 40 45

Asp Lys Arg Ile Ala Asp Pro Thr Lys Ser Tyr Phe Pro His Ser Ile  
 50 55 60

Ser Arg Thr Pro Arg Arg Lys Tyr Thr Tyr Ile Leu Val Leu Thr Ser  
 65 70 75 80

Leu Asn Gly Thr Phe Glu Ser Lys His Val Val Ile Pro Phe Lys Pro  
 85 90 95

Asp Gly Leu Lys Leu Gly Arg Pro Val Ala Asn Ser Asn Ser Ser Ser  
 100 105 110

Ser Ser Ser Leu Arg Gly Gly Lys Arg Val Asp Ser His Thr Phe Ser  
 115 120 125

Gln Val Arg Ser Asp Asn Gly Asn Phe Asp Ser Arg Val Leu Ser Arg  
 130 135 140

Asn His Ala Leu Leu Ser Cys Asp Pro Leu Thr Gly Lys Val Tyr Ile  
 145 150 155 160

Arg Asp Leu Lys Ser Ser Asn Gly Thr Phe Ile Asn Gly Gln Arg Ile  
 165 170 175

Gly Ser Asn Asp Val Glu Ile Lys Val Gly Asp Val Ile Asp Leu Gly  
 180 185 190

Thr Asp Ile Asp Thr Lys Ile Glu His Arg Lys Ile Ser Ala Thr Val  
 195 200 205

Glu Glu Leu Phe Val Gln Pro Leu Leu Glu Ser Pro Ile Phe Glu Asn  
 210 215 220

Glu Asp Ser Asp Asp Cys His Thr Ile Thr Glu Lys Glu Glu Ala Ala  
 225 230 235 240

Ala Ile Thr Ser His Ile Tyr Gly Asp Ser Asn Asn Leu Glu Leu Glu  
 245 250 255

Glu Val Ile Leu Gly Ser Asp Thr Glu Ile Leu Ser Gly Ile Phe Ile  
 260 265 270

Asn Asn Cys Ile Gly Thr Ser Pro Thr Leu Ser Asn Ile Ile Lys Thr  
 275 280 285

Leu Ala Met Glu Ile Pro Phe Ser Lys Cys Asp Asn Phe Lys Leu Gln  
 290 295 300

Ser Met Glu Asn Phe Leu Ile Asn Tyr Thr Thr His Leu Glu Tyr Thr  
 305 310 315 320

Asn Lys Leu Leu Val Glu Lys Asn Asp Gln Gln Leu Val Lys Leu Gln  
 325 330 335

Asn Gly Leu Arg Arg Lys Leu Ser Gly Lys Tyr Glu Lys Ile Ile Glu  
 340 345 350

Gln Asn Arg Asn Gln Val Lys Gln Leu Glu Arg Asp His Met Phe Phe  
 355 360 365

Lys Lys Ser Phe Glu Val Lys Lys Arg Arg Asn Asn Glu Lys Gln Lys  
 370 375 380

Ser Met Glu Arg Glu Ile Glu Asp Leu Lys Thr Arg Leu Glu Val Glu  
 385 390 395 400

Arg Tyr Lys Asn Ser Gln Met Met Lys Lys Asn Lys Gln Lys Glu Gln  
 405 410 415

Glu Leu Ser Thr Ala Ser Lys Lys Lys Thr Thr Glu His Asp Thr Arg  
 420 425 430

Gly Val Pro Gly Met Asn Pro Lys Gly Thr Asp Lys Phe Ser Ile Lys  
 435 440 445

Asn Thr Leu Cys Asn His Phe Thr Leu Leu Thr Phe Gly Thr Ile Ser  
 450 455 460

Ile Gly Ile Ile Ala Ile Val Phe Lys Ile Leu Ser Pro Asn  
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<210> 191

<211> 2849

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 191

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<210> 192

<211> 782

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 192

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Thr	Val	Pro	Asp	Glu	His	His	Asp	Phe	Arg	Lys	Pro	Thr	Ala	Lys	Val
			20					25					30		
Val	Thr	Thr	Gln	Leu	Thr	Ile	Ala	Thr	Ser	Leu	Gly	Ile	Phe	Ala	Leu
			35				40					45			
Leu	Ser	Phe	Ser	Ile	Leu	Leu	Lys	Lys	Trp	Pro	Arg	Leu	Tyr	Ala	Ser
	50						55				60				
Arg	Arg	Tyr	Lys	Asp	Asp	Gly	Asn	Leu	Arg	Leu	Pro	Ser	Trp	Asn	Gln
65					70				75					80	
Ser	Ser	Leu	Phe	Gly	Trp	Leu	Thr	Val	Leu	Tyr	Lys	Ile	Arg	Asp	Glu
				85					90					95	
Gln	Ile	Leu	Glu	Tyr	Ala	Gly	Leu	Asp	Ala	Tyr	Val	Phe	Leu	Ser	Phe
			100					105					110		
Phe	Lys	Met	Cys	Ile	Lys	Leu	Leu	Ser	Ile	Phe	Cys	Phe	Phe	Ser	Val
		115					120				125				
Cys	Val	Ile	Ser	Pro	Val	Arg	Tyr	His	Phe	Thr	Gly	Lys	Ile	Asp	Asp
		130				135					140				
Gly	Asn	Asp	Asp	Asp	Asp	Ser	Glu	Ser	Ser	Leu	Ile	His	Leu	Val	Lys
145					150					155				160	

Arg Ile Val Glu Gly Ser Gly Asp Gly Asp Asn His Ser Ala Pro Glu  
165 170 175

Arg Thr Asn Val Tyr Leu Trp Met Tyr Val Leu Phe Thr Tyr Phe Phe  
180 185 190

Thr Phe Ile Ala Ile Lys Met Ala Val Ala Glu Thr Lys His Val Val  
195 200 205

Ser Thr Arg Gln Ala Tyr Leu Gly Lys Gln Asn Thr Ile Thr Asp Arg  
210 215 220

Thr Ile Arg Leu Ser Gly Ile Pro Ile Glu Leu Arg Asp Ser Glu Ala  
225 230 235 240

Leu Lys Thr Arg Ile Glu Gln Leu Lys Ile Gly Thr Val Ser Ser Ile  
245 250 255

Thr Ile Cys Arg Glu Trp Gly Pro Leu Asn Lys Leu Phe His Cys Arg  
260 265 270

Lys Lys Ile Leu Lys Asn Leu Glu Leu Lys Tyr Ser Glu Cys Pro Arg  
275 280 285

Glu Leu Arg Thr Arg Gln Pro Tyr Ser Glu Asn Tyr His Leu Leu Gly  
290 295 300

Asn Glu Gln Ser Gly Ala Val Thr His Gly Glu Asn Val Pro Ser Ser  
305 310 315 320

Asn Asn Asn Asp Glu Asp Thr Ile Leu Tyr Ser Gln Ile Ser Leu Gly  
325 330 335

Glu Arg Pro Lys Met Lys Ile Gly Tyr Arg Gly Ile Phe Gly Lys Glu  
340 345 350

Val Asp Ala Ile Glu Tyr Leu Glu Gln Gln Leu Lys Phe Ile Asp Ala  
355 360 365

Glu Ile Ile Glu Ala Arg Lys Gln His Tyr Ser Ala Thr Pro Thr Ala  
370 375 380

Phe Val Thr Met Asp Ser Val Ala Asn Ala Gln Met Ala Ala Gln Ala  
385 390 395 400

Val Leu Asp Pro Arg Val His Tyr Phe Ile Thr Arg Leu Ala Pro Ala  
405 410 415

Pro His Asp Ile Lys Trp Asp His Val Cys Leu Ser Arg Lys Asp Arg  
 420 425 430

Leu Thr Lys Val Tyr Ser Thr Thr Val Phe Ile Gly Leu Ser Ser Leu  
 435 440 445

Phe Leu Val Ile Pro Val Ser Tyr Leu Ala Thr Leu Leu Asn Leu Lys  
 450 455 460

Thr Leu Ser Lys Phe Trp Pro Ser Val Gly Gln Leu Leu Lys Asp His  
 465 470 475 480

Gln Trp Ala Ala Asn Ile Val Thr Gly Leu Leu Pro Thr Tyr Leu Phe  
 485 490 495

Thr Leu Leu Asn Phe Gly Ile Pro Tyr Phe Tyr Glu Tyr Leu Thr Ser  
 500 505 510

Tyr Gln Gly Leu Val Ser Tyr Ser Glu Glu Glu Ile Ser Leu Val Ser  
 515 520 525

Lys Asn Phe Phe Tyr Ile Phe Val Asn Leu Phe Leu Val Phe Thr Leu  
 530 535 540

Ala Gly Thr Ala Ser Asn Tyr Trp Ala Tyr Leu Ser Asp Thr Thr Lys  
 545 550 555 560

Ile Ala Tyr Gln Leu Ala Thr Ser Val Lys Glu Phe Ser Leu Phe Tyr  
 565 570 575

Val Asp Leu Ile Ile Leu Gln Gly Ile Gly Met Phe Pro Phe Lys Leu  
 580 585 590

Leu Leu Val Gly Ser Leu Ile Gly Phe Pro Leu Val Lys Ile Lys Ala  
 595 600 605

Lys Thr Pro Arg Gln Arg Asn Glu Leu Tyr Asn Pro Pro Ile Phe Asn  
 610 615 620

Phe Gly Leu Gln Leu Pro Gln Pro Ile Leu Ile Leu Ile Ile Thr Leu  
 625 630 635 640

Ile Tyr Ser Val Met Ser Thr Lys Ile Leu Thr Ser Gly Leu Ala Tyr  
 645 650 655

Phe Ile Ile Gly Phe Tyr Val Tyr Lys Tyr Gln Leu Ile Phe Ala Thr  
 660 665 670



Asp His Leu Pro His Ser Thr Gly Lys Val Trp Pro Leu Ile Phe Arg  
675 680 685

Arg Ile Ile Val Gly Leu Leu Leu Phe Gln Leu Thr Met Thr Gly Thr  
690 695 700

Leu Ala Gly Phe Glu Gly Gly Trp Val Leu Ser Ser Cys Leu Phe Pro  
705 710 715 720

Leu Pro Val Val Thr Leu Cys Phe Leu Tyr Asp Phe Glu Lys Asn Tyr  
725 730 735

Leu Pro Leu Ser Lys Tyr Ile Ala Leu Ser Ser Ile Arg Glu Tyr Glu  
740 745 750

Arg Asp Asn Ser Thr Val Asn Ser Ala Asn Glu Glu Glu Ser Tyr Ala  
755 760 765

Tyr Pro Tyr Ala Val Ser Glu Leu Glu Gly Pro Met Leu Asp  
770 775 780

<210> 193

<211> 1781

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 193

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cacaaggaga cccacggcag tgcaaaagta gcatctgact tacagaagat gctaaataaa 180
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actctttcac ataataaagt atgtaaacta tatagataga agatgtcccg tgtctttttg 360
tctactaaat gatgatctgc tcatttaaag tcgccgcgac tactttgaca aaaaaaaaaa 420
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aaggcacata gcagcacaca atgtcgacac aaaaccagct tattccacaa gcttatattt 540
ctaactttca taacagattg acaaacgaag atgatggtat ccccatcttt acaatggctc 600
aacaacaag gcagcataaa agggctaaag tggtaacta tgcggaatat gacaacgatc 660
tctttgatga attcaatatg aacgggttcta atttcaacaa tgctgatata cactataaag 720
ataatgcagt gtctcatgaa aatactccgg cacttacaaa tgggtgttacc atggacggtt 780
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```

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&lt;210&gt; 194

&lt;211&gt; 426

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 194

```

Met Ser His Gln Asn Gln Leu Ile Pro Gln Ala Tyr Ile Ser Asn Phe
  1              5              10              15

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```

His Asn Arg Leu Thr Asn Glu Asp Asp Gly Ile Pro Ile Phe Thr Met
      20              25              30

```

```

Ala Gln Gln Thr Arg Gln His Lys Arg Ala Lys Val Val Asn Tyr Ala
      35              40              45

```

```

Glu Tyr Asp Asn Asp Leu Phe Asp Glu Phe Asn Met Asn Gly Ser Asn
      50              55              60

```

```

Phe Asn Asn Ala Asp Thr His Tyr Lys Asp Asn Ala Val Ser His Glu
      65              70              75              80

```

```

Asn Thr Pro Ala Leu Thr Asn Gly Val Thr Met Asp Gly Ser Glu Tyr
      85              90              95

```

```

Asn Val Leu Glu Asn Met Asn Gly Ala Asp Ser Ile Ile Ser Asn Asn
      100              105              110

```

```

Lys Tyr Asp Ala Gly Ser Asn Met Val Val Glu Ser Leu Ser Gly Leu
      115              120              125

```

```

Asn Ser Asn Asn Asn Ala Ser Asn Gly Pro Ser Asn Lys Ala Gln Ala
      130              135              140

```

```

Gln Asp Ile Gly Asn Ala Val Leu Pro Asp Leu Gln Asp Gln His His

```

145                                      150                                      155                                      160  
 Asn Pro Phe Asn Ile Leu Arg Tyr Pro Lys Ile Arg Asp Thr Phe Ile  
    165                                      170                                      175  
 Asn Gly Lys Val Val Ser Pro Tyr Arg Leu Asn Thr Asp Gln Glu Thr  
    180                                      185                                      190  
 Lys Ala Asn Ala Asn Ser Gly Glu Ala Ile Met Ile Pro Ile Thr Leu  
    195                                      200                                      205  
 Asp Ile Glu His Met Gly His Thr Ile Lys Asp Gln Phe Leu Trp Asn  
    210                                      215                                      220  
 Tyr Asn Asp Asp Ser Ile Ser Pro Glu Glu Phe Ala Ser Ile Tyr Cys  
    225                                      230                                      235                                      240  
 Lys Asp Leu Asp Met Thr Ser Ala Thr Leu Gln Thr Gln Ile Ala Asn  
    245                                      250                                      255  
 Ile Ile Lys Glu Gln Leu Lys Asp Leu Glu Asn Ile Ala Ala Thr Glu  
    260                                      265                                      270  
 Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Gln  
    275                                      280                                      285  
 Asp Arg Phe Phe Glu Asp Asn Phe Gln Trp Asn Leu Asn Asp Lys Ser  
    290                                      295                                      300  
 Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Gln Asp Leu Gly Leu  
    305                                      310                                      315                                      320  
 Thr Arg Glu Phe Ile Pro Leu Ile Ser Gln Ser Leu His Glu Thr Ile  
    325                                      330                                      335  
 Leu Lys Ile Lys Lys Asp Trp Val Asp Gly His Leu Ile Gln Asp His  
    340                                      345                                      350  
 Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp  
    355                                      360                                      365  
 Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Glu Ile Leu Thr  
    370                                      375                                      380  
 Lys Glu Glu Ile Gln Lys Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg  
    385                                      390                                      395                                      400  
 Arg Leu Lys Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg

405

410

415

Leu Asp Asp Leu Glu Thr Thr Met Arg Met  
420 425

&lt;210&gt; 195

&lt;211&gt; 815

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 195

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ccatcatctt cgtttgtaa tctgttatga aagttagaaa tataagcttg tggaataagc 720
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&lt;210&gt; 196

&lt;211&gt; 104

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 196

Met Arg His Cys Ile Ile Phe Ile Val Cys Ile Ser Ile Val Glu Ile  
1 5 10 15

Arg Thr Val His Ile Glu Phe Ile Lys Glu Ile Val Val Ile Phe Arg  
20 25 30

Ile Val Asp His Phe Ser Pro Phe Met Leu Pro Cys Leu Leu Ser His  
35 40 45

Cys Lys Asp Gly Asp Thr Ile Ile Phe Val Cys Gln Ser Val Met Lys  
50 55 60

Val Arg Asn Ile Ser Leu Trp Asn Lys Leu Val Leu Val Arg His Cys

246

```

      65              70              75              80
Val Leu Leu Cys Ala Phe Leu Leu Ser Phe Phe Asn Val Leu His Ser
      85              90              95
Ile Ile Ser Ile Cys Arg Ile Phe
      100

```

```
<210> 197
<211> 737
<212> DNA
<213> Saccharomyces cerevisiae
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<400> 197						
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acaaaacagg	gcattctcaca	tatttcgcgt	ctgggtgttct	tttagctcat	tccgatatta	180
ttccaagacg	gaattttcat	ctagagaaaa	tgcattccgtg	cattttcata	aaccacaca	240
attaaaatgc	cttgcgaaaa	ggaggactcg	tccgtgcaac	tgttgaaaaa	aatagacgga	300
gcatcatacg	ttcgagtggg	aaattatgga	gagttttcca	agctctatgg	catgtagagt	360
cgtgattgct	gctgtacgct	tttgcacaa	attgaattctt	caatctaaag	aattaaattt	420
tctaattttc	atgtagaaat	atttcaactg	ttagtttttt	atttcagggt	gaatatagta	480
cgacaaaata	tcaaggaaaa	atggctagag	aaatcaccga	catcaaaaaa	tttttgggaat	540
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ccggtaagcc	attcagacaa	accaagttca	aggtttagagg	ctcttcttct	ttgtacactt	660
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<210> 198
<211> 78
<212> PRT
<213> Saccharomyces cerevisiae
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```

<400> 198
Met Ala Arg Glu Ile Thr Asp Ile Lys Gln Phe Leu Glu Leu Thr Arg
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Arg Ala Asp Val Lys Thr Ala Thr Val Lys Ile Asn Lys Lys Leu Asn
      20             25             30

Lys Ala Gly Lys Pro Phe Arg Gln Thr Lys Phe Lys Val Arg Gly Ser
      35             40             45

Ser Ser Leu Tyr Thr Leu Val Ile Asn Asp Ala Gly Lys Ala Lys Lys
  50             55             60

```

Leu Ile Gln Ser Leu Pro Pro Thr Leu Lys Val Asn Arg Leu

65

70

75

&lt;210&gt; 199

&lt;211&gt; 1331

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 199

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agttggaata a

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1331

&lt;210&gt; 200

&lt;211&gt; 127

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 200

Met Ala Lys Gln Ser Leu Asp Val Ser Ser Asp Arg Arg Lys Ala Arg

1

5

10

15

Lys Ala Tyr Phe Thr Ala Pro Ser Ser Gln Arg Arg Val Leu Leu Ser

20

25

30

Ala Pro Leu Ser Lys Glu Leu Arg Ala Gln Tyr Gly Ile Lys Ala Leu  
 35 40 45

Pro Ile Arg Arg Asp Asp Glu Val Leu Val Val Arg Gly Ser Lys Lys  
 50 55 60

Gly Gln Glu Gly Lys Ile Ser Ser Val Tyr Arg Leu Lys Phe Ala Val  
 65 70 75 80

Gln Val Asp Lys Val Thr Lys Glu Lys Val Asn Gly Ala Ser Val Pro  
 85 90 95

Ile Asn Leu His Pro Ser Lys Leu Val Ile Thr Lys Leu His Leu Asp  
 100 105 110

Lys Asp Arg Lys Ala Leu Ile Gln Arg Lys Gly Gly Lys Leu Glu  
 115 120 125

&lt;210&gt; 201

&lt;211&gt; 1376

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 201

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 cccatgtggt ggaggggaag aatatattga aatgtaaatg ttcttaagtt cggttgaact 180  
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 gattcaaagg cgaagtgcgt aggattgtaa ctcttatatc tttaggatac ttacaatttt 360  
 gtactgtttt caagaccact gtaaccgata ataaaccgga ggacacattt taaccacta 420  
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tattgccagc cagacaattc ggttacgtta ttttgactac ttctgcgggt attatggacc 1320  
 atgaggaagc tagaagaaag cacgtttccg gtaaaatctt gggttttgtc tatta 1376

<210> 202

<211> 130

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 202

Met Thr Arg Ser Ser Val Leu Ala Asp Ala Leu Asn Ala Ile Asn Asn  
 1 5 10 15

Ala Glu Lys Thr Gly Lys Arg Gln Val Leu Leu Arg Pro Ser Ser Lys  
 20 25 30

Val Ile Ile Lys Phe Leu Gln Val Met Gln Lys His Gly Tyr Ile Gly  
 35 40 45

Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln  
 50 55 60

Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asn  
 65 70 75 80

Val Lys Ile Gly Asp Ile Glu Lys Trp Thr Ala Asn Leu Leu Pro Ala  
 85 90 95

Arg Gln Phe Gly Tyr Val Ile Leu Thr Thr Ser Ala Gly Ile Met Asp  
 100 105 110

His Glu Glu Ala Arg Arg Lys His Val Ser Gly Lys Ile Leu Gly Phe  
 115 120 125

Val Tyr  
 130

<210> 203

<211> 1340

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 203

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 ctgactaatt gcattacagc cgaccaagg caatatcagt ttaataaaat atcatgtatc 120  
 tcaccctctt cttggtatta gtaaagagac gcctgatctt gtaacagtgg tgaagattgt 180



```

actagagcag aatcaagaat ttaaaaagtg taaaggcaag gcagaggcga tgtacataaa 240
acttcgaagt aagaaatatt taatagttct cgccacatca ctatgcagct atataaaaac 300
tactataaac gtttggtttg ttccttacgc acaatatect tgcctagaaa tcgtttttga 360
aatttaaatt tttattacca tttatttgat tcgccttcag aaaaatatgg aagagtgcac 420
atttaaaaag gactatttca gcatatagta aaagtcaggt tatttgttta tttgcgatat 480
cagagtaact taaactaact atgcagggca cttttaaaag gttttaccat cccacgctta 540
cgcggtatgtc cttcttggtat aaattcctca agcctatgat ggcaacggct tcccaaagg 600
aataccagat caaacaactg gtcaagccaa taggcttaac acaagcacca aggaaaagca 660
ccaaatactc ccagggggaaac tctttgaggg atatgtttga ttcggaaaag acaaaccaca 720
gagttaaaga gttggccggt gaattcagca aatctggact ttatgacgtg caagtcttcc 780
aaaagacaaa ggggaaattg tttatagctc cagtttcata ttggaaagaa gataaagctt 840
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catcctggcg ccagccattt tatttcgaat gttctagagg ccaatggcca ttttccgtca 1200
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agtttgccaa acgtctgtga                                     1340

```

&lt;210&gt; 204

&lt;211&gt; 279

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 204

```

Met Gln Gly Thr Phe Lys Arg Phe Tyr His Pro Thr Leu Thr Arg Met
  1              5              10              15

```

```

Ser Phe Leu Asp Lys Phe Leu Lys Pro Met Met Ala Thr Ala Ser Pro
          20              25              30

```

```

Lys Glu Tyr Gln Ile Lys Gln Leu Val Lys Pro Ile Gly Leu Thr Gln
      35              40              45

```

```

Ala Pro Arg Lys Ser Thr Lys Tyr Ser Gln Gly Asn Ser Leu Arg Asp
      50              55              60

```

```

Met Phe Asp Ser Glu Lys Thr Asn His Arg Val Lys Glu Leu Ala Val
      65              70              75              80

```

```

Glu Phe Ser Lys Ser Gly Leu Tyr Asp Val Gln Val Phe Gln Lys Thr
          85              90              95

```

```

Lys Gly Lys Leu Phe Ile Ala Pro Val Ser Tyr Trp Lys Glu Asp Lys
      100              105              110

```

Ala Leu Phe Phe Pro His Leu Ile Gly Thr Ala Met Asp Gly Thr Lys  
 115 120 125

Gln Gln Asn Ile Glu Asp Met Leu Arg Gly Lys Thr Ser Ile Val Arg  
 130 135 140

Leu Phe Ser Thr Ala Ser Gly Asp Lys Leu Ser Ser Ser Tyr Phe Gln  
 145 150 155 160

Gly Ile Val Asp Asp Asn Lys Lys Thr Asp Tyr Leu Thr Glu Ala Asp  
 165 170 175

Ala Arg Leu Ser Leu Asn Asp Ser Asn Val Gln Ile Ile Glu Val Asn  
 180 185 190

Leu Val Glu Asn Ala Val Lys Ser Ala Leu Val Lys Thr Leu Ala Arg  
 195 200 205

Trp Ala Asn Arg Val Pro Ser Trp Arg Gln Pro Phe Tyr Phe Glu Cys  
 210 215 220

Ser Arg Gly Gln Trp Pro Phe Ser Val Arg Glu Glu Leu Phe Cys Asn  
 225 230 235 240

Asn Val Phe Ser Gly Tyr Val Phe Leu Val Asp Gln Gln Leu Lys Ile  
 245 250 255

Arg Trp Ala Ala Cys Gly Glu Ala Thr Pro Ser Glu Lys Glu Ala Leu  
 260 265 270

Trp Lys Phe Ala Lys Arg Leu  
 275

&lt;210&gt; 205

&lt;211&gt; 1754

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 205

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 ggcattgccg ctactagttt tcaaggcatc attagtgtat gtcattgtcac tattcatgct 180  
 tgaattatta tcttcctcat cgctataatt ataggaatcg attcttcttt ttttgaaaaa 240  
 gaacttttta tctgtgttgg agtccgaatc ctccatgttt tggcgtactg aaggcttaag 300  
 ttcttcgacc tctctcggtt gtactatttc gaaattttgg atttttgta ttgttttgac 360

```

ataatgtaaa tactagatgc gcgctctaag gcctcagtat taaaaattgc aagatatccc 420
taacttgata attatttgaa agtcgcataa cgtacgataa attcgatact gcgaggatat 480
tatcaacgta tttaacacct atgaacgaag cagatgttac aaaatttggt aataatgcc 540
ggaaaacgct gaccgatgct caacttttat gttcaagtgc taatttaagg attgtagata 600
ttaagaaaaa attgtcatct tggcagttga gtattttcaa actcaatttt ctaatagttg 660
gcttgagaca gcaaggaaag tttctttaca ctattttaaa ggaaggcatt gggacaaagc 720
taatccagaa acaatggaat caagctgtct tagtggctct agttgatgag atgaagtact 780
ggcaatatga aatcacttct aaagtacaaa ggttgatgg tatagtaaat gaattgagca 840
tatcagaaaa agatgatacc gatccctcta aactaggaga ttacatctcg agagacaacg 900
ttaacttatt gaatgacaaa ctgaaagaag tgccagtaat tgagcgtcaa attgaaaaca 960
ttaagcttca atacgaaaat atggtcagaa aagttaacaa agaactgatt gataccaagt 1020
tgacggacgt aactcaaaaa ttccaaagta aatttggtat agataacctg atggaaacaa 1080
atgttgcaga gcagtttagc agggaaactaa cggaccttga aaaagattta gcagagataa 1140
tgaattcatt gacacagcac tttgataaga cattgctggt acaagataaa aaaattgata 1200
acgatgaacg tgaggagctg tttaaggtgg tacaaggcga cgacaaagaa ctatacaaca 1260
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tttatgataa ttttgaagaa agctacggtg acttagttct agaagcaaag aggagaaaag 1560
atgtggcaaa cagaatgaaa actatattga aagattgtga aaagcagttg cagaatttag 1620
atgctcagga ccaggaagaa cgtcagaatt ttatagcgga aaatggaact tatcttcctg 1680
agacaatctg gcccggtaaa attgacgatt tttcttcctt gtacacttta aattacaacg 1740
tgaagaatcc ttag                                     1754

```

&lt;210&gt; 206

&lt;211&gt; 417

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 206

```

Met Asn Glu Ala Asp Val Thr Lys Phe Val Asn Asn Ala Arg Lys Thr
  1                      5                      10                      15

```

```

Leu Thr Asp Ala Gln Leu Leu Cys Ser Ser Ala Asn Leu Arg Ile Val
          20                      25                      30

```

```

Asp Ile Lys Lys Lys Leu Ser Ser Trp Gln Leu Ser Ile Ser Lys Leu
          35                      40                      45

```

```

Asn Phe Leu Ile Val Gly Leu Arg Gln Gln Gly Lys Phe Leu Tyr Thr
          50                      55                      60

```

```

Ile Leu Lys Glu Gly Ile Gly Thr Lys Leu Ile Gln Lys Gln Trp Asn
          65                      70                      75                      80

```

```

Gln Ala Val Leu Val Val Leu Val Asp Glu Met Lys Tyr Trp Gln Tyr

```

85

90

95

Glu Ile Thr Ser Lys Val Gln Arg Leu Asp Gly Ile Val Asn Glu Leu  
 100 105 110

Ser Ile Ser Glu Lys Asp Asp Thr Asp Pro Ser Lys Leu Gly Asp Tyr  
 115 120 125

Ile Ser Arg Asp Asn Val Asn Leu Leu Asn Asp Lys Leu Lys Glu Val  
 130 135 140

Pro Val Ile Glu Arg Gln Ile Glu Asn Ile Lys Leu Gln Tyr Glu Asn  
 145 150 155 160

Met Val Arg Lys Val Asn Lys Glu Leu Ile Asp Thr Lys Leu Thr Asp  
 165 170 175

Val Thr Gln Lys Phe Gln Ser Lys Phe Gly Ile Asp Asn Leu Met Glu  
 180 185 190

Thr Asn Val Ala Glu Gln Phe Ser Arg Glu Leu Thr Asp Leu Glu Lys  
 195 200 205

Asp Leu Ala Glu Ile Met Asn Ser Leu Thr Gln His Phe Asp Lys Thr  
 210 215 220

Leu Leu Leu Gln Asp Lys Lys Ile Asp Asn Asp Glu Arg Glu Glu Leu  
 225 230 235 240

Phe Lys Val Val Gln Gly Asp Asp Lys Glu Leu Tyr Asn Ile Phe Lys  
 245 250 255

Thr Leu His Glu Val Ile Asp Asp Val Asp Lys Thr Ile Leu Asn Leu  
 260 265 270

Gly Gln Phe Leu Gln Ala Lys Ile Lys Glu Lys Thr Glu Leu His Ser  
 275 280 285

Glu Val Ser Glu Ile Ile Asn Asp Phe Asn Arg Asn Leu Glu Tyr Leu  
 290 295 300

Leu Ile Phe Lys Asp Ile Ser Asn Leu Ile Asp Ser Phe Lys Asn Ser  
 305 310 315 320

Cys Thr Gln Asp Ile Gln Thr Thr Lys Glu Leu Cys Glu Phe Tyr Asp  
 325 330 335

Asn Phe Glu Glu Ser Tyr Gly Asn Leu Val Leu Glu Ala Lys Arg Arg

254

340

345

350

Lys Asp Val Ala Asn Arg Met Lys Thr Ile Leu Lys Asp Cys Glu Lys  
 355 360 365

Gln Leu Gln Asn Leu Asp Ala Gln Asp Gln Glu Glu Arg Gln Asn Phe  
 370 375 380

Ile Ala Glu Asn Gly Thr Tyr Leu Pro Glu Thr Ile Trp Pro Gly Lys  
 385 390 395 400

Ile Asp Asp Phe Ser Ser Leu Tyr Thr Leu Asn Tyr Asn Val Lys Asn  
 405 410 415

Pro

&lt;210&gt; 207

&lt;211&gt; 1342

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 207

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 aatgatttga cgtaaaagca agtctcattc aagaaactgt aaaatccgta cacactactg 120  
 aattttacat ccatacattt ttttgaaatt tcatgttttt ttgaaaaatt ggaaaagggc 180  
 taaattatcc gtcgggggtgt cctcctagct cggtcacaacc taggcaaatt cgtttactgg 240  
 ggccatccaa gctcatcctt ccagagattc gcctttcaga ggcaaagaac tcgtctccgc 300  
 aggctctctg ttccggggagg aggagaattc ttgcgcggaa actgggtgat gcctgggcta 360  
 tggttaattct gacacctttg ctatcctaac tggaaaagggt ccttagtaat aacaatatca 420  
 ggtactttta cattgtttaa gatatactat tagtgaaaaa ccgatcttac gaaaagccaa 480  
 tagagcagaa agtggttaaag atgtcttttag ttgtacaaga acaagggttc ttccaacaca 540  
 ttttacggta tgttttacga gtacagtgc gatatgttga gagagtttca cattacatgg 600  
 gataatagct taatattgctg attgaaaata tgtgagtgc ctccgatgga ataataaacg 660  
 tcacgggtta ccaaatacga ggccgaatta actctacgct actataaaaa ttatcactag 720  
 attttaaagt aatacacagt ttattggaaa atacaatata tgactcaatg cgaattttaa 780  
 aatttcagtc aatacagctt gacaaattca tatttatcgt ccttccatgt tcgtacgcca 840  
 ttccaaaatg atgcgccatg ttgaaaattt ctcgaagaac ctagcagtgg tgtgaaataa 900  
 attactaaca ataagatgta caattttttg tgcgcccatt acaatcagtt tgttgaacac 960  
 caatgtcgat ggtaacatta aaattgttta cgctttgacc actattaagg gtgttggtcg 1020  
 tcgttactcc aacttgggtc gtaagaaggc tgatgttgat ttgcacaaga gagctgggtga 1080  
 attgacccaa gaagaattgg aaagaattgt ccaaattcatg caaaacccaa ctcattacaa 1140  
 gatcccagcc tggttcttaa accgtcaaaa cgacattact gatggtaagg actaccacac 1200  
 tttggctaac aacgtcgaat ccaagttgag agatgacttg gaaagattaa agaagatcag 1260  
 agcccaccgt ggtattagac acttctgggg tttacgtgtt agaggtaaac acaccaagac 1320  
 cactggtaga agaagagctt aa 1342

<210> 208  
 <211> 146  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 208

Met Ser Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg  
 1 5 10 15

Leu Leu Asn Thr Asn Val Asp Gly Asn Ile Lys Ile Val Tyr Ala Leu  
 20 25 30

Thr Thr Ile Lys Gly Val Gly Arg Arg Tyr Ser Asn Leu Val Cys Lys  
 35 40 45

Lys Ala Asp Val Asp Leu His Lys Arg Ala Gly Glu Leu Thr Gln Glu  
 50 55 60

Glu Leu Glu Arg Ile Val Gln Ile Met Gln Asn Pro Thr His Tyr Lys  
 65 70 75 80

Ile Pro Ala Trp Phe Leu Asn Arg Gln Asn Asp Ile Thr Asp Gly Lys  
 85 90 95

Asp Tyr His Thr Leu Ala Asn Asn Val Glu Ser Lys Leu Arg Asp Asp  
 100 105 110

Leu Glu Arg Leu Lys Lys Ile Arg Ala His Arg Gly Ile Arg His Phe  
 115 120 125

Trp Gly Leu Arg Val Arg Gly Gln His Thr Lys Thr Thr Gly Arg Arg  
 130 135 140

Arg Ala  
 145

<210> 209  
 <211> 1268  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 209

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```

ccatacacca tagcaccagt acactatatt tttatgaatt ttactaagaa ttattcctgc 180
aggagctcca ctgaaaaaaaa aagagcagca tggatgtccg gtagaagtgc tactgagtaa 240
atgggaagga cgcggtagat ccagtgtgga atcaaggtgg tgccggtgtg aagccgcctc 300
ggccggctgg actctccagg ccggagtgat gattgccacg ctgaacgtaa cacagtttca 360
caataccagt gtctctatta gtgagttcca atgtatagtt agtagtggtt ttttgatata 420
tgtgagtggg agcagatttg aacttagtta gttgtattcg cctttgagga aaccaagcaa 480
aaaaccgatc tagactaatc atggctgttg gtaagaataa gagactatcc agaggtaaga 540
agggtttgaa gaagaagggtc gttgacccat ttaccagaaa ggaatgggtc gatattaaag 600
ccccatccac ttttgaaaac agaaatgttg gtaagacttt agttaacaag tccactgggt 660
tgaagaatgc ttccgatgct ttgaagggtg gagttgtcga agtttggttg gctgacttgc 720
aaggttctga agaccattct ttcagaaagg tcaagttgag agtcgatgaa gttcaaggta 780
agaacttggt gaccaacttc cacggtatgg acttcactac cgacaaattg agatcaatgg 840
tcagaaaatg gcaaactttg atcgaagcta atgttaccgt taagacttcc gatgattacg 900
ttttgagaat ctttgctatt gccttcacca gaaagcaagc taaccaagtt aagagacact 960
cttacgctca atcttccac atcagagcta tcagaaaagt tatttctgaa atcttgacca 1020
gagaagttca aaactctact ttggctcaat tgacctcaa attgattcca gaagttatca 1080
acaaggaaat cgaaaatgct accaaggaca tcttccact acaaaacatc cacgtagtaa 1140
aggttaagtt attgaaacaa ccaaagttcg acgttggtgc tttgatggct ttgcatgggt 1200
aaggttccgg tgaagaaaag ggtaagaagg tttctggtt caaggatgaa gtcttggaag 1260
ctgtgtaa 1268

```

&lt;210&gt; 210

&lt;211&gt; 255

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 210

```

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Arg Gly Lys Lys Gly Leu
  1             5             10             15

```

```

Lys Lys Lys Val Val Asp Pro Phe Thr Arg Lys Glu Trp Phe Asp Ile
          20             25             30

```

```

Lys Ala Pro Ser Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Val
          35             40             45

```

```

Asn Lys Ser Thr Gly Leu Lys Asn Ala Ser Asp Ala Leu Lys Gly Arg
          50             55             60

```

```

Val Val Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser
          65             70             75             80

```

```

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu
          85             90             95

```

```

Leu Thr Asn Phe His Gly Met Asp Phe Thr Thr Asp Lys Leu Arg Ser
          100            105            110

```

Met Val Arg Lys Trp Gln Thr Leu Ile Glu Ala Asn Val Thr Val Lys  
 115 120 125

Thr Ser Asp Asp Tyr Val Leu Arg Ile Phe Ala Ile Ala Phe Thr Arg  
 130 135 140

Lys Gln Ala Asn Gln Val Lys Arg His Ser Tyr Ala Gln Ser Ser His  
 145 150 155 160

Ile Arg Ala Ile Arg Lys Val Ile Ser Glu Ile Leu Thr Arg Glu Val  
 165 170 175

Gln Asn Ser Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val  
 180 185 190

Ile Asn Lys Glu Ile Glu Asn Ala Thr Lys Asp Ile Phe Pro Leu Gln  
 195 200 205

Asn Ile His Val Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp  
 210 215 220

Val Gly Ala Leu Met Ala Leu His Gly Glu Gly Ser Gly Glu Glu Lys  
 225 230 235 240

Gly Lys Lys Val Ser Gly Phe Lys Asp Glu Val Leu Glu Thr Val  
 245 250 255

<210> 211  
 <211> 2042  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 211  
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 ctttatttcc acttctttac aagctttctg cctttctcta tgacgtcttt cccaaaacac 180  
 tacctcttga cagcacttgt tgttttcggt tttctctaag aatatcacta ttttcacttt 240  
 tttcaccttt tccaccatta cgtcggtaag caacagcatt acgccggcct caccttagag 300  
 gggaagaata agggatcttt ggaactgaag gaaaataagg gagaggagg aaacaaggag 360  
 gcggtgaaag gggatcgaca gggattttaa agccactcat ggagtcgtat tcctagcatg 420  
 attagattac cggagttag aagaggatct gcaatagaag aggagacaac tacaaaagaa 480  
 ctgttaatta agagaagaag atgaagcaat tcaagttggt taatgcggtt tccgcatcat 540  
 ttgtgcttat tggcttagtg ttggccaatt cagattcagt gttcgacaag tggacgcagg 600  
 aagacctggc cgattattta cgtgataata agaagagctt ggaaaagtac gctacagact 660  
 ccattgagga cttgaaaacg gaggcacgc aggtatggga caaacacgcg cagcccaaac 720



```

catggtggca ggtgtggtct agtgacagca gtagcgtgag caacagtaac cccggatggt 780
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cagacagtct acgtaacttc ttgaagaaaa acggcgtgga tgttgacgac gctaaggctt 900
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tagttcagaa agtcaaggaa aacatctacc gaacttcaga aaaggcagaa cagcagcgtc 1140
tgggtttgct agaaagcttg gatttggtc accaacaat attagacaca tcgggacaaa 1200
taaaagacac tgtatttgac aagtgggtc gtgatcagtt aaccaattgg ttggagagcc 1260
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aagaaaattc tgccaatttg aaagatgata tctactggta cctggactat atgaaaagag 1380
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aaaatttcct cacaaatttg tactccaagt tcagaggtaa gactgacaat gtgatcaatg 1500
atactttttt gggtggccta gactcttggc caaaggacaa attgaaaatg tttttgatag 1560
ctcgtggtat taagtactca atgctgtcta ctgaacatca attgagagaa ttagtcaaaa 1620
aatccagaaa cgaaaaactc aagatcctgc caaaagacta caaaaaatac tttgacaaca 1680
gtaactggtc tttggatgac ataaagggtt gggttgctga caaaaaggac gacttccaag 1740
attctcagac ttactccaca attatgcagg attttgacaa ggtttccaaa aacacaaatg 1800
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acctattgca gtacctaaaa tcattcgggt ttccggttaa acagacttct acgaaggacg 1920
acttaatcaa cttggccaag cagaatacgc aatggttggt cggcactgtt aaggagcctg 1980
cttacaagag gtacctacat aacgttaaaa actggtcgaa aagcatatta gggttcaact 2040
aa

```

&lt;210&gt; 212

&lt;211&gt; 513

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 212

```

Met Lys Gln Phe Lys Leu Val Asn Ala Val Ser Ala Ser Phe Val Leu
  1              5              10              15

```

```

Ile Gly Leu Val Leu Ala Asn Ser Asp Ser Val Phe Asp Lys Trp Thr
          20              25              30

```

```

Gln Glu Asp Leu Ala Asp Tyr Leu Arg Asp Asn Lys Lys Ser Leu Glu
          35              40              45

```

```

Lys Tyr Ala Thr Asp Ser Ile Glu Asp Leu Lys Thr Glu Ala Ser Gln
          50              55              60

```

```

Val Trp Asp Lys His Ala Gln Pro Lys Pro Trp Trp Gln Val Trp Ser
          65              70              75              80

```

```

Ser Asp Ser Ser Ser Val Ser Asn Ser Asn Pro Gly Trp Phe Gly Tyr
          85              90              95

```

Thr Gly Ser Ser Asp His Pro Val Ser Asp Trp Leu Phe Asp Thr Trp  
 100 105 110  
 Ser Thr Asp Ser Leu Arg Asn Phe Leu Lys Lys Asn Gly Val Asp Val  
 115 120 125  
 Asp Asp Ala Lys Ala Ser Lys Asp Ser Leu Val Lys Thr Ala Lys Glu  
 130 135 140  
 Asn Phe Asn Lys Ile Ser Lys Ser Leu Lys Ser Ser Gly Tyr Tyr Pro  
 145 150 155 160  
 Ser Ser Ser Tyr Phe Asp Ser Trp Ser Thr Lys Asp Leu Gln Asn Trp  
 165 170 175  
 Leu Asn Asp Asn Gly Ile Asp Tyr Asp Lys Ala Val Gln Ser Lys Asp  
 180 185 190  
 Glu Leu Val Gln Lys Val Lys Glu Asn Ile Tyr Arg Thr Ser Glu Lys  
 195 200 205  
 Ala Glu Gln Gln Arg Leu Gly Leu Leu Glu Ser Leu Asp Leu Ala His  
 210 215 220  
 Gln Gln Ile Leu Asp Thr Ser Gly Gln Ile Lys Asp Thr Val Phe Asp  
 225 230 235 240  
 Lys Trp Ser Ser Asp Gln Leu Thr Asn Trp Leu Glu Ser His Lys Val  
 245 250 255  
 Asn Ile Asp Lys Asn Met Ala Lys Lys His Asp Tyr Leu Val Arg Met  
 260 265 270  
 Ala Lys Glu Asn Ser Ala Asn Leu Lys Asp Asp Ile Tyr Trp Tyr Leu  
 275 280 285  
 Asp Tyr Met Lys Arg Glu Ser Ser Pro Phe Leu Thr Lys Thr Pro Glu  
 290 295 300  
 Tyr Val Gly Ser Val Trp Asp Ser Ser Lys Asn Phe Leu Thr Asn Leu  
 305 310 315 320  
 Tyr Ser Lys Phe Arg Gly Lys Thr Asp Asn Val Ile Asn Asp Thr Phe  
 325 330 335  
 Leu Val Gly Leu Asp Ser Trp Pro Lys Asp Lys Leu Lys Met Phe Leu  
 340 345 350

Asp Ala Arg Gly Ile Lys Tyr Ser Met Leu Ser Thr Glu His Gln Leu  
 355 360 365  
 Arg Glu Leu Val Lys Lys Ser Arg Asn Glu Lys Leu Lys Ile Leu Pro  
 370 375 380  
 Lys Asp Tyr Gln Lys Tyr Phe Asp Asn Ser Asn Trp Ser Leu Asp Asp  
 385 390 395 400  
 Ile Lys Gly Trp Phe Ala Asp Lys Lys Asp Asp Phe Gln Asp Ser Gln  
 405 410 415  
 Thr Tyr Ser Thr Ile Met Gln Asp Phe Asp Lys Val Ser Lys Asn Thr  
 420 425 430  
 Asn Asp Ala Lys Asp Gln Ile Ala Lys Thr Trp Ser Asn Thr Phe Gln  
 435 440 445  
 Ser Trp Ser Gln Glu Asp Leu Leu Gln Tyr Leu Lys Ser Phe Gly Val  
 450 455 460  
 Pro Val Lys Gln Thr Ser Thr Lys Asp Asp Leu Ile Asn Leu Ala Lys  
 465 470 475 480  
 Gln Asn Thr Gln Trp Leu Phe Gly Thr Val Lys Glu Pro Ala Tyr Lys  
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 Arg Tyr Leu His Asn Val Lys Asn Trp Ser Lys Ser Ile Leu Gly Phe  
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Asn

<210> 213

<211> 2192

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 213

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 ggctttgggc gttagtaaga acaaaaagaa aagaagagaa caaaaaagaa acgatacggg 360

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cagtaacgtg caggtaaaac atgagattaa gaaccgccat tgccacactg tgcctcacgg 540
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<210> 214

<211> 563

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 214

Met Arg Leu Arg Thr Ala Ile Ala Thr Leu Cys Leu Thr Ala Phe Thr

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Ser Ala Thr Ser Asn Asn Ser Tyr Ile Ala Thr Asp Gln Thr Gln Asn

20 25 30

Ala Phe Asn Asp Thr His Phe Cys Lys Val Asp Arg Asn Asp His Val

35 40 45

Ser Pro Ser Cys Asn Val Thr Phe Asn Glu Leu Asn Ala Ile Asn Glu  
 50 55 60  
 Asn Ile Arg Asp Asp Leu Ser Ala Leu Leu Lys Ser Asp Phe Phe Lys  
 65 70 75 80  
 Tyr Phe Arg Leu Asp Leu Tyr Lys Gln Cys Ser Phe Trp Asp Ala Asn  
 85 90 95  
 Asp Gly Leu Cys Leu Asn Arg Ala Cys Ser Val Asp Val Val Glu Asp  
 100 105 110  
 Trp Asp Thr Leu Pro Glu Tyr Trp Gln Pro Glu Ile Leu Gly Ser Phe  
 115 120 125  
 Asn Asn Asp Thr Met Lys Glu Ala Asp Asp Ser Asp Asp Glu Cys Lys  
 130 135 140  
 Phe Leu Asp Gln Leu Cys Gln Thr Ser Lys Lys Pro Val Asp Ile Glu  
 145 150 155 160  
 Asp Thr Ile Asn Tyr Cys Asp Val Asn Asp Phe Asn Gly Lys Asn Ala  
 165 170 175  
 Val Leu Ile Asp Leu Thr Ala Asn Pro Glu Arg Phe Thr Gly Tyr Gly  
 180 185 190  
 Gly Lys Gln Ala Gly Gln Ile Trp Ser Thr Ile Tyr Gln Asp Asn Cys  
 195 200 205  
 Phe Thr Ile Gly Glu Thr Gly Glu Ser Leu Ala Lys Asp Ala Phe Tyr  
 210 215 220  
 Arg Leu Val Ser Gly Phe His Ala Ser Ile Gly Thr His Leu Ser Lys  
 225 230 235 240  
 Glu Tyr Leu Asn Thr Lys Thr Gly Lys Trp Glu Pro Asn Leu Asp Leu  
 245 250 255  
 Phe Met Ala Arg Ile Gly Asn Phe Pro Asp Arg Val Thr Asn Met Tyr  
 260 265 270  
 Phe Asn Tyr Ala Val Val Ala Lys Ala Leu Trp Lys Ile Gln Pro Tyr  
 275 280 285  
 Leu Pro Glu Phe Ser Phe Cys Asp Leu Val Asn Lys Glu Ile Lys Asn  
 290 295 300

Lys Met Asp Asn Val Ile Ser Gln Leu Asp Thr Lys Ile Phe Asn Glu  
 305 310 315 320  
 Asp Leu Val Phe Ala Asn Asp Leu Ser Leu Thr Leu Lys Asp Glu Phe  
 325 330 335  
 Arg Ser Arg Phe Lys Asn Val Thr Lys Ile Met Asp Cys Val Gln Cys  
 340 345 350  
 Asp Arg Cys Arg Leu Trp Gly Lys Ile Gln Thr Thr Gly Tyr Ala Thr  
 355 360 365  
 Ala Leu Lys Ile Leu Phe Glu Ile Asn Asp Ala Asp Glu Phe Thr Lys  
 370 375 380  
 Gln His Ile Val Gly Lys Leu Thr Lys Tyr Glu Leu Ile Ala Leu Leu  
 385 390 395 400  
 Gln Thr Phe Gly Arg Leu Ser Glu Ser Ile Glu Ser Val Asn Met Phe  
 405 410 415  
 Glu Lys Met Tyr Gly Lys Arg Leu Asn Gly Ser Glu Asn Arg Leu Ser  
 420 425 430  
 Ser Phe Phe Gln Asn Asn Phe Phe Asn Ile Leu Lys Glu Ala Gly Lys  
 435 440 445  
 Ser Ile Arg Tyr Thr Ile Glu Asn Ile Asn Ser Thr Lys Glu Gly Lys  
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 Lys Lys Thr Asn Asn Ser Gln Ser His Val Phe Asp Asp Leu Lys Met  
 465 470 475 480  
 Pro Lys Ala Glu Ile Val Pro Arg Pro Ser Asn Gly Thr Val Asn Lys  
 485 490 495  
 Trp Lys Lys Ala Trp Asn Thr Glu Val Asn Asn Val Leu Glu Ala Phe  
 500 505 510  
 Arg Phe Ile Tyr Arg Ser Tyr Leu Asp Leu Pro Arg Asn Ile Trp Glu  
 515 520 525  
 Leu Ser Leu Met Lys Val Tyr Lys Phe Trp Asn Lys Phe Ile Gly Val  
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 Ala Asp Tyr Val Ser Glu Glu Thr Arg Glu Pro Ile Ser Tyr Lys Leu  
 545 550 555 560

Asp Ile Gln

&lt;210&gt; 215

&lt;211&gt; 998

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 215

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tattcatttg ggactgccta attcaagggc ctccagatac gccatacgct gatgggtgtt 660
ttaatgctaa gctagagttt cctaaagact atccgttatc tccacctaaa cttactttca 720
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&lt;210&gt; 216

&lt;211&gt; 165

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 216

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Met Ser Lys Thr Ala Gln Lys Arg Leu Leu Lys Glu Leu Gln Gln Leu
  1           5           10          15

Ile Lys Asp Ser Pro Pro Gly Ile Val Ala Gly Pro Lys Ser Glu Asn
    20           25           30

Asn Ile Phe Ile Trp Asp Cys Leu Ile Gln Gly Pro Pro Asp Thr Pro
    35           40           45

Tyr Ala Asp Gly Val Phe Asn Ala Lys Leu Glu Phe Pro Lys Asp Tyr
    50           55           60

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Pro Leu Ser Pro Pro Lys Leu Thr Phe Thr Pro Ser Ile Leu His Pro  
65 70 75 80

Asn Ile Tyr Pro Asn Gly Glu Val Cys Ile Ser Ile Leu His Ser Pro  
85 90 95

Gly Asp Asp Pro Asn Met Tyr Glu Leu Ala Glu Glu Arg Trp Ser Pro  
100 105 110

Val Gln Ser Val Glu Lys Ile Leu Leu Ser Val Met Ser Met Leu Ser  
115 120 125

Glu Pro Asn Ile Glu Ser Gly Ala Asn Ile Asp Ala Cys Ile Leu Trp  
130 135 140

Arg Asp Asn Arg Pro Glu Phe Glu Arg Gln Val Lys Leu Ser Ile Leu  
145 150 155 160

Lys Ser Leu Gly Phe  
165

<210> 217

<211> 1091

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 217

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ttgcatcgca tccagttctc atgcaatata gttgtatacc atgtcggtga aaggaaccag 180
agtaaact tctaccagta tttctttacg gttcggatca aaaccatcac tcattcggtc 240
attcttaccg tacgataaac caaattacaa ggaaaagtat ccctaattag agatcactgc 300
atccgtaata gttttttttc tattttggac ttttgtaaaa aagggattag ggatacgttg 360
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ataccgaaaa attaatcaca ctcaatgcga ctgtgatagc tgataagtgg agctcagaaa 480
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tctctaattg cagaatggac cttttttcca agaattcca caatggccgc gtatccaaat 660
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tggtcagta a 1091
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&lt;210&gt; 218

&lt;211&gt; 196

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 218

Met Lys Ala Thr Ile Gln Arg Val Thr Ser Val Phe Gly Val Pro Arg  
 1 5 10 15

Ala Ser Val Phe Val Pro Arg Ile Ser Thr Pro Phe Ile Leu His Asn  
 20 25 30

Tyr Ile Ser Asn Gly Arg Met Asp Leu Phe Ser Lys Glu Phe His Asn  
 35 40 45

Gly Arg Val Ser Lys Ser Asp Leu Trp Ser Ser Asn Lys Glu Glu Glu  
 50 55 60

Leu Leu Val Ser Gln Arg Lys Lys Arg Pro Ile Ser Pro His Leu Thr  
 65 70 75 80

Val Tyr Glu Pro Glu Met Ser Trp Tyr Leu Ser Ser Leu His Arg Ile  
 85 90 95

Ser Gly Val Leu Leu Ala Leu Gly Phe Tyr Ala Phe Thr Ile Thr Leu  
 100 105 110

Gly Val Thr Thr Ile Met Gly Met Asp Thr Thr Phe Gln Asp Leu Asn  
 115 120 125

Lys Trp Tyr His Glu Lys Met Pro Lys Trp Ser Gln Trp Val Ala Lys  
 130 135 140

Gly Ser Ala Ala Tyr Leu Phe Ala Phe His Phe Gly Asn Gly Ile Arg  
 145 150 155 160

His Leu Ile Trp Asp Met Gly Tyr Glu Leu Thr Asn Arg Gly Val Ile  
 165 170 175

Lys Thr Gly Ser Ile Val Leu Ala Gly Thr Leu Val Leu Gly Thr Tyr  
 180 185 190

Leu Leu Ala Gln  
 195

<210> 219  
 <211> 1121  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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 gttctgcaga atgatgtttg atagtatcga taatggagtg agatcaagag aaaaaaatg 240  
 aatatgtcag ccaaccaagt tctgagtagg cagtaaata gtagcatag tgtatttatc 300  
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 ggagagtatt ttgacaagat tgggttaaact actacggtca gttccgtaac cagtacgatt 420  
 gtacacataa ggaaacaact gttaaagataa acaataaggg cttccaatgc cattgtaaga 480  
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 gtaagaagaa atcagctact gctgttgccc atgtcaaggc cggtaagggt ttgatcaagg 780  
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 cttaccatca aaaatatgtc gatgaacaat ccaagaacga attgaagaag gctttcactt 1020  
 cttacgacag aaccttggtg attgctgatt ctagaagacc agaaccaaag aaattcgggtg 1080  
 gtaagggtgc tcgttccaga ttccaaaaat cttaccgtta a 1121

<210> 220  
 <211> 143  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 220  
 Met Tyr Ser Glu Tyr Lys Ala Ser Thr Phe Gly Lys Lys Lys Ser Ala  
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 Thr Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Val Asn  
 20 25 30  
 Gly Ser Pro Ile Thr Leu Val Glu Pro Glu Ile Leu Arg Phe Lys Val  
 35 40 45  
 Tyr Glu Pro Leu Leu Leu Val Gly Leu Asp Lys Phe Ser Asn Ile Asp  
 50 55 60  
 Ile Arg Val Arg Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala  
 65 70 75 80

Ile Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr  
                             85                            90                            95

Val Asp Glu Gln Ser Lys Asn Glu Leu Lys Lys Ala Phe Thr Ser Tyr  
                             100                            105                            110

Asp Arg Thr Leu Leu Ile Ala Asp Ser Arg Arg Pro Glu Pro Lys Lys  
                             115                            120                            125

Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg  
                             130                            135                            140

<210> 221  
 <211> 707  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 221  
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 tttccaaaaa aacctaaaca tatgatgcaa acctccaatg agactcaacg taacatgcaa 180  
 gtaaatacag aagggttaaga gatagttgtc ttaaaggggt accgaaagca tttaggggag 240  
 gcttaaggga ggggtgccgat cctatgaagt attaatacgt aatgccaaaa ggaattgttg 300  
 aacatctgaa gtggatagat taatcgtaca gtaatcgtac agtactatgt cttactgatg 360  
 tcgggaatct caggggcgac cgccccggc tagaattatc tatataacgg taaaaagaat 420  
 aaaactctat tctagttctc gccatttacc ttgactttaa tgaaccaata aaagaaattt 480  
 ctacaaccaa gacatccaga atgaatacag accaacaata agtgagcgaa atatttcaga 540  
 gctcaaagga aaaattgcag ggcatgcaa aggtagttag tgacgctttt aagaaaatgg 600  
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 aagagcaata caacaagctc aaaggggcgg ggcataagaa ggagtag 707

<210> 222  
 <211> 68  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 222  
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Glu Lys Leu Gln Gly Asp Ala Lys Val Val Ser Asp Ala Phe Lys Lys  
                             20                            25                            30

Met Ala Ser Gln Asp Lys Asp Gly Lys Thr Thr Asp Ala Asp Glu Ser

35

40

45

Glu Lys His Asn Tyr Gln Glu Gln Tyr Asn Lys Leu Lys Gly Ala Gly  
 50 55 60

His Lys Lys Glu  
 65

&lt;210&gt; 223

&lt;211&gt; 1877

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 223

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tggtcgcgat gtgcttttgg atagcctgga atacgaaatc tttgtcttcc tgtaaagtcg 300
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1877

270

<210> 224  
 <211> 458  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 224

Met Ile Thr Gln Pro Ala Lys Cys Pro Leu Leu Ile Arg Ile Ser Ala  
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Phe Arg Ser Gly Ser Ser Phe Leu Leu Tyr Val His Cys Lys Ser Ile  
 20 25 30

Asn Lys Ser Trp Gln Pro Lys Pro Gly Asn Pro Leu Arg Asn Ala Arg  
 35 40 45

Leu Asn Tyr Ile Asn Ile Lys Asp Met Trp Arg Glu Ala Ser Leu Pro  
 50 55 60

Ser His Phe Ala Phe His Asp Leu Lys Trp Phe Phe His Asn Arg Arg  
 65 70 75 80

Ala Pro Thr Arg Asn Met Ala Val Gly Gly Asn Asn Trp Ser Met Trp  
 85 90 95

Leu Arg Met Ser Arg Val His Leu Arg Gln Ile Thr Lys Ser Leu Asp  
 100 105 110

Arg Thr Leu Ile Ser Leu Ser His Gly Asn Phe Ser His Gln Tyr Asn  
 115 120 125

Arg Asn Ile Phe Val Thr Trp Trp Lys Ser Leu Phe Glu Ala Ser Thr  
 130 135 140

Ala Phe Arg Arg Ala Ser Gly Leu Thr Val Ser Pro Leu Thr Arg Arg  
 145 150 155 160

Gly Ile Ala Arg Phe Asp His Phe Arg Pro Val Pro Asn Val Ser Lys  
 165 170 175

Phe Ala Ser Phe Pro Arg Val Pro Lys Gly Ala Pro Arg Gly Leu Phe  
 180 185 190

Thr Asn Trp Asn Met Thr Thr Ser Lys Arg Leu Leu Gly Gln Arg Ala  
 195 200 205

Tyr Ser Thr Ser Ser Ile Lys Phe Thr Gln Glu Ala Val Asn Asn Met

210		215		220
Thr Ile Ser Leu Arg Cys Phe Phe Asn Ser Leu Gly Gly Leu Asn Gln				
225		230		240
Cys Ser His Ser Asn Ser Cys Lys Ala Tyr Gln Asn Ala Ser Asn Val				
	245		250	255
Thr Ser Lys Gln Asp His Val Gln Pro Val Ala Leu Lys Lys Leu Ser				
	260		265	270
Gln Lys Asp Ile Asn Phe Ile Arg Asn Leu Glu Leu Phe Lys Ile Met				
	275		280	285
Lys Thr Gln Asn Glu Val Val Asp Glu Thr Ser Ala Tyr Tyr Met Glu				
	290		295	300
Lys Pro Gly Ser Tyr Ile Glu Phe Thr Ile Ser Glu Phe Asn Val Asn				
305		310		320
Gly Thr Phe Ser Ala Pro Leu Ser Phe Leu Asp Pro Ser Leu Leu Ala				
	325		330	335
Asp Leu Asp Glu Met Ile Arg Asn Tyr Lys Tyr Glu Leu Lys Ser Ile				
	340		345	350
Tyr Ser Ser Val Asp Met Ile Leu Gln Asn Tyr Gly Ser Leu Pro Ile				
	355		360	365
Thr Phe His Arg Asn Lys Ile Arg Ile His Phe Pro Asn Ser Thr Val				
	370		375	380
Val Glu Thr Glu Lys Leu Ile Ala Gly Leu Asn Ile Ala Thr Gly Val				
385		390		400
Ile Tyr Ala Asp Thr Ser Pro Asp Ile Ser Leu Glu Gly Thr Asn Leu				
	405		410	415
Asn Ala Leu Val Asn Val Asp Asn Ser Gly Ser Val Trp Ser Phe Val				
	420		425	430
Lys Glu Pro Ser Phe Pro Ser Arg Ser Ala Phe Ser Pro Ile Leu Ser				
	435		440	445
Asp Ala Ser Tyr Asp Thr Tyr Glu Leu Val				
450		455		

<210> 225  
 <211> 1228  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 225  
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 gtagaaaacc gattgtttca aaaagatctt tgtggacaag tacggcagtg catgaatccg 720  
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 gaacttttga gtccttatag aaatgctaatt attatgatca aagcgattat atcatttact 840  
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 atcgtaagaa atattattac taacaaggaa gatcattgaa ttacgatcgc atatcgaaat 960  
 agaaggtgtt gtcgtcgcta agaaggattt caaccaagct aagcacgaag aaattgatac 1020  
 caagaacttg tatgttatca aggttttgca atccttgact tctaagggtt acgttaagac 1080  
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 atcccaaaga cctcaaagaa gatactaa 1228

<210> 226  
 <211> 105  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 226  
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 Gln Glu Gly Val Val Val Ala Lys Lys Asp Phe Asn Gln Ala Lys His  
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 Glu Glu Ile Asp Thr Lys Asn Leu Tyr Val Ile Lys Ala Leu Gln Ser  
 35 40 45  
 Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr Tyr  
 50 55 60

Tyr Tyr Thr Leu Thr Glu Glu Gly Val Glu Tyr Leu Arg Glu Tyr Leu  
65 70 75 80

Asn Leu Pro Glu His Ile Val Pro Gly Thr Tyr Ile Gln Glu Arg Asn  
85 90 95

Pro Ser Gln Arg Pro Gln Arg Arg Tyr  
100 105

<210> 227

<211> 3998

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 227

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&lt;210&gt; 228

&lt;211&gt; 1165

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 228

Met Thr Glu Glu Asp Arg Lys Leu Thr Val Glu Thr Glu Thr Val Glu

1

5

10

15

Ala Pro Val Ala Asn Asn Leu Leu Leu Ser Asn Asn Ser Asn Val Val

20	25	30
Ala Pro Asn Pro Ser Ile Pro Ser Ala Ser Thr Ser Thr Ser Pro Leu		
35	40	45
His Arg Glu Ile Val Asp Asp Ser Val Ala Thr Ala Asn Thr Thr Ser		
50	55	60
Asn Val Val Gln His Asn Leu Pro Thr Ile Asp Asn Asn Leu Met Asp		
65	70	75
		80
Ser Asp Ala Thr Ser His Asn Gln Asp His Trp His Ser Asp Ile Asn		
85	90	95
Arg Ala Gly Thr Ser Met Ser Thr Ser Asp Ile Pro Thr Asp Leu His		
100	105	110
Leu Glu His Ile Gly Ser Val Ser Ser Thr Asn Asn Asn Ser Asn Asn		
115	120	125
Ala Leu Ile Asn His Asn Pro Leu Ser Ser His Leu Ser Asn Pro Ser		
130	135	140
Ser Ser Leu Arg Asn Lys Lys Ser Ser Leu Leu Val Ala Ser Asn Pro		
145	150	155
		160
Ala Phe Ala Ser Asp Val Glu Leu Ser Lys Lys Lys Pro Ala Val Ile		
165	170	175
Ser Asn Asn Met Pro Thr Ser Asn Ile Ala Leu Tyr Gln Thr Ala Arg		
180	185	190
Ser Ala Asn Ile His Gly Pro Ser Ser Thr Ser Ala Ser Lys Ala Phe		
195	200	205
Arg Lys Ala Ser Ala Phe Ser Asn Asn Thr Ala Pro Ser Thr Ser Asn		
210	215	220
Asn Ile Gly Ser Asn Thr Pro Pro Ala Pro Leu Leu Pro Leu Pro Ser		
225	230	235
		240
Leu Ser Gln Gln Asn Lys Pro Lys Ile Ile Glu Arg Pro Thr Met His		
245	250	255
Val Thr Asn Ser Arg Glu Ile Leu Leu Gly Glu Asn Leu Leu Asp Asp		
260	265	270
Thr Lys Ala Lys Asn Ala Pro Ala Asn Ser Thr Thr His Asp Asn Gly		

277

530	535	540
Met Ser Gly His Asn His Leu Asp Glu Leu Ser Ser Ile Lys Gln Glu		
545	550	555 560
Pro Pro His Gln Leu Gln Gln Gln Pro Pro Met Asp Val Gln Ser		
	565	570 575
Val Asp Ser Tyr Thr Ser Asp Asn Pro Asp Ser Asn Val Ile Ala Lys		
	580	585 590
Ser Pro Asp Lys Arg Ser Ser Leu Val Ser Leu Ser Lys Val Ser Pro		
	595	600 605
His Leu Leu Ser Ser Thr Ser Ser Asn Gly Asn Thr Ile Ser Cys Pro		
	610	615 620
Asn Val Ala Thr Asn Ser Gln Glu Leu Glu Pro Asn Asn Asp Ile Ser		
	625	630 635 640
Thr Lys Lys Ser Leu Ser Asn Ser Thr Leu Arg His Ser Ser Ala Asn		
	645	650 655
Arg Asn Ser Asn Tyr Gly Asp Asn Lys Arg Pro Leu Arg Thr Thr Val		
	660	665 670
Ser Lys Ile Phe Asp Ser Asn Pro Asn Gly Ala Pro Leu Arg Arg Tyr		
	675	680 685
Ser Gly Val Pro Asp His Val Asn Leu Glu Asp Tyr Ile Glu Gln Pro		
	690	695 700
His Asn Tyr Pro Thr Met Gln Asn Ser Val Lys Lys Asp Glu Phe Tyr		
	705	710 715 720
Asn Ser Arg Asn Asn Lys Phe Pro His Gly Leu Asn Phe Tyr Gly Asp		
	725	730 735
Asn Asn Val Ile Glu Glu Glu Asn Asn Gly Asp Ser Ser Asn Val Asn		
	740	745 750
Arg Pro Gln His Thr Asn Leu Gln His Glu Phe Ile Pro Glu Asp Asn		
	755	760 765
Glu Ser Asp Glu Asn Asp Ile His Ser Met Phe Tyr Tyr Asn His Lys		
	770	775 780
Asn Asp Leu Glu Thr Lys Pro Leu Ile Ser Asp Tyr Gly Glu Asp Glu		

279

1045

1050

1055

Gly Ala Phe Asn Arg Asn Tyr Asp Val Ser Val Ser Ser Val Lys Leu  
 1060 1065 1070

Leu Ser Pro Gly Ser Arg Glu Ala Lys His Glu Asn Asp Asp Asp Asp  
 1075 1080 1085

Asp Asp Asp Gly Asp Asp Gly Asp Asp Glu Asn Asn Thr Asn Glu Arg  
 1090 1095 1100

Gln Tyr Lys Ser Lys Pro Asn Ala Arg Asp Asp Lys Glu Asp Asp Thr  
 1105 1110 1115 1120

Lys Lys Trp Lys Leu Leu Ile Lys His Asp Tyr Glu Leu Ile Val Arg  
 1125 1130 1135

Gly Ser Met Lys Tyr Glu Val Pro Phe Phe Asn Thr Gln Lys Ser Thr  
 1140 1145 1150

Ala Ile Gln Lys Asp Ser Met Val His Pro Gly Lys Lys  
 1155 1160 1165

&lt;210&gt; 229

&lt;211&gt; 1076

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 229

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280

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1076

&lt;210&gt; 230

&lt;211&gt; 191

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 230

Met Lys Tyr Ile Gln Thr Glu Gln Gln Ile Glu Ile Pro Glu Gly Val  
1 5 10 15

Thr Val Ser Ile Lys Ser Arg Ile Val Lys Val Val Gly Pro Arg Gly  
20 25 30

Thr Leu Thr Lys Asn Leu Lys His Ile Asp Val Thr Phe Thr Lys Val  
35 40 45

Asn Asn Gln Leu Ile Lys Val Ala Val His Asn Gly Asp Arg Lys His  
50 55 60

Val Ala Ala Leu Arg Thr Val Lys Ser Leu Val Asp Asn Met Ile Thr  
65 70 75 80

Gly Val Thr Lys Gly Tyr Lys Tyr Lys Met Arg Tyr Val Tyr Ala His  
85 90 95

Phe Pro Ile Asn Val Asn Ile Val Glu Lys Asp Gly Ala Lys Phe Ile  
100 105 110

Glu Val Arg Asn Phe Leu Gly Asp Lys Lys Ile Arg Asn Val Pro Val  
115 120 125

Arg Asp Gly Val Thr Ile Glu Phe Ser Thr Asn Val Lys Asp Glu Ile  
130 135 140

Val Leu Ser Gly Asn Ser Val Glu Asp Val Ser Gln Asn Ala Ala Asp  
145 150 155 160

Leu Gln Gln Ile Cys Arg Val Arg Asn Lys Asp Ile Arg Lys Phe Leu  
165 170 175

Asp Gly Ile Tyr Val Ser His Lys Gly Phe Ile Val Glu Asp Met  
180 185 190

&lt;210&gt; 231

281

&lt;211&gt; 1373

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 231

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&lt;210&gt; 232

&lt;211&gt; 290

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 232

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Met Leu Arg Arg Gln Ala Arg Glu Arg Arg Glu Tyr Leu Tyr Arg Lys
 1             5             10             15

Ala Gln Glu Leu Gln Asp Ser Gln Leu Gln Gln Lys Arg Gln Ile Ile
          20             25             30

Lys Gln Ala Leu Ala Gln Gly Lys Pro Leu Pro Lys Glu Leu Ala Glu
          35             40             45

Asp Glu Ser Leu Gln Lys Asp Phe Arg Tyr Asp Gln Ser Leu Lys Glu
          50             55             60

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Ser Glu Glu Ala Asp Asp Leu Gln Val Asp Asp Glu Tyr Ala Ala Thr  
65 70 75 80

Ser Gly Ile Met Asp Pro Arg Ile Ile Val Thr Thr Ser Arg Asp Pro  
85 90 95

Ser Thr Arg Leu Ser Gln Phe Ala Lys Glu Ile Lys Leu Leu Phe Pro  
100 105 110

Asn Ala Val Arg Leu Asn Arg Gly Asn Tyr Val Met Pro Asn Leu Val  
115 120 125

Asp Ala Cys Lys Lys Ser Gly Thr Thr Asp Leu Val Val Leu His Glu  
130 135 140

His Arg Gly Val Pro Thr Ser Leu Thr Ile Ser His Phe Pro His Gly  
145 150 155 160

Pro Thr Ala Gln Phe Ser Leu His Asn Val Val Met Arg His Asp Ile  
165 170 175

Ile Asn Ala Gly Asn Gln Ser Glu Val Asn Pro His Leu Ile Phe Asp  
180 185 190

Asn Phe Thr Thr Ala Leu Gly Lys Arg Val Val Cys Ile Leu Lys His  
195 200 205

Leu Phe Asn Ala Gly Pro Lys Lys Asp Ser Glu Arg Val Ile Thr Phe  
210 215 220

Ala Asn Arg Gly Asp Phe Ile Ser Val Arg Gln His Val Tyr Val Arg  
225 230 235 240

Thr Arg Glu Gly Val Glu Ile Ala Glu Val Gly Pro Arg Phe Glu Met  
245 250 255

Arg Leu Phe Glu Leu Arg Leu Gly Thr Leu Glu Asn Lys Asp Ala Asp  
260 265 270

Val Glu Trp Gln Leu Arg Arg Phe Ile Arg Thr Ala Asn Lys Lys Asp  
275 280 285

Tyr Leu  
290

<210> 233

283

&lt;211&gt; 1418

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 233

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gtgagttgga attacaagtc gccaagacct tcatcgatct agaaagctcc tctccagaac 600
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gtgaattgga aaagaaattc cctgaccgtc atgttatttt cttggctgaa agaagaatct 1140
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gagttagata tttggttggg ggtaacaaga tccaaaaggt tttggttagac tccaaggatg 1320
ttcaacaaat cgactacaag ttggaatctt tccaagctgt ctacaacaag ttgactggca 1380
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```

&lt;210&gt; 234

&lt;211&gt; 190

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 234

```

Met Ser Ser Val Gln Ser Lys Ile Leu Ser Gln Ala Pro Ser Glu Leu
  1              5              10              15

Glu Leu Gln Val Ala Lys Thr Phe Ile Asp Leu Glu Ser Ser Ser Pro
      20              25              30

Glu Leu Lys Ala Asp Leu Arg Pro Leu Gln Ile Lys Ser Ile Arg Glu
      35              40              45

Ile Asp Val Thr Gly Gly Lys Lys Ala Leu Val Leu Phe Val Pro Val
      50              55              60

```

Pro Ala Leu Ser Ala Tyr His Lys Val Gln Thr Lys Leu Thr Arg Glu  
65 70 75 80

Leu Glu Lys Lys Phe Pro Asp Arg His Val Ile Phe Leu Ala Glu Arg  
85 90 95

Arg Ile Leu Pro Lys Pro Ser Arg Thr Ser Arg Gln Val Gln Lys Arg  
100 105 110

Pro Arg Ser Arg Thr Leu Thr Ala Val His Asp Lys Val Leu Glu Asp  
115 120 125

---

Met Val Phe Pro Thr Glu Ile Val Gly Lys Arg Val Arg Tyr Leu Val  
130 135 140

Gly Gly Asn Lys Ile Gln Lys Val Leu Leu Asp Ser Lys Asp Val Gln  
145 150 155 160

Gln Ile Asp Tyr Lys Leu Glu Ser Phe Gln Ala Val Tyr Asn Lys Leu  
165 170 175

Thr Gly Lys Gln Ile Val Phe Glu Ile Pro Ser Gln Thr Asn  
180 185 190

&lt;210&gt; 235

&lt;211&gt; 1333

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 235

ttcatcacca atatagacta atgcgttttg gaacgccaaa ccgcagtgac aaatagcaaa 60  
tatgtagctg tcatatcggc atataataac agttttctac caaatgctgt cctacattca 120  
gagatcttac atccttacat ctaaagtaaa acctagacat ttacttcgag ttatactttt 180  
tttttattta tctatttttt ctcttgcgga catttaacac ctgaattccg cctaacgcca 240  
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ggttacagca gctggcccg cagagtgattg ggctcacagga aatagcgcaa ccttctcttt 360  
tgcccgggaa aggcgggttca atctaccttc gaagggctag tacatgagcg cgaaggaggc 420  
agataatagc accattaagt ggtccaaatg catcttgaaa tctaatacctt aatagaggaa 480  
aacaacaatt atcagtaaaa atgggtatgt tataaccata attcctaata gtgaataaaa 540  
tcaggaccaa taaagaaaag ctaatttgat ttttattgtc aatgaaattt cataatcgtc 600  
atgaatgcat aaacagacac acctagcaac tgtataatct gcgcctaaaa agggcgtata 660  
cacaaaacta aacgatgcgc aataaaaagt cagcagtcag caatgaaacc gagatatgca 720  
gcaacagagt atcatatgca tggaggatcc tttctgtttt tctgataata tgctctgaaa 780  
aagctccaaa cagcacagta gcctatttgt gaagctcaaa aaaggcttct atttcctcgc 840  
ctatcttcag attgtgcagt gatattcttt gaggaaggaa acgtagaggg gataagttgg 900

285

ataactgtta tttcttttca atagtctaga ttttgcttac caccttactg attttttcta 960  
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 gactaccaag aagggttggtt tgagattgga atgtgtcaaa tgtaagacca gagcccaatt 1260  
 gaccttgaag agatgcaagc acttcgaatt ggggtggtgaa aagaagcaaa aggggtcaagc 1320  
 tttgcaattc tga 1333

<210> 236

<211> 116

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 236

Met Val Arg Cys Leu Ile Tyr Phe Phe Tyr Leu Val Asn Val Pro Lys  
 1 5 10 15

Thr Arg Lys Thr Tyr Cys Lys Gly Lys Thr Cys Arg Lys His Thr Gln  
 20 25 30

His Lys Val Thr Gln Tyr Lys Ala Gly Lys Ala Ser Leu Phe Ala Gln  
 35 40 45

Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser Gly Phe Gly Gly Gln Thr  
 50 55 60

Lys Pro Val Phe His Lys Lys Ala Lys Thr Thr Lys Lys Val Val Leu  
 65 70 75 80

Arg Leu Glu Cys Val Lys Cys Lys Thr Arg Ala Gln Leu Thr Leu Lys  
 85 90 95

Arg Cys Lys His Phe Glu Leu Gly Gly Glu Lys Lys Gln Lys Gly Gln  
 100 105 110

Ala Leu Gln Phe  
 115

<210> 237

<211> 1223

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 237

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gggccacgtc agttccacac aataacattt acgtagtgtt cagcggaagc agttacatct 60
caactaacat aattgctggt gagcctacaa cactgcatgc gtaaacgtca acgggattac 120
gttagtatct ttggcgcgcg gtaaattctc ttgttttttt ttcttgattt cacttctttt 180
catgttcctt tggaataatc taattcctca tgattaaatg agactgtttt ttgtttccgt 240
aacatccata ctttctctgt ataattattt tgctgtaaag ttgttttttt ttatgaaaaa 300
aacattttct tttcttgaga tgaggcgccg cgagcctttc tcccatgggc agtggtgaaat 360
tttccaaatc aatgcagctc ttgaaatac aacagcattt ttcatacatt ttaagcaatt 420
tctagtttgt agatattgtt agattagttt ttgaacattg ttttgataac tgaaaataaa 480
acagcaaaca aactacaaaa atggctcgtt taatctctaa gaaaagaaaag ctagtcgctg 540
acgggtgtct ctacgctgaa ttgaacgaat tcttcaccag agaattagct gaagaagggt 600
actccggtgt tgaagtcctg gtcactccaa ccaagaccga agttatcatc agagctacca 660
gaactcaaga tgttttgggt gaaaacggta gaagaatcaa cgaattaaact ttgttggttc 720
aaaagagatt caagtacgct ccagggtacta ttgtcttata tgctgaaaga gttcaagacc 780
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agagcagaac tgggtccaaag gctttgccag atgctgtcac catcattgaa ccaaaagaag 1140
aagaaccaat tcttgctcca tctgtcaagg actacagacc agctgaagaa actgaagctc 1200
aagctgaacc agttgaagct tag 1223

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&lt;210&gt; 238

&lt;211&gt; 240

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 238

Met Val Ala Leu Ile Ser Lys Lys Arg Lys Leu Val Ala Asp Gly Val  
1 5 10 15

Phe Tyr Ala Glu Leu Asn Glu Phe Phe Thr Arg Glu Leu Ala Glu Glu  
20 25 30

Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Thr Lys Thr Glu Val  
35 40 45

Ile Ile Arg Ala Thr Arg Thr Gln Asp Val Leu Gly Glu Asn Gly Arg  
50 55 60

Arg Ile Asn Glu Leu Thr Leu Leu Val Gln Lys Arg Phe Lys Tyr Ala  
65 70 75 80

Pro Gly Thr Ile Val Leu Tyr Ala Glu Arg Val Gln Asp Arg Gly Leu  
85 90 95

Ser Ala Val Ala Gln Ala Glu Ser Met Lys Phe Lys Leu Leu Asn Gly

100	105	110
Leu Ala Ile Arg Arg Ala Ala Tyr Gly Val Val Arg Tyr Val Met Glu		
115	120	125
Ser Gly Ala Lys Gly Cys Glu Val Val Val Ser Gly Lys Leu Arg Ala		
130	135	140
Ala Arg Ala Lys Ala Met Lys Phe Ala Asp Gly Phe Leu Ile His Ser		
145	150	155
		160
<hr/>		
Gly Gln Pro Val Asn Asp Phe Ile Asp Thr Ala Thr Arg His Val Leu		
165	170	175
Met Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Arg Asp Pro		
180	185	190
Ala Lys Ser Arg Thr Gly Pro Lys Ala Leu Pro Asp Ala Val Thr Ile		
195	200	205
Ile Glu Pro Lys Glu Glu Glu Pro Ile Leu Ala Pro Ser Val Lys Asp		
210	215	220
Tyr Arg Pro Ala Glu Glu Thr Glu Ala Gln Ala Glu Pro Val Glu Ala		
225	230	235
		240

&lt;210&gt; 239

&lt;211&gt; 2168

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 239

```

ctttgataaa ttaatacggg aagataccgt gtgaactatt ataataactg ccacgcttat 60
agcatgtacg ctatacat ttt acgtgctgag ctccctaggaa agctcatgag cagccactgt 120
atcgtgggagc ataactacaa caaagaatac acagcggtcac atagaggggt tttgagagga 180
gaagttgaaa taggacttga tcttggggga gaggggattt gaaagcacc attcaggagt 240
atgtgtctgt aattgaagtg ttagcgcgcg attcacctgt aataagagt atgatttgat 300
agcgccattc tacatcatat ggcaaattgt gaaaaactgt acgcgcgaaac taaaattttt 360
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aggacgggctc tgacaagggc atatgcgtta agattgattg ttcaatattc ataaaacagg 480
atctttcaag ggacgataaa atggatgagc aagttatttt tacaacaaat acctcaggaa 540
caatagcttc tgtacactca tttgaacaga taaatttgag gcaatgctcc actcaatcaa 600
gaaatagctg tgttcaagta ggaaataaat acctttttat tgctcaagca caaaaagcat 660

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taatcaatgt ctacaatctg tcaggttctt tcaaaagaga atctgttgaa cagcgcttac 720
cattacctga aatcctaaaa tgtctggaag tagttgaaaa tgatgggtgtg cagtatgata 780
gaattcaagg tgtcaatcat aatttaccag acttcaatct tccgtacctt ttacttggct 840
ccaccgaatc gggtaaattg tacatatggg agttaaattc agggatttta ttgaacgtga 900
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ccgctaaaaga tgaggaaatt acagaactta agaccaacat agaagcatta actcatgcct 2100
acaaggagtt acgtgacatg cacgaaaagc tgtacgagga acaccaacag atgcttgaca 2160
agcaataa 2168

```

&lt;210&gt; 240

&lt;211&gt; 555

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 240

```

Met Asp Glu Gln Val Ile Phe Thr Thr Asn Thr Ser Gly Thr Ile Ala
  1              5              10              15

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Ser Val His Ser Phe Glu Gln Ile Asn Leu Arg Gln Cys Ser Thr Gln
      20              25              30

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Ser Arg Asn Ser Cys Val Gln Val Gly Asn Lys Tyr Leu Phe Ile Ala
      35              40              45

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Gln Ala Gln Lys Ala Leu Ile Asn Val Tyr Asn Leu Ser Gly Ser Phe
      50              55              60

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Lys Arg Glu Ser Val Glu Gln Arg Leu Pro Leu Pro Glu Ile Leu Lys
      65              70              75              80

```

289

Cys Leu Glu Val Val Glu Asn Asp Gly Val Gln Tyr Asp Arg Ile Gln  
                                   85                                  90                                  95  
 Gly Val Asn His Asn Leu Pro Asp Phe Asn Leu Pro Tyr Leu Leu Leu  
                                   100                                  105                                  110  
 Gly Ser Thr Glu Ser Gly Lys Leu Tyr Ile Trp Glu Leu Asn Ser Gly  
                                   115                                  120                                  125  
 Ile Leu Leu Asn Val Lys Pro Met Ala His Tyr Gln Ser Ile Thr Lys  
                                   130                                  135                                  140

---

Ile Lys Ser Ile Leu Asn Gly Lys Tyr Ile Ile Thr Ser Gly Asn Asp  
 145                                  150                                  155                                  160  
 Ser Arg Val Ile Ile Trp Gln Thr Val Asp Leu Val Ser Ala Ser Asn  
                                   165                                  170                                  175  
 Asp Asp Pro Lys Pro Leu Cys Ile Leu His Asp His Thr Leu Pro Val  
                                   180                                  185                                  190  
 Thr Asp Phe Gln Val Ser Ser Ser Gln Gly Lys Phe Leu Ser Cys Thr  
                                   195                                  200                                  205  
 Asp Thr Lys Leu Phe Thr Val Ser Gln Asp Ala Thr Ile Arg Cys Tyr  
                                   210                                  215                                  220  
 Asp Leu Ser Leu Ile Gly Ser Lys Lys Lys Gln Lys Ala Asn Glu Asn  
 225                                  230                                  235                                  240  
 Asp Val Ser Ile Gly Lys Thr Pro Val Leu Leu Ala Thr Phe Thr Thr  
                                   245                                  250                                  255  
 Pro Tyr Ser Ile Lys Ser Ile Val Leu Asp Pro Ala Asp Arg Ala Cys  
                                   260                                  265                                  270  
 Tyr Ile Gly Thr Ala Glu Gly Cys Phe Ser Leu Asn Leu Phe Tyr Lys  
                                   275                                  280                                  285  
 Leu Lys Gly Asn Ala Ile Val Asn Leu Leu Gln Ser Ala Gly Val Asn  
                                   290                                  295                                  300  
 Thr Val Gln Lys Gly Arg Val Phe Ser Leu Val Gln Arg Asn Ser Leu  
 305                                  310                                  315                                  320  
 Thr Gly Gly Glu Asn Glu Asp Leu Asp Ala Leu Tyr Ala Met Gly Gln  
                                   325                                  330                                  335



Leu Val Cys Glu Asn Val Leu Asn Ser Asn Val Ser Cys Leu Glu Ile  
 340 345 350  
 Ser Met Asp Gly Thr Leu Leu Leu Ile Gly Asp Thr Glu Gly Lys Val  
 355 360 365  
 Ser Ile Ala Glu Ile Tyr Ser Lys Gln Ile Ile Arg Thr Ile Gln Thr  
 370 375 380  
 Leu Thr Thr Ser Gln Asp Ser Val Gly Glu Val Thr Asn Leu Leu Thr  
 385 390 395 400  
 Asn Pro Tyr Arg Leu Glu Arg Gly Asn Leu Leu Phe Glu Gly Glu Ser  
 405 410 415  
 Lys Gly Lys Gln Pro Ser Asn Asn Asn Gly His Asn Phe Met Lys Ile  
 420 425 430  
 Pro Asn Leu Gln Arg Val Ile Phe Asp Gly Lys Asn Lys Gly His Leu  
 435 440 445  
 His Asp Ile Trp Tyr Gln Ile Gly Glu Pro Glu Ala Glu Thr Asp Pro  
 450 455 460  
 Asn Leu Ala Leu Pro Leu Asn Asp Phe Asn Ala Tyr Leu Glu Gln Val  
 465 470 475 480  
 Lys Thr Gln Glu Ser Ile Phe Ser His Ile Gly Lys Val Ser Ser Asn  
 485 490 495  
 Val Lys Val Ile Asp Asn Lys Ile Asp Ala Thr Ser Ser Leu Asp Ser  
 500 505 510  
 Asn Ala Ala Lys Asp Glu Glu Ile Thr Glu Leu Lys Thr Asn Ile Glu  
 515 520 525  
 Ala Leu Thr His Ala Tyr Lys Glu Leu Arg Asp Met His Glu Lys Leu  
 530 535 540  
 Tyr Glu Glu His Gln Gln Met Leu Asp Lys Gln  
 545 550 555

<210> 241  
 <211> 1115  
 <212> DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 241

```

aatgcgctcc cgtacgtcag tggctgttgc tgaaacgaga caatttctca attcgtttgt 60
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gtgctcactt ctctcgtctt ttattaggtg tgtgtgttgt gcgtaatttt cgtttcgctg 180
attactttat atagtgtagt ttgttcttga atgtaataaa gacttctgtt ttattttgtt 240
ttgttattta gaaacagtct atctgggtta acttaaacga gtgagcttaa gataatctga 300
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gaattttcct ttaaggagta acttaagcat ttagctgcac attaaacact ttttttttta 420
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cagcgcttta taattgaaat atgaagttct cttctgttac tgctattact ctageccaccg 540
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catcggacgg tagtttaact actaccacct ctactcatat cactcacaag tatggtaagt 660
tcaacaagac ttccaagtcc aagaccccaa accacactgg tactcacaag tacggtaagt 720
tcaacaagac ctccaagtct aagaccccaa accataccgg tactcacaag tatggtaagt 780
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tcaacaagac ctccaagtct aagaccccaa accataccgg tactcacaag tatggtaagt 960
tcaacaaaac caaacatgac actaccactt atggtcctgg tgaaaaggcc cgtaagaaca 1020
atgccgcccc tgggccatct aatttcaact ccataaaatt gtttggtgtt accgctggta 1080
gtgctgccgt agccggtgcc ttattactat tataa 1115

```

&lt;210&gt; 242

&lt;211&gt; 204

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 242

```

Met Lys Phe Ser Ser Val Thr Ala Ile Thr Leu Ala Thr Val Ala Thr
  1              5              10              15

Val Ala Thr Ala Lys Lys Gly Glu His Asp Phe Thr Thr Thr Leu Thr
          20              25              30

Leu Ser Ser Asp Gly Ser Leu Thr Thr Thr Thr Ser Thr His Thr Thr
          35              40              45

His Lys Tyr Gly Lys Phe Asn Lys Thr Ser Lys Ser Lys Thr Pro Asn
          50              55              60

His Thr Gly Thr His Lys Tyr Gly Lys Phe Asn Lys Thr Ser Lys Ser
          65              70              75              80

Lys Thr Pro Asn His Thr Gly Thr His Lys Tyr Gly Lys Phe Asn Lys
          85              90              95

```

Thr Ser Lys Ser Lys Thr Pro Asn His Thr Gly Thr His Lys Tyr Gly  
 100 105 110

Lys Phe Asn Lys Thr Ser Lys Ser Lys Thr Pro Asn His Thr Gly Thr  
 115 120 125

His Lys Tyr Gly Lys Phe Asn Lys Thr Ser Lys Ser Lys Thr Pro Asn  
 130 135 140

His Thr Gly Thr His Lys Tyr Gly Lys Phe Asn Lys Thr Lys His Asp  
 145 150 155 160

Thr Thr Thr Tyr Gly Pro Gly Glu Lys Ala Arg Lys Asn Asn Ala Ala  
 165 170 175

Pro Gly Pro Ser Asn Phe Asn Ser Ile Lys Leu Phe Gly Val Thr Ala  
 180 185 190

Gly Ser Ala Ala Val Ala Gly Ala Leu Leu Leu Leu  
 195 200

&lt;210&gt; 243

&lt;211&gt; 1115

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 243

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 gttttagttc tgtatatcac gatcaagata tcataacaatc ataaattcaa ttattcttct 120  
 gtttccctc ttgaggcatc aaacgagtggt ttgactgata cacaccaaca tactaaggca 180  
 acttttctgg ctgccc aaag ctgtggcacg tatgaaactg cttttcggct gcataaaaca 240  
 accatgtgga gtttttactg tattcgcatt tcgccccgct agcattcttc gttcatgcta 300  
 aaaatgaggc gtgggctaata attcagtatt aataattccg gcacccgcac agcccatacc 360  
 ggaaaagggg ctggctgttg ggcttggcaa aaaactcaat ctgagcagtc atttataaag 420  
 aaagacttta atttgtcttg ctaaacactt gtaagccttc caaatataga tcacttaaga 480  
 caatctaaca agtgtccaaa atgtctgcaa acgaattcta ctcaagtggc caacaaggtc 540  
 aatataacca gcaaaacaac caagaaagaa ctggtgctcc aaacaacggg caatatgggtg 600  
 ccgacaatgg taaccccaac ggtgaacgtg gtttattttc cactattgta ggtggcagtg 660  
 ccggtgcgta cgctggatct aagggtgtcg acaaccattc taagttgagt ggtgtgctgg 720  
 gcgcatagg tgggtgcattc cttgccaaca agatatctga tgagcgtaaa gagcataagc 780  
 aacaagagca atacggcaac tcaaacttcg gaggtgctcc tcaaggtgga cacaacaacc 840  
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 tcaaggtttc ggaagacaag gcccaacagg atttgagggt cctggtccac aagagtttgg 960  
 tggccagggt ggccaaggat tcggtggtcc aaatcctcaa gaattcggcg gccagggtgc 1020  
 caaggattcg gtggtccaaa cctcaggaa ttcgggggcc aaggctcgtca aggattcaat 1080  
 ggcggttcac gttggtgaat ggctcaacag agtga 1115

<210> 244  
 <211> 204  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 244

Met Ser Ala Asn Glu Phe Tyr Ser Ser Gly Gln Gln Gly Gln Tyr Asn  
 1 5 10 15

Gln Gln Asn Asn Gln Glu Arg Thr Gly Ala Pro Asn Asn Gly Gln Tyr  
 20 25 30

Gly Ala Asp Asn Gly Asn Pro Asn Gly Glu Arg Gly Leu Phe Ser Thr  
 35 40 45

Ile Val Gly Gly Ser Ala Gly Ala Tyr Ala Gly Ser Lys Val Ser Asn  
 50 55 60

Asn His Ser Lys Leu Ser Gly Val Leu Gly Ala Ile Gly Gly Ala Phe  
 65 70 75 80

Leu Ala Asn Lys Ile Ser Asp Glu Arg Lys Glu His Lys Gln Gln Glu  
 85 90 95

Gln Tyr Gly Asn Ser Asn Phe Gly Gly Ala Pro Gln Gly Gly His Asn  
 100 105 110

Asn His His Arg Gln Thr Ile Thr Thr Ile Thr Val Asp Leu Ala Val  
 115 120 125

Gln Ala Ala Leu Ala Val Lys Val Ser Glu Asp Lys Ala His Lys Asp  
 130 135 140

Leu Glu Val Leu Val His Lys Ser Leu Val Val Gln Val Ala Lys Asp  
 145 150 155 160

Ser Val Val Gln Ile Leu Lys Asn Ser Ala Ala Arg Trp Pro Arg Ile  
 165 170 175

Arg Trp Ser Lys Pro Ser Gly Ile Arg Gly Pro Arg Ser Ser Arg Ile  
 180 185 190

Gln Trp Arg Phe Thr Leu Val Asn Gly Ser Thr Glu  
 195 200

294

<210> 245  
 <211> 1313  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 245  
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 gatctgccga tttaggaatc gtactgtaga ttgctcttgg cgacagatat agtgaaatac 240  
 cttttaaaaa gtggatacag gttgcctatc actaccgcca tttcactagc aagtagagta 300  
 ttgagaaaac ggtaaacttt gaaagttgca gatgcagaat atatatctgg tttttagtgg 360  
 ctatccgcta aacgggacga tcgcatttta gccgccgaca gtgttaatat aagtaatgaa 420  
 cttgggttaa tttgattacg cgtcacagct actaataaaa taagaccgag agttttaatc 480  
 agctagtgcg taccaaaaca atgagtaacc aacacagccc tcagccattt tgtttggaca 540  
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 ataaagtaca gacaaatggg ccgcaacggc acgatttcat agtcactcta gaaataaaac 1080  
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 gggaaaaatc aggcgccagc ataaaaataa tacctattag tgataaaatg actgcacatg 1200  
 aaaggaacca ccctgaatct gttcaacaaa caataactaat ttcgggtgac ttatactcaa 1260  
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<210> 246  
 <211> 270  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 246  
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 Val Lys Leu Leu Glu Glu Leu Gln Glu Gly Lys Gln Phe Asn Asn Lys  
 20 25 30  
 Asn Ile Phe Pro Glu Lys Ala Leu Tyr Leu Lys Leu Ala Leu Asp Tyr  
 35 40 45  
 Ser Phe Phe Arg Lys Asn Leu Leu Glu Phe Cys Val His Leu Asp Lys  
 50 55 60

Ile Lys Gly Val Ile Arg Pro Asn Tyr Asp Thr Ile Tyr Ile Leu Cys  
 65 70 75 80  
 Leu Leu Glu Val Asp Leu Leu Asn Leu Val Phe Thr Asp Asn Ile Leu  
 85 90 95  
 Glu Ile Cys Leu Pro Arg Phe Val Ser Arg Glu Asp Leu Arg Val Phe  
 100 105 110  
 Asn Asn Thr Phe Tyr Thr Tyr His Asp Asn Arg Leu Arg Ile Leu Gln  
 115 120 125  
 Glu Asp Phe Ser Gln Leu Phe Lys Lys Ile Lys Thr Lys Ala Ser Val  
 130 135 140  
 Leu Cys Phe Thr Val Glu Glu Ile Phe Leu Thr Asn Gln Glu Ile Leu  
 145 150 155 160  
 Pro Gln Asn Ser Thr Val Ala Glu Leu Gln Lys Ser Thr Asn Lys Val  
 165 170 175  
 Gln Thr Asn Gly Pro Gln Arg His Asp Phe Ile Val Thr Leu Glu Ile  
 180 185 190  
 Lys Leu Asn Lys Thr Gln Ile Thr Phe Leu Ile Gly Ala Lys Gly Thr  
 195 200 205  
 Arg Ile Glu Ser Leu Arg Glu Lys Ser Gly Ala Ser Ile Lys Ile Ile  
 210 215 220  
 Pro Ile Ser Asp Lys Met Thr Ala His Glu Arg Asn His Pro Glu Ser  
 225 230 235 240  
 Val Gln Gln Thr Ile Leu Ile Ser Gly Asp Leu Tyr Ser Ile Ala Leu  
 245 250 255  
 Ala Val Thr Ser Ile Glu Ser Ala Leu Ile Thr Leu Asp Leu  
 260 265 270

&lt;210&gt; 247

&lt;211&gt; 1766

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 247

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tatttcttgt tgtatacgca gcggccaact agtggcagca agaattgaat gaacgattca 240
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ttgataagaa acttatcgac agcagacact tgatctttgg caaccccatg gctcatagaa 1740
taaaaaat 1766

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&lt;210&gt; 248

&lt;211&gt; 421

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 248

Met Val Arg Ile Leu Pro Ile Ile Leu Ser Ala Leu Ser Ser Lys Leu

1

5

10

15

Val Ala Ser Thr Ile Leu His Ser Ser Ile His Ser Val Pro Ser Gly

20

25

30

Gly Glu Ile Ile Ser Ala Glu Asp Leu Lys Glu Leu Glu Ile Ser Gly

35

40

45

Asn Ser Ile Cys Val Asp Asn Arg Cys Tyr Pro Lys Ile Phe Glu Pro

50                                      55                                      60  
 Arg His Asp Trp Gln Pro Ile Leu Pro Gly Gln Glu Leu Pro Gly Gly  
 65                                      70                                      75                                      80  
 Leu Asp Ile Arg Ile Asn Met Asp Thr Gly Leu Lys Glu Ala Lys Leu  
 85                                      90                                      95  
 Asn Asp Glu Lys Asn Val Gly Asp Asn Gly Ser His Glu Leu Ile Val  
 100                                      105                                      110  
~~Ser Ser Glu Asp Met Lys Ala Ser Pro Gly Asp Tyr Glu Phe Ser Ser~~  
~~115                                      120                                      125~~  
 Asp Phe Lys Glu Met Arg Asn Ile Ile Asp Ser Asn Pro Thr Leu Ser  
 130                                      135                                      140  
 Ser Gln Asp Ile Ala Arg Leu Glu Asp Ser Phe Asp Arg Ile Met Glu  
 145                                      150                                      155                                      160  
 Phe Ala His Asp Tyr Lys His Gly Tyr Lys Ile Ile Thr His Glu Phe  
 165                                      170                                      175  
 Ala Leu Leu Ala Asn Leu Ser Leu Asn Glu Asn Leu Pro Leu Thr Leu  
 180                                      185                                      190  
 Arg Glu Leu Ser Thr Arg Val Ile Thr Ser Cys Leu Arg Asn Asn Pro  
 195                                      200                                      205  
 Pro Val Val Glu Phe Ile Asn Glu Ser Phe Pro Asn Phe Lys Ser Lys  
 210                                      215                                      220  
 Ile Met Ala Ala Leu Ser Asn Leu Asn Asp Ser Asn His Arg Ser Ser  
 225                                      230                                      235                                      240  
 Asn Ile Leu Ile Lys Arg Tyr Leu Ser Ile Leu Asn Glu Leu Pro Val  
 245                                      250                                      255  
 Thr Ser Glu Asp Leu Pro Ile Tyr Ser Thr Val Val Leu Gln Asn Val  
 260                                      265                                      270  
 Tyr Glu Arg Asn Asn Lys Asp Lys Gln Leu Gln Ile Lys Val Leu Glu  
 275                                      280                                      285  
 Leu Ile Ser Lys Ile Leu Lys Ala Asp Met Tyr Glu Asn Asp Asp Thr  
 290                                      295                                      300  
 Asn Leu Ile Leu Phe Lys Arg Asn Ala Glu Asn Trp Ser Ser Asn Leu



[illegible]

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<210> 249
<211> 821
<212> DNA
<213> Saccharomyces cerevisiae
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tcacacttgt	accgctttta	gtgacatggg	ccatactggt	attagggcct	cttggtgtga	240
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cactggtcct	gacccatatt	acgaatcaga	tatttgatat	atctttgggtg	ttgcaagacc	360
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tcgatgaacc	tgatgcggtg	agaaatttca	acacaataaa	gggaagtcgg	atttttaaga	480
ttcccagatt	actattcaga	atgttttttta	aagtctccaa	ttttacttca	ctaacattac	540
tgctgctaatt	tcctattgta	ggaccaatct	tggaacaatca	actaatggcc	ccaaaaagaa	600
cctttaccta	tttgacagagg	tacttttttac	taaagggatt	cagtaagaaa	caggccaaag	660
attttcagta	cgagcattac	gcaagtttca	tatgtttcgg	tatgtctgcc	ggtctactag	720
agttaatacc	cttcttcaca	atagtcacca	tatctagcaa	cactgttggt	gcagctaaat	780
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**<210> 250**

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 250

Met Phe Phe Lys Val Ser Asn Phe Thr Ser Leu Thr Leu Leu Ser Leu  
 1 5 10 15

Ile Pro Ile Val Gly Pro Ile Leu Ala Asn Gln Leu Met Ala Pro Lys  
 20 25 30

Arg Thr Phe Thr Tyr Leu Gln Arg Tyr Phe Leu Leu Lys Gly Phe Ser  
 35 40 45

Lys Lys Gln Ala Lys Asp Phe Gln Tyr Glu His Tyr Ala Ser Phe Ile  
 50 55 60

Cys Phe Gly Met Ser Ala Gly Leu Leu Glu Leu Ile Pro Phe Phe Thr  
 65 70 75 80

Ile Val Thr Ile Ser Ser Asn Thr Val Gly Ala Ala Lys Trp Cys Thr  
 85 90 95

Ser Leu Leu Lys Gly Glu Arg Lys Lys Glu  
 100 105

&lt;210&gt; 251

&lt;211&gt; 1256

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 251

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 ttaagtccaa cttgcaagaa tatattagtt tggctgaaga ttcttcatct ggattttcct 660  
 taagcagtct gccatctggt gtttttagaca tcggttttagc tttggcttcc gccactgatg 720  
 actcctacac tactttgtac tctgaggttg actttgctgc tgttagcaag atgttgacca 780  
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&lt;210&gt; 252

&lt;211&gt; 251

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 252

Met Ala Tyr Ile Lys Ile Ala Leu Leu Ala Ala Ile Ala Ala Leu Ala  
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Ser Ala Gln Thr Gln Glu Glu Ile Asp Glu Leu Asn Val Ile Leu Asn  
 20 25 30

Asp Val Lys Ser Asn Leu Gln Glu Tyr Ile Ser Leu Ala Glu Asp Ser  
 35 40 45

Ser Ser Gly Phe Ser Leu Ser Ser Leu Pro Ser Gly Val Leu Asp Ile  
 50 55 60

Gly Leu Ala Leu Ala Ser Ala Thr Asp Asp Ser Tyr Thr Thr Leu Tyr  
 65 70 75 80

Ser Glu Val Asp Phe Ala Ala Val Ser Lys Met Leu Thr Met Val Pro  
 85 90 95

Trp Tyr Ser Ser Arg Leu Leu Pro Glu Leu Glu Ser Leu Leu Gly Thr  
 100 105 110

Ser Thr Thr Ala Ala Ser Ser Thr Glu Ala Ser Ser Ala Ala Thr Ser  
 115 120 125

Ser Ala Val Ala Ser Ser Ser Glu Thr Thr Ser Ser Ala Val Ala Ser  
 130 135 140

Ser Ser Glu Ala Thr Ser Ser Ala Val Ala Ser Ser Ser Glu Ala Ser  
 145 150 155 160

Ser Ser Ala Ala Thr Ser Ser Ala Val Ala Ser Ser Ser Glu Ala Thr  
 165 170 175

301

Ser Ser Thr Val Ala Ser Ser Thr Lys Ala Ala Ser Ser Thr Lys Ala  
 180 185 190

Ser Ser Ser Ala Val Ser Ser Ala Val Ala Ser Ser Thr Lys Ala Ser  
 195 200 205

Ala Ile Ser Gln Ile Ser Asp Gly Gln Val Gln Ala Thr Ser Thr Val  
 210 215 220

Ser Glu Gln Thr Glu Asn Gly Ala Ala Lys Ala Val Ile Gly Met Gly  
 225 230 235 240

Ala Gly Val Met Ala Ala Ala Ala Met Leu Leu  
 245 250

<210> 253

<211> 2693

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 253

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aaaagaagaa gaaaaaaaaa aagaaatcat tgttcttatt cggcaaaaata tga 2693

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&lt;210&gt; 254

&lt;211&gt; 730

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 254

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Met Ile Ser Val Cys Pro Gln Asn Asp Leu Gln Lys Cys Tyr Arg Ser
  1                   5                   10                   15

```

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Leu Thr Phe Asp Val Pro Gly Gln Gln Phe Glu Glu Arg Asn Glu Gln
      20                   25                   30

```

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Asn Leu Lys Lys Arg Ala Lys Lys Lys Gly Ser Phe Gln Pro Ser Val
      35                   40                   45

```

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Ala Phe Asp Thr Val Pro Ser Thr Ala Gly Tyr Ser Ser Ile Asp Asp
      50                   55                   60

```

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Ser Arg Glu Gly Phe Lys Gly Val Pro Val Pro Asn Tyr Tyr Thr Met
      65                   70                   75                   80

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Glu Glu Cys Tyr Asp Asp Glu Thr Asp Ser Phe Ser Pro Asn Leu Gln
      85                   90                   95

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Tyr Tyr Leu Arg Asp Thr Phe Gln Ser Ser Pro Phe Leu Asn Thr Arg
      100                  105                  110

```

303

Lys Glu Asn Lys Ser Glu Ser Ser Ser Phe Pro Met Arg Ser Ser Lys  
 115 120 125  
 Leu Leu Glu Lys Asn Ser Asp Ile Lys Lys Tyr Phe Leu Val Ser Lys  
 130 135 140  
 Asn Gly Lys Ile Val Arg Arg Asp Tyr Pro Ser Thr Pro Val Ile Val  
 145 150 155 160  
 Asn Glu Thr Leu Met Ile Asn Arg Phe Glu Lys Asn Trp Ile Lys Leu  
 165 170 175  
 Trp Arg Gln Arg Lys Leu Gln Ile Asn Glu Arg Leu Asn Asp Lys Lys  
 180 185 190  
 Lys Trp Phe Thr Tyr Pro Glu Leu Ile Phe Ser Glu Glu Arg Ile Lys  
 195 200 205  
 Pro Leu Tyr Arg Gly Asp Asp Ser Ala Pro Cys Thr Lys Glu Gln Lys  
 210 215 220  
 Arg Lys His Lys Ile Leu Gln Gln Lys Val Gly Tyr Pro Asn Asn Pro  
 225 230 235 240  
 Lys Thr Ile Val Cys His Ile Asn Gly Lys Lys His Thr Trp Val Ala  
 245 250 255  
 Leu Asp Trp Thr Val Tyr Lys Phe Ala Arg Asn Leu Asp His Ile Val  
 260 265 270  
 Val Ile Thr Thr Leu Pro Lys Met Ile Ser Asn Arg Lys Lys Thr Ala  
 275 280 285  
 Lys Asp Asp Thr Glu Trp Ala Pro Gly Tyr Gln Lys Glu Val Ile Asp  
 290 295 300  
 Gln Lys Leu Asn Asp Ile Phe Asp Tyr Ile Leu Gln Leu Val Lys Val  
 305 310 315 320  
 Val Lys Ile Ser Val Lys Ile Thr Leu Glu Ile Ile Val Gly Lys Ile  
 325 330 335  
 Lys Lys Ser Leu Val Asp Val Ile Asn Val His Thr Pro Asp Phe Leu  
 340 345 350  
 Val Leu Ala Thr Leu Lys His Glu Arg Asn Glu Asn Leu Ile Thr Tyr  
 355 360 365

304

Lys Ser Lys Lys Leu Thr Asp Val Phe Pro Val Ser Tyr Pro Ile Pro  
 370 375 380  
 Thr Phe Val Val Pro Ser Lys Arg Met Tyr Ser Phe Glu Leu Asn Leu  
 385 390 395 400  
 Gln Arg Glu Val Asn Glu His Tyr Val Ser Lys Asn His Met Lys His  
 405 410 415  
 Glu His Thr Asp Val Glu Ser Met Ser Ser Ser Met Phe Lys Lys Asn  
 420 425 430

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Thr Ile Ser Asp Ile Ser Ser His Ile Ser Val Asp Ser Tyr Ala Glu  
 435 440 445  
 Asp Phe Lys Arg Gln Gly Tyr Ile Lys Lys Gln Phe Asn Thr Ser Asn  
 450 455 460  
 Asp Ser Ile Pro Arg Lys Leu Thr Gly Leu Ala Gln His Ser Arg Arg  
 465 470 475 480  
 Lys Ile Thr Gly Asp Ile Glu Lys Leu Gln Asp Asp Glu Lys Asp Arg  
 485 490 495  
 Glu Cys Thr Lys Glu Lys Leu Leu Leu Lys Lys Ile Asp Ile Ile Ile  
 500 505 510  
 Arg Glu Ser Leu Lys Ser Ser Leu Ala Ile Glu Thr Leu Pro Gly Lys  
 515 520 525  
 Asn Val Ser Gln Ser Ser His Gly Asp Gln Ile Ser Ser Phe Lys Asn  
 530 535 540  
 Ala Leu Ile Gly Asn Gly Ser Lys Asn Thr Lys Phe Arg Lys Ser Leu  
 545 550 555 560  
 Ile Pro Tyr Ser Ser Ser Glu Glu Gln Asn Thr Thr Thr Thr Ile Lys  
 565 570 575  
 Leu Ser Ser Ser Pro Thr Ser Gln Ile Lys Phe Ala Thr Ser Val Lys  
 580 585 590  
 His Lys Asp Gly Arg Ala Ala Leu Gly Lys Ala Arg Asn Leu Pro Asp  
 595 600 605  
 Ile Arg His Ser Ile Ser Phe Asp Lys Glu Asn Ser Phe Asp Pro Ser  
 610 615 620

305

Asp Lys Ser Ser Ser Val Asp Asn Ser Ile Pro Leu Arg Lys Val Lys  
625 630 635 640

Ser Ala Gly Ala Leu Arg Lys Val Lys Thr Asn Asp Ser Ser Ser Ser  
645 650 655

Ala Gly Ser Lys Lys Ser Ser Ser Ser Phe Ser Thr Val Asn Thr Phe  
660 665 670

Thr Gly Gly Gly Val Gly Ile Phe Lys Val Phe Lys Ser Gly Ser Ser  
675 680 685

Ser Gly Asn Lys Ser Ser Ser Arg Arg Asn Ser Ser Ser Gly Asp Val  
690 695 700

Phe Glu Ser Asp Asp Arg Asn Asp Lys Lys Lys Lys Lys Lys Lys Lys  
705 710 715 720

Lys Lys Ser Leu Phe Leu Phe Gly Lys Ile  
725 730

<210> 255

<211> 2270

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 255

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ttaaaattgc ttgttcggac aatattctat gtctggcaac ttctgatgat actttcaaga 180
caaacgccgc aattgaccaa actattgaac taaacgcaag ttcaatatac ataatatattg 240
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catacataga ttaagtaaat aggatctgct agaaaaatta tatatagatc aatcatctta 420
ttaaggatc ttgtttaagc caaaagtct gtcccaaat tcctcactgt agctactaaa 480
acaacctata cgcaagaaag atgtcattga cagccgatga atacaaacaa caaggtaacg 540
ctgcatttac cgctaaggat tacgataaag cgatagagct cttcactaaa gctattgaag 600
tttctgaaac tccaaaccat gttttatatt ctaacaggtc cgcctgttat acttctttaa 660
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ctaagggtta taatagactc ggtgccgcc acttaggtct tggcgatctc gacgaagctg 780
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tggatcaggt tcatcgtacc caacaggcaa gacaggcaca gcctgattta ggggtgacac 900
agttgtttgc tgacccaaat ttaattgaaa atttaaagaa gaacccaaaa actagcgaaa 960
tgatgaagga ccctcaatta gtggctaaac tgattgggta caaacaaaat ccgcaagcta 1020
ttggccaaga tctgtttact gatccaagat taatgaccat catggctaca ttgatggggg 1080
```



```

ttgatttaaa catggatgat ataaaccaat caaactccat gccaaaggaa ccggaaccca 1140
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aaaattcctc taaagcacca cagaagaag aaagtaagga atccgagcca atggaagttg 1260
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```

&lt;210&gt; 256

&lt;211&gt; 589

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 256

```

Met Ser Leu Thr Ala Asp Glu Tyr Lys Gln Gln Gly Asn Ala Ala Phe
  1             5             10             15

Thr Ala Lys Asp Tyr Asp Lys Ala Ile Glu Leu Phe Thr Lys Ala Ile
      20             25             30

Glu Val Ser Glu Thr Pro Asn His Val Leu Tyr Ser Asn Arg Ser Ala
      35             40             45

Cys Tyr Thr Ser Leu Lys Lys Phe Ser Asp Ala Leu Asn Asp Ala Asn
      50             55             60

Glu Cys Val Lys Ile Asn Pro Ser Trp Ser Lys Gly Tyr Asn Arg Leu
      65             70             75             80

Gly Ala Ala His Leu Gly Leu Gly Asp Leu Asp Glu Ala Glu Ser Asn
      85             90             95

Tyr Lys Lys Ala Leu Glu Leu Asp Ala Ser Asn Lys Ala Ala Lys Glu
      100            105            110

```

307

Gly Leu Asp Gln Val His Arg Thr Gln Gln Ala Arg Gln Ala Gln Pro  
115 120 125

Asp Leu Gly Leu Thr Gln Leu Phe Ala Asp Pro Asn Leu Ile Glu Asn  
130 135 140

Leu Lys Lys Asn Pro Lys Thr Ser Glu Met Met Lys Asp Pro Gln Leu  
145 150 155 160

Val Ala Lys Leu Ile Gly Tyr Lys Gln Asn Pro Gln Ala Ile Gly Gln  
165 170 175

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Asp Leu Phe Thr Asp Pro Arg Leu Met Thr Ile Met Ala Thr Leu Met  
180 185 190

Gly Val Asp Leu Asn Met Asp Asp Ile Asn Gln Ser Asn Ser Met Pro  
195 200 205

Lys Glu Pro Glu Thr Ser Lys Ser Thr Glu Gln Lys Lys Asp Ala Glu  
210 215 220

Pro Gln Ser Asp Ser Thr Thr Ser Lys Glu Asn Ser Ser Lys Ala Pro  
225 230 235 240

Gln Lys Glu Glu Ser Lys Glu Ser Glu Pro Met Glu Val Asp Glu Asp  
245 250 255

Asp Ser Lys Ile Glu Ala Asp Lys Glu Lys Ala Glu Gly Asn Lys Phe  
260 265 270

Tyr Lys Ala Arg Gln Phe Asp Glu Ala Ile Glu His Tyr Asn Lys Ala  
275 280 285

Trp Glu Leu His Lys Asp Ile Thr Tyr Leu Asn Asn Arg Ala Ala Ala  
290 295 300

Glu Tyr Glu Lys Gly Glu Tyr Glu Thr Ala Ile Ser Thr Leu Asn Asp  
305 310 315 320

Ala Val Glu Gln Gly Arg Glu Met Arg Ala Asp Tyr Lys Val Ile Ser  
325 330 335

Lys Ser Phe Ala Arg Ile Gly Asn Ala Tyr His Lys Leu Gly Asp Leu  
340 345 350

Lys Lys Thr Ile Glu Tyr Tyr Gln Lys Ser Leu Thr Glu His Arg Thr  
355 360 365

308

Ala Asp Ile Leu Thr Lys Leu Arg Asn Ala Glu Lys Glu Leu Lys Lys  
370 375 380

Ala Glu Ala Glu Ala Tyr Val Asn Pro Glu Lys Ala Glu Glu Ala Arg  
385 390 395 400

Leu Glu Gly Lys Glu Tyr Phe Thr Lys Ser Asp Trp Pro Asn Ala Val  
405 410 415

Lys Ala Tyr Thr Glu Met Ile Lys Arg Ala Pro Glu Asp Ala Arg Gly  
420 425 430

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Tyr Ser Asn Arg Ala Ala Ala Leu Ala Lys Leu Met Ser Phe Pro Glu  
435 440 445

Ala Ile Ala Asp Cys Asn Lys Ala Ile Glu Lys Asp Pro Asn Phe Val  
450 455 460

Arg Ala Tyr Ile Arg Lys Ala Thr Ala Gln Ile Ala Val Lys Glu Tyr  
465 470 475 480

Ala Ser Ala Leu Glu Thr Leu Asp Ala Ala Arg Thr Lys Asp Ala Glu  
485 490 495

Val Asn Asn Gly Ser Ser Ala Arg Glu Ile Asp Gln Leu Tyr Tyr Lys  
500 505 510

Ala Ser Gln Gln Arg Phe Gln Pro Gly Thr Ser Asn Glu Thr Pro Glu  
515 520 525

Glu Thr Tyr Gln Arg Ala Met Lys Asp Pro Glu Val Ala Ala Ile Met  
530 535 540

Gln Asp Pro Val Met Gln Ser Ile Leu Gln Gln Ala Gln Gln Asn Pro  
545 550 555 560

Ala Ala Leu Gln Glu His Met Lys Asn Pro Glu Val Phe Lys Lys Ile  
565 570 575

Gln Thr Leu Ile Ala Ala Gly Ile Ile Arg Thr Gly Arg  
580 585

<210> 257

<211> 710

<212> DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 257

```

ctgcagaagt acagctgcct ttatttcttg tggtcattta ttgcttttat tttcaagtca 60
gatatacaag aaaatcaaat cccatcgta acgtcacgta taaacgatta atttacagta 120
ataccatact ctaccaacat tatttttagtc cgacgttcag tcctgtaggt gttccaaatc 180
cttctggcat tgacttctgt gcagaaaccc ttcaaaatga gttccacttt acgtcagatc 240
gcataacaac cggatcatata ttttttctt ttgctaaacc ccctactgca agcactttta 300
agaaaaagaa caataaatgc gtctttattg ctgtgtggaa gtgatttttg tctttcggac 360
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aagggcgcac atcggtcccc ctaagaatag cgaagcgata ttacactgaa cactacaatg 480
tcaaatagta ctcaataaat atgactgtaa aaatatgtga ctgtgaagge gaatgttga 540
aggactcttg tcattgtggg agcacctgcc ttccaagctg ttctggcggg gaaaagtga 600
aatgtgatca cagcacgga agccctcaat gtaagagttg tggtgaaaaa tgcaaatgcg 660
aaaccacgtg cacttgtgaa aagagtaa atgcaattgtga aaaatgttag 710

```

&lt;210&gt; 258

&lt;211&gt; 69

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 258

```

Met Thr Val Lys Ile Cys Asp Cys Glu Gly Glu Cys Cys Lys Asp Ser
 1             5             10             15

Cys His Cys Gly Ser Thr Cys Leu Pro Ser Cys Ser Gly Gly Glu Lys
      20             25             30

Cys Lys Cys Asp His Ser Thr Gly Ser Pro Gln Cys Lys Ser Cys Gly
      35             40             45

Glu Lys Cys Lys Cys Glu Thr Thr Cys Thr Cys Glu Lys Ser Lys Cys
      50             55             60

Asn Cys Glu Lys Cys
      65

```

&lt;210&gt; 259

&lt;211&gt; 1474

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 259

```

aaaccatac acaatgaacc ttatcacacc caaacatatg atatggtatt aaaaaatgaa 60
aaaaattcat tattcttttag cgtaattatt gaagaaaaaa cagtgcgcgc ggttaatttt 120

```

```

tgtcactcag taactagaga gaagccgaat gtactccccc ggctagctgg agaccatggc 180
tctgcctagg atttctctta tgctttcctt tcaccaatca ctttggtccg gcgaggcccg 240
cgaagctcgc tttctttcag cctagcaatc atgttcttgc cagcgtcgta gactactgta 300
tggcagttgc tgcacttgcc atgaatatcc tagtgaagcc tctatgcaat aatccagtta 360
ctgcgttaga atcctggtaa aatgtctaata cttattacat tacagcaacg tattagattt 420
tgattgaaaa ttagtccttg cgacttggtta tatatcttat ttaagaaaag ctgaaaggaa 480
gaaagatcat cacgaacaac atgtctgctc cacaagccaa gattttgtct caagctccaa 540
ctgaattgga attacaagtt gctcaagctt tcggtgaatt ggaaaattct tctccagaat 600
tgaaagctga gttgagacct ttgcaattca agtccatcag agaagtatgt tattaatttg 660
aatctaaact taagaataat ggagagtaac aaaggaaaaa agtgtgaacg ggacgatacc 720
agaatgtttc aatctagaaa agtataaaaag ataaggacta ggactcaaat gtatttggt 780
gactatcgcc tgaaccttga tgctaagcaa ataccatata ttcaagaaaa agcctactcc 840
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gttaattaca atcgggtccaa gttctaagcg gtgctgtcca tgcataatc atttacaagt 960
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tagatatttg gttggtggta acaagatcca aaaggttttg ttagactcaa aggatgtcca 1380
acaaatcgac tacaattgg aatctttcca agctgtttac aacaaattga ctggtaagca 1440
aattgttttc gaaattccaa gtgaaactca ttag 1474

```

&lt;210&gt; 260

&lt;211&gt; 190

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 260

```

Met Ser Ala Pro Gln Ala Lys Ile Leu Ser Gln Ala Pro Thr Glu Leu
 1             5             10             15

Glu Leu Gln Val Ala Gln Ala Phe Val Glu Leu Glu Asn Ser Ser Pro
      20             25             30

Glu Leu Lys Ala Glu Leu Arg Pro Leu Gln Phe Lys Ser Ile Arg Glu
      35             40             45

Ile Asp Val Ala Gly Gly Lys Lys Ala Leu Ala Ile Phe Val Pro Val
      50             55             60

Pro Ser Leu Ala Gly Phe His Lys Val Gln Thr Lys Leu Thr Arg Glu
      65             70             75             80

Leu Glu Lys Lys Phe Gln Asp Arg His Val Ile Phe Leu Ala Glu Arg
      85             90             95

```

311

Arg Ile Leu Pro Lys Pro Ser Arg Thr Ser Arg Gln Val Gln Lys Arg  
 100 105 110

Pro Arg Ser Arg Thr Leu Thr Ala Val His Asp Lys Ile Leu Glu Asp  
 115 120 125

Leu Val Phe Pro Thr Glu Ile Val Gly Lys Arg Val Arg Tyr Leu Val  
 130 135 140

Gly Gly Asn Lys Ile Gln Lys Val Leu Leu Asp Ser Lys Asp Val Gln  
 145 150 155 160

Gln Ile Asp Tyr Lys Leu Glu Ser Phe Gln Ala Val Tyr Asn Lys Leu  
 165 170 175

Thr Gly Lys Gln Ile Val Phe Glu Ile Pro Ser Glu Thr His  
 180 185 190

<210> 261

<211> 803

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 261

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 tcactctcac cttagtcgtt ctttatcaac caaaaataaa aaaatgcttc aatccgttgt 180  
 ctttttcgct cttttaacct tcgcaagttc tgtgtcagcg atttattcaa acaatactgt 240  
 ttctacaact accacttttag cgcccagcta ctccttggtg cccaagaga ctaccatata 300  
 gtacgccgac gacaccacta ctttttttgt cacctcaacg gtctactcca cgagctgggt 360  
 cacctcaact tcagccacca ttaccaatgc ggccctctcc tccttgtcca cctcttcggc 420  
 ctctggatct gtaacccag aatccacca tgaaattacc tccacctga ctatcacgtc 480  
 cactttgctg ctaacccttc atgactccac tactttgtct ccatcatcta ctgcagcaag 540  
 tgtcagtgac gaagattcaa acaacaaaga tgcaaagggtc aagtcctttg aacagggttc 600  
 aacttccaat ggttgcggtc caatcacaaa gtttgtcact gtcaccaatg agcccggtac 660  
 ccagtacgtt acagtcaccc caaatacgac tacacaatac gttactgtca ccggtgcacc 720  
 ttctgttacc actacctctc caggtaacgt acaatgggtac aacaccactt cgattactaa 780  
 ttcgaccagt tgggtgaatta tga 803

<210> 262

<211> 100

<212> PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 262

Met Thr Pro Leu Leu Cys Leu His His Leu Leu Gln Gln Val Ser Val

1 5 10 15

Thr Lys Ile Gln Thr Thr Lys Met Gln Arg Ser Ser Pro Leu Asn Arg

20 25 30

Leu Gln Leu Pro Met Val Ala Ser Gln Ser Gln Ser Leu Ser Leu Ser

35 40 45

Pro Met Ser Pro Leu Pro Ser Thr Leu Gln Ser Pro Gln Ile Arg Leu

50 55 60

His Asn Thr Leu Leu Ser Pro Val His Leu Leu Leu Pro Leu Pro Leu

65 70 75 80

Gln Val Thr Tyr Asn Gly Thr Thr Pro Leu Arg Leu Leu Ile Arg Pro

85 90 95

Val Gly Glu Leu

100

&lt;210&gt; 263

&lt;211&gt; 1255

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 263

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aacacacgtc ctttaaagat cccctgatag gtttcattaa aggcaacttc catacacgtt 120  
gaagtgccaa tttttccct acatccaagc attctgggtt tgtatgggtg ttacaccggt 180  
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acgcacgctc ttttgcaaaa atatccatta attgcatgta acttagatta aactggtat 420  
taagatttcg caattttggg ctggattatt aaggtcgagt agcaaagttt agcaagaaca 480  
gtacgaacta agtagccaag atgttgatgc caaaggaaga cagaaacaag atccaccaat 540  
acttattcca aggtatgttt tagaataact ttcagaaagc atgaagatac acggaaagtc 600  
aagcgaggga agttatgctg atacacagta gcggtagtgt gcattcacat acacgatgtt 660  
tcaaacacac agatggatac catgcatatg aggttaaagg atttcttatg aatatattag 720  
tggattacat agaagaaatt acaaggaacc gtgtgacgac attttcgaaa ggacagcaca 780  
aggccatcga ccctggagac gtatgaaata tgggtatacgt cctatatattg ggcaagaaaa 840  
cggtaaaact gttttacgcg gagatccaac ttttgatcct taccgagtac cacgaatcat 900  
ctatatgatc tttttactaa cttatcttca atttcaacgg agagatgtaa acatcattct 960  
ctcctatgat aatttctttt tttatacaga aggtgttgtt gtcgccaaga aggatttcaa 1020  
ccaagccaag cacgaagaaa ttgacaccaa gaacttgtat gtcattaagg ctttacaatc 1080

cttgacttct aagggttacg tcaagactca attctcatgg caatactact actacacctt 1140  
 gactgaagaa ggtgttgaat acttgagaga atacttgaac ttgccagaac acattgttcc 1200  
 aggtacctac attcaagaaa gaaacccaac tcaaagacca caaagaagat attaa 1255

<210> 264

<211> 105

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 264

Met Leu Met Pro Lys Glu Asp Arg Asn Lys Ile His Gln Tyr Leu Phe  
 1 5 10 15

Gln Glu Gly Val Val Val Ala Lys Lys Asp Phe Asn Gln Ala Lys His  
 20 25 30

Glu Glu Ile Asp Thr Lys Asn Leu Tyr Val Ile Lys Ala Leu Gln Ser  
 35 40 45

Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr Tyr  
 50 55 60

Tyr Tyr Thr Leu Thr Glu Glu Gly Val Glu Tyr Leu Arg Glu Tyr Leu  
 65 70 75 80

Asn Leu Pro Glu His Ile Val Pro Gly Thr Tyr Ile Gln Glu Arg Asn  
 85 90 95

Pro Thr Gln Arg Pro Gln Arg Arg Tyr  
 100 105

<210> 265

<211> 1432

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 265

tatttacaag ctagataaaa aaaaaatcaa atagcaagct attctgtcat atcttaaggt 60  
 gctgattgtt ttagggcacg aagtaaacaa gctcttcccc aaaacaataa atacggtttt 120  
 cgggactgtt caccctgaca ttttacgttt ccgacggcgc gatgctatct ttgaattttt 180  
 atctctttca ggtaacccca tgaccagtag ggcggcttac taccgaagag aaaaatgtcc 240  
 gcggcctaga cagttacttc ccaggccagg gccaggccac acggacagag gcagattcca 300  
 agttgttccg catagtctgt ctagctcttt ctcaattttc cgccagattc tgtctaattt 360  
 ctttcgcgtc gagttggcaa cagtacgaag aagtaactct aatagataga tataaccgtt 420  
 tttgagggca ttatttttgc agaagataat agaagagaac cgtaacaaag gaatcaagca 480



```

aagaaaaagt atgtaataga atgtattgta tgcttggtga atgaatgtca atgtagctat 540
tttatatggt gagctcaaat tgaatgaaca tatcgtggaa atttaaaata ctgaagaata 600
cccaataagt caatgcaacc tgtgaatgtt tttcctgaaa tacgccgaat actgaatagc 660
attattacca taaattgctt ctagaaggaa ggcggtgtac catttaatac tgatgatatg 720
gttaatatca tttgagaagt cttcacatga ggactataga actaccatcc aggaattata 780
gaggaaatta actgaatcag agatctatgt tgaacattc atttacatgt aattgtctgc 840
aataaagcaa ttttttgaa atatgcaagt ttactaaca gaataaattc ttttttgatt 900
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gagacaatac gtcaagcaat tcttgaccaa ggatttaaaa ttccattac ctacagagt 1380
ccaaaaatct accaagactt tctcttaca gagaccatca accttctact aa 1432

```

&lt;210&gt; 266

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 266

```

Met Tyr Leu Ala His Phe Lys Glu Tyr Gln Val Ile Gly Arg Arg Leu
  1             5             10            15

```

```

Pro Thr Glu Ser Val Pro Glu Pro Lys Leu Phe Arg Met Arg Ile Phe
          20             25            30

```

```

Ala Ser Asn Glu Val Ile Ala Lys Ser Arg Tyr Trp Tyr Phe Leu Gln
          35             40            45

```

```

Lys Leu His Lys Val Lys Lys Ala Ser Gly Glu Ile Val Ser Ile Asn
          50             55            60

```

```

Gln Ile Asn Glu Ala His Pro Thr Lys Val Lys Asn Phe Gly Val Trp
          65             70            75            80

```

```

Val Arg Tyr Asp Ser Arg Ser Gly Thr His Asn Met Tyr Lys Glu Ile
          85             90            95

```

```

Arg Asp Val Ser Arg Val Ala Ala Val Glu Thr Leu Tyr Gln Asp Met
          100            105           110

```

```

Ala Ala Arg His Arg Ala Arg Phe Arg Ser Ile His Ile Leu Lys Val
          115            120           125

```

315

Ala Glu Ile Glu Lys Thr Ala Asp Val Lys Arg Gln Tyr Val Lys Gln  
 130 135 140

Phe Leu Thr Lys Asp Leu Lys Phe Pro Leu Pro His Arg Val Gln Lys  
 145 150 155 160

Ser Thr Lys Thr Phe Ser Tyr Lys Arg Pro Ser Thr Phe Tyr  
 165 170

<210> 267  
 <211> 932  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 267  
 cttcttaciaa gttaatgaat agtatatata tgtaaaaaaa aattctgctt catgtatata 60  
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 acatcttggc atattaaatg gttatttcgg ggtttgttc ggctcaacgg tgatataaaa 180  
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 tggttgaagg tttggctaac gaccagaaa acaagggtcc attgatcaag gttgctgatg 780  
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<210> 268  
 <211> 143  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 268  
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Glu Gln Thr Ala Glu Val Thr Ile Glu Asp Ala Leu Lys Val Val Leu  
 20 25 30

Arg Thr Ala Leu Val His Asp Gly Leu Ala Arg Gly Leu Arg Glu Ser

35

40

45

Thr Lys Ala Leu Thr Arg Gly Glu Ala Leu Leu Val Val Leu Val Ser  
 50 55 60

Ser Val Thr Glu Ala Asn Ile Ile Lys Leu Val Glu Gly Leu Ala Asn  
 65 70 75 80

Asp Pro Glu Asn Lys Val Pro Leu Ile Lys Val Ala Asp Ala Lys Gln  
 85 90 95

~~Leu Gly Glu Trp Ala Gly Leu Gly Lys Ile Asp Arg Glu Gly Asn Ala~~  
 100 105 110

Arg Lys Val Val Gly Ala Ser Val Val Val Val Lys Asn Trp Gly Ala  
 115 120 125

Glu Thr Asp Glu Leu Ser Met Ile Met Glu His Phe Ser Gln Gln  
 130 135 140

&lt;210&gt; 269

&lt;211&gt; 800

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 269

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 aaaataatct cttcgtacta tccttcatgt cgccttttat tataaagtat gctaggtagt 240  
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 ggatactgaa taacctgtta accacattga tccaggacat tgtagctcgg gaaaccactc 600  
 aacaacaatt gctgaagaca agatatccgg atcttcgcag ttattatttc gaccgaacg 660  
 gatctctcga tattaatgga ctacagaagc aacaagagtc ctctcagtat attcactgtg 720  
 agaattgtgg cagggatgtg tccgcaaaca gactagcagc tcatttacag agatgtttga 780  
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&lt;210&gt; 270

&lt;211&gt; 99

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

317

&lt;400&gt; 270

Met Thr Glu Glu Thr Ile Thr Ile Asp Ser Ile Ser Asn Gly Ile Leu  
 1 5 10 15

Asn Asn Leu Leu Thr Thr Leu Ile Gln Asp Ile Val Ala Arg Glu Thr  
 20 25 30

Thr Gln Gln Gln Leu Leu Lys Thr Arg Tyr Pro Asp Leu Arg Ser Tyr  
 35 40 45

Tyr Phe Asp Pro Asn Gly Ser Leu Asp Ile Asn Gly Leu Gln Lys Gln  
 50 55 60

Gln Glu Ser Ser Gln Tyr Ile His Cys Glu Asn Cys Gly Arg Asp Val  
 65 70 75 80

Ser Ala Asn Arg Leu Ala Ala His Leu Gln Arg Cys Leu Ser Arg Gly  
 85 90 95

Ala Arg Arg

&lt;210&gt; 271

&lt;211&gt; 1605

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 271

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 tgatcatcgac gcgcccggagc atcggaaggt tggaacgtgc gcgattgcac caatcccact 180  
 ggggccgtgc attctgtagg caggaagcca ctggacactc tgcccgttcc cacttggaag 240  
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 cgttggagga atgccgctac ctaggtaagt ctactgggtg ggaattccag taccgacgtc 360  
 taggaacatc atgatgctgc agtttctttg aaatttcata tacagtgtta ccaaggataa 420  
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<210> 272

<211> 236

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 272

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Gly Gln Glu Val Asp Gly Glu Ala Val Gly Asp Glu Phe Lys Gly Tyr  
 35 40 45

Val Phe Lys Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys  
 50 55 60

Gln Gly Val Leu Leu Pro Thr Arg Ile Lys Leu Leu Leu Thr Lys Asn  
 65 70 75 80

Val Ser Cys Tyr Arg Pro Arg Arg Asp Gly Glu Arg Lys Arg Lys Ser  
 85 90 95

Val Arg Gly Ala Ile Val Gly Pro Asp Leu Ala Val Leu Ala Leu Val  
 100 105 110

Ile Val Lys Lys Gly Glu Gln Glu Leu Glu Gly Leu Thr Asp Thr Thr  
 115 120 125

Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn Asn Ile Arg Lys Phe  
 130 135 140

Phe Gly Leu Ser Lys Glu Asp Asp Val Arg Asp Phe Val Ile Arg Arg  
 145 150 155 160

Glu Val Thr Lys Gly Glu Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln  
 165 170 175  
 Arg Leu Val Thr Pro Gln Arg Leu Gln Arg Lys Arg His Gln Arg Ala  
 180 185 190  
 Leu Lys Val Arg Asn Ala Gln Ala Gln Arg Glu Ala Ala Ala Glu Tyr  
 195 200 205  
 Ala Gln Leu Leu Ala Lys Arg Leu Ser Glu Arg Lys Ala Glu Lys Ala  
 210 215 220

Glu Ile Arg Lys Arg Arg Ala Ser Ser Leu Lys Ala  
 225 230 235

<210> 273

<211> 4331

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 273

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 atcatgcctt cacttttgcc ttcccatctt tctttttgct gcaaaataaa gggaagaggg 240  
 gtaaaaaacgc aaggaagaac aagaagaaga gggtagtgc aaaaaaagaa aagaagaaaa 300  
 aaaaaaaaaa gtaatcttga taccgtgagc aaataagcta acggaaagcg taagaaagaa 360  
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<210> 274  
 <211> 1276  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 274

Met Ile Thr Asn Thr Glu Phe Asp Val Pro Val Asp Trp Leu Tyr Lys  
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~~Gly Lys Ser Arg Arg Lys Thr Asn Thr Lys Pro Ser Arg Pro Ser Thr~~  
 20 25 30

Ser Pro Ala Ser Ser Ser Ser Thr Ser Ser Ser Lys Asn Gly Asp Asn  
 35 40 45

Ser Thr Ser Gly Asn Arg Ser Ser Asn Asp Lys Pro Arg Ala Arg Ser  
 50 55 60

Ser Ser Val Ser Asn Ala Ala Leu Cys Asn Thr Glu Lys Pro Asp Leu  
 65 70 75 80

Lys Arg Asn Asp Gly Asn Thr Ser Ala Ser Asp Thr Asp Asn Ile Pro  
 85 90 95

Leu Leu Thr Pro Ile Asn Ser Gly Asn Arg Ser Asp Ser Ala Asp Ile  
 100 105 110

Asp Asn Pro Ala Thr Val Asp Ala Ile Asp Leu Ile Asp Asn Asp Asp  
 115 120 125

Asn Gly Ser Ser Thr Gln Phe Val Arg Lys Lys Arg Ser Thr Ser Ile  
 130 135 140

Ser Asn Ala Val Val Ser Ser Lys Pro Arg Leu Ala Ser Ser Ala Ile  
 145 150 155 160

Asn Ala Thr Ala Ser Ser Ser Val Gly Lys Gly Lys His Pro Pro Ile  
 165 170 175

Ser Ser Pro Ser Asn Ala Thr Leu Lys Arg Ser Asn Ser Thr Ser Gly  
 180 185 190

Glu Lys Thr Lys Arg Ser Ile Phe Gly Ser Leu Phe Ser Lys Arg Ser  
 195 200 205

Thr Ser Ser Ser Ala Ser Thr Ala Lys Lys Pro Leu Pro Val Val Asn

322



210	215	220
Thr Ser Thr Thr Glu Asn Glu Ser Gly Gly Ile Lys Ala Val Ala Thr		
225	230	235 240
Pro Asp Pro Arg Val Lys Glu Ile Ser Ser Pro Met Arg Gly Val Ala		
	245	250 255
Pro Thr Ala Ser Lys Pro Gln Thr Pro Ile Leu Pro Ser Pro Ala Leu		
	260	265 270
<hr/>		
Ala Val Lys Asp Leu Ser Thr Val Ser Leu Lys Arg Val Ser Phe Ala		
275	280	285
Val Asp Lys Phe Glu Ser Asp Pro Pro Gln Gln Leu Pro Ser Arg Thr		
290	295	300
Pro Lys Lys Gly Asn Ile Leu Ile Pro Asp Asp Met Ile Ser Glu Val		
305	310	315 320
Pro Ser Ile Ser Val Gly Ile Ser Ser Ser Asn Gln Ser Ala Lys Ser		
	325	330 335
Thr Asn Ser Asn Ile Lys Gly Pro Leu Tyr Thr Lys Lys Ser Lys Glu		
	340	345 350
Tyr Ile Leu Ala Leu Glu Asn Gln Lys Leu Ala Leu Arg Glu Ala Ala		
355	360	365
Lys His Gln Gln Glu Ala His Phe Ala Ala Asn Arg Ile Ala Phe Glu		
370	375	380
Val Ala Asn Phe Lys Thr Ala Ser Asp Ala Gly Gly Lys Leu Thr Glu		
385	390	395 400
Lys Ser Ser Glu Gly Thr Ile Thr Lys Gln Arg Glu Glu Val Ser Pro		
	405	410 415
Pro Asn Val Glu Ala Asp Arg Glu Leu Glu Asn Asn Lys Leu Ala Glu		
	420	425 430
Asn Leu Ser Lys Ala Gly Ile Asp Lys Pro Ile His Met His Glu His		
	435	440 445
Tyr Phe Lys Glu Pro Asp Gln Asp Lys Tyr Gln Asp Gly His Ser Ile		
450	455	460
Glu Asn Asn Glu Val Thr Leu Asp Val Ile Tyr Thr Arg Cys Cys His		

323

465		470		475		480
Leu Arg Glu Ile Leu Pro Ile Pro Ser Thr Leu Arg Gln Val Lys Asp						
	485			490		495
Lys Thr Ala Pro Leu Gln Ile Leu Lys Phe Leu Asn Pro Lys Pro Thr						
	500		505			510
Leu Ile Asp Ile Leu Ser Phe Cys Asp Phe Ile Thr Ile Ala Pro Ile						
	515		520			525

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His Thr Ile Val Phe Asp Asn Val Ala Leu Asn Gln Asp Met Phe Arg						
	530		535			540
Ile Ile Ile Ser Ala Leu Val Asn Ser Thr Val Leu Asp Lys Leu Ser						
	545		550		555	560
Leu Arg Asn Val Arg Ile Asp Gln Asp Gly Trp Lys Leu Leu Cys Lys						
	565		570			575
Phe Leu Leu Leu Asn Lys Ser Leu Asn Lys Leu Asp Ile Ser Gln Thr						
	580		585			590
Lys Ile Lys Ser Asp Leu Ala Glu Ser Leu Tyr Arg His Asn Met Asp						
	595		600			605
Trp Asn Leu Phe Thr Asp Val Leu Ser Gln Arg Ser His Lys Pro Ile						
	610		615			620
Glu Glu Leu Leu Phe Asn Gly Ile Gln Phe Ser Lys Ile Pro Tyr Ser						
	625		630		635	640
Cys Phe Ala Arg Leu Leu Thr Ser Phe Ala Thr Gln Lys Asn Phe Pro						
	645		650			655
Glu Ser Gly Ile Arg Leu Gly Leu Ala Gly Ala Thr Thr Ser Asn Ile						
	660		665			670
Ser Gln Asp Cys Leu Lys Phe Ile Phe Asn Trp Met Ser Gln Tyr Asn						
	675		680			685
Val Gln Gly Val Asp Leu Ala Phe Asn Asp Leu Ser Thr Met Ile Lys						
	690		695			700
Pro Met Val Gly Lys Leu Ser Ala Leu Ser Tyr Asp Asn Leu Arg Tyr						
	705		710		715	720
Phe Ile Leu Asn Ser Thr Asn Ile Ser Thr Ser Tyr Asp Leu Ala Leu						

725

730

735

Leu Leu Lys Tyr Leu Ser Lys Leu Pro Asn Leu Ile Phe Leu Asp Leu  
 740 745 750

Ser Asn Leu Ser Gln Cys Phe Pro Asp Ile Leu Pro Tyr Met Tyr Lys  
 755 760 765

Tyr Leu Pro Arg Phe Pro Asn Leu Lys Arg Ile His Leu Asp Ser Asn  
 770 775 780

~~Asn Leu Thr Leu Lys Glu Leu Ala Val Val Cys Asn Ile Leu Ile Lys~~  
 785 790 795 800

Cys Lys Ser Leu Ser His Val Ser Met Thr Asn Gln Asn Val Glu Asn  
 805 810 815

Phe Tyr Leu Met Asn Gly Thr Asp Ser Pro Val Gln Gln Thr Asn Thr  
 820 825 830

Asp Gly Asp Leu Asp Ser Ser Ser Thr Leu Asp Val Lys Gly Gln Phe  
 835 840 845

Ala Lys Asn Ser Phe Ser Ser Thr Leu Tyr Ala Phe Ala Arg Asp Ser  
 850 855 860

Pro Asn Leu Ile Gly Leu Asp Phe Asp Tyr Asp Leu Ile Ser Glu Glu  
 865 870 875 880

Ile Gln Ser Arg Ile Ala Leu Cys Leu Met Arg Asn Met Lys Arg Thr  
 885 890 895

Met Asp Ser Thr Phe Gln Leu Asp Glu Leu Asp Ser Gln Asp Asp Leu  
 900 905 910

Leu Phe Asp Gly Ser Leu Val Thr Met Thr Ala Glu Ser Val Leu Glu  
 915 920 925

Lys Leu Asn Leu Leu Ser Asp Lys Ser Thr Lys Val Lys Lys Asp Thr  
 930 935 940

Thr Lys Arg Tyr Leu Leu Lys Lys Tyr Ile Glu Lys Phe His Ile Leu  
 945 950 955 960

His His Asn Val Gln His Thr Ile Asp Thr Met Phe Glu Lys Arg Lys  
 965 970 975

Ser Gly Glu Leu Pro Leu Gln Glu Lys Glu Asn Leu Val Arg Leu Leu

325

980	985	990
Leu Leu Glu Gln Asn Leu Cys Asn Ile Leu Glu Leu Phe Ser His Asn		
995	1000	1005
Pro Asn Leu Asn Asp Val Leu Gly Ser Ser Arg Asp Asp Ser Lys Glu		
1010	1015	1020
Ser Val Asp Ser Ser Glu Asp Ser Lys Leu Pro Ala Leu Lys His Val		
1025	1030	1035 1040
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Glu Ser Gly Tyr His Val Pro Glu Glu Lys Ile Gln Pro Glu Asn Asp		
1045	1050	1055
Val Ile Thr Ala Arg Pro His Leu Met Ala Thr Asp Ser Gly Lys Thr		
1060	1065	1070
Ile Asp Val Phe Thr Gly Lys Pro Leu Val Phe Lys His Thr Ser Ser		
1075	1080	1085
Ser Thr Ser Val Gly Cys Lys Lys Gln Glu Glu Glu Gly Glu Leu		
1090	1095	1100
His Lys Trp Gly Phe Phe Val Gln Gln Gln Arg Ser Leu Tyr Pro Glu		
1105	1110	1115 1120
Asn Glu Ser Thr Arg Gln Thr Pro Phe Ala Ser Gly Asp Thr Pro Ile		
1125	1130	1135
Asn Thr Glu Thr Ala Gly Lys Ser Thr Ser Ser Pro Ser Val Ser Thr		
1140	1145	1150
Ser Asn Asn Glu Thr Ala Thr Thr Ser Leu Phe Ser Pro Ala Asn Pro		
1155	1160	1165
Lys Ile Leu Pro Lys Ile Pro Ser Gly Ala Val Leu Arg Ser Ala Ile		
1170	1175	1180
Met Lys Ala Lys Gly Ile Asp Ser Ile Asp Asp Leu Ile Gln Asn Val		
1185	1190	1195 1200
Asn Ser Asn Asn Ile Glu Leu Glu Asn Ile Tyr Gly Glu Ser Ile Gln		
1205	1210	1215
Asn Ser Ala Ser Thr Phe Thr Pro Gly Val Asp Ser Asp Val Ser Ala		
1220	1225	1230
Pro Asn Thr Asp Lys Gly Ser Val Glu Thr Leu Pro Ala Val Ser Thr		

1235

1240

1245

Asp Asp Pro Asn Cys Glu Val Lys Val Thr Ala Thr Tyr Asp Lys Leu  
 1250 1255 1260

Leu Asn Asn Leu Ser Met Glu Arg Ser Il Arg Leu  
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&lt;210&gt; 275

&lt;211&gt; 1262

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 275

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ga 1262

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&lt;210&gt; 276

&lt;211&gt; 253

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 276

Met Leu Lys Leu Ala Arg Pro Phe Ile Pro Pro Leu Ser Arg Asn Asn  
 1 5 10 15

327

Ala Ile Ser Ser Gly Ile Val Leu Thr Ser Arg Arg Phe Gln Ser Ser  
20 25 30

Phe Thr Phe Leu Ser Asn Gln Ser Leu Leu Ser Lys Asn Gln Met Lys  
35 40 45

Ser Lys Arg Lys Lys Gly Ser Lys Lys Ala Ala Tyr His Arg Gln Pro  
50 55 60

---

Pro Glu His Glu His Thr Ala Pro Leu Ile Lys Gln Asn Lys Thr Ile  
65 70 75 80

Thr Lys Lys Glu His Ser Asp Val Arg Gly Ser His Leu Lys Lys Lys  
85 90 95

Arg Ser Asp Phe Ser Trp Leu Pro Arg Val Pro Ser Thr Ser His Leu  
100 105 110

Lys Gln Ser Asp Met Thr Thr Asn Val Leu Tyr Ser Gly Tyr Arg Pro  
115 120 125

Leu Phe Ile Asn Pro Asn Asp Pro Lys Leu Lys Glu Asp Thr Gly Ser  
130 135 140

Thr Leu Tyr Glu Phe Ala Met Lys Leu Glu Asp Leu Asn Glu Pro Leu  
145 150 155 160

Ser Pro Trp Ile Ser Ser Ala Thr Gly Leu Glu Phe Phe Ser Glu Trp  
165 170 175

Glu Asn Ile Pro Ser Glu Leu Leu Lys Asn Leu Lys Pro Phe His Pro  
180 185 190

Pro Lys Glu Lys Ser Met Asn Thr Asn Glu Leu Ile His Val Ser Ala  
195 200 205

Lys Arg Asn Thr Leu Val Asp Asn Lys Thr Ser Glu Thr Leu Gln Arg  
210 215 220

Lys Met Asp Glu Phe Ser Lys Arg Arg Gly Lys Gly Arg Lys Lys Ser  
225 230 235 240

Val Val Thr Leu Leu Gln Met Lys Lys Lys Leu Glu Gly  
245 250

<210> 277  
 <211> 1940  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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 gatctctttt gttgttgata ctaaccagta aagttgagag ttataacaat gaaaatagga 600  
 tgctgtgcga ctttttttat ccacagttag gtggagtcga attccatata tatcatttat 660  
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<210> 278  
 <211> 461  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 278  
 Met Ser Ser Ser His Lys Val Glu Ser Tyr Asn Asn Glu Asn Arg Met

1	5	10	15
Leu Cys Asp Phe Phe Tyr Pro Gln Leu Gly Gly Val Glu Phe His Ile	20	25	30
Tyr His Leu Ser Gln Lys Leu Ile Asp Leu Gly His Ser Val Val Ile	35	40	45
Ile Thr His Ala Tyr Lys Asp Arg Val Gly Val Arg His Leu Thr Asn	50	55	60
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Thr Phe Pro Thr Val Phe Ser Thr Phe Pro Ile Ile Arg Asn Ile Leu	85	90	95
Leu Arg Glu Gln Ile Gln Ile Val His Ser His Gly Ser Ala Ser Thr	100	105	110
Phe Ala His Glu Gly Ile Leu His Ala Asn Thr Met Gly Leu Arg Thr	115	120	125
Val Phe Thr Asp His Ser Leu Tyr Gly Phe Asn Asn Leu Thr Ser Ile	130	135	140
Trp Val Asn Lys Leu Leu Thr Phe Thr Leu Thr Asn Ile Asp Arg Val	145	150	155
Ile Cys Val Ser Asn Thr Cys Lys Glu Asn Met Ile Val Arg Thr Glu	165	170	175
Leu Ser Pro Asp Ile Ile Ser Val Ile Pro Asn Ala Val Val Ser Glu	180	185	190
Asp Phe Lys Pro Arg Asp Pro Thr Gly Gly Thr Lys Arg Lys Gln Ser	195	200	205
Arg Asp Lys Ile Val Ile Val Val Ile Gly Arg Leu Phe Pro Asn Lys	210	215	220
Gly Ser Asp Leu Leu Thr Arg Ile Ile Pro Lys Val Cys Ser Ser His	225	230	235
Glu Asp Val Glu Phe Ile Val Ala Gly Asp Gly Pro Lys Phe Ile Asp	245	250	255
Phe Gln Gln Met Ile Glu Ser His Arg Leu Gln Lys Arg Val Gln Leu			

330



260

265

270

Leu Gly Ser Val Pro His Glu Lys Val Arg Asp Val Leu Cys Gln Gly  
 275 280 285

Asp Ile Tyr Leu His Ala Ser Leu Thr Glu Ala Phe Gly Thr Ile Leu  
 290 295 300

Val Glu Ala Ala Ser Cys Asn Leu Leu Ile Val Thr Thr Gln Val Gly  
 305 310 315 320

Gly Ile Pro Glu Val Leu Pro Asn Glu Met Thr Val Tyr Ala Glu Gln  
 325 330 335

Thr Ser Val Ser Asp Leu Val Gln Ala Thr Asn Lys Ala Ile Asn Ile  
 340 345 350

Ile Arg Ser Lys Ala Leu Asp Thr Ser Ser Phe His Asp Ser Val Ser  
 355 360 365

Lys Met Tyr Asp Trp Met Asp Val Ala Lys Arg Thr Val Glu Ile Tyr  
 370 375 380

Thr Asn Ile Ser Ser Thr Ser Ser Ala Asp Asp Lys Asp Trp Met Lys  
 385 390 395 400

Met Val Ala Asn Leu Tyr Lys Arg Asp Gly Ile Trp Ala Lys His Leu  
 405 410 415

Tyr Leu Leu Cys Gly Ile Val Glu Tyr Met Leu Phe Phe Leu Leu Glu  
 420 425 430

Trp Leu Tyr Pro Arg Asp Glu Ile Asp Leu Ala Pro Lys Trp Pro Lys  
 435 440 445

Lys Thr Val Ser Asn Glu Thr Lys Glu Ala Arg Glu Thr  
 450 455 460

&lt;210&gt; 279

&lt;211&gt; 2900

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 279

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331

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gaggcgaaca aacacatcta tacatatata tacatctata tggatataaa aacgactaat 300
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2900

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<210> 280  
 <211> 799  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 280

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Leu Asn Ala Ser Thr Val Ser His Gln Ser Lys Pro Phe Arg Gln Phe  
 20 25 30

Ser Thr Arg Ser Arg Ala Lys Ser Asn Ala Ser Phe Lys Gly Leu Arg  
 35 40 45

Arg Val Leu Thr His Asp Gly Thr Leu Asp Asn Asp Tyr Phe Asn Lys  
 50 55 60

His Asn Val Ser Gln Lys Cys Lys Ser Ser Asp Ala Leu Phe Arg Lys  
 65 70 75 80

Arg Thr Ile Ser Gly Leu Asn Met Thr Ala Leu Thr Arg Val Lys Ser  
 85 90 95

Asn Gln Gly Lys Arg Ser Ala Ser Phe His Ser Pro Val His Asn Thr  
 100 105 110

Leu Leu Ser Pro Lys Asn Ser Ser His Ser Asn Thr Gly Thr Ala Gly  
 115 120 125

Phe Gly Leu Lys Pro Arg Arg Ser Lys Ser Thr Gln Ser Val Leu Ser  
 130 135 140

Leu Arg Asp Ala Gln Glu Ser Lys Lys Ser Glu Ser Thr Thr Asp Glu  
 145 150 155 160

Glu Val Glu Cys Phe Ser Glu Asp Asn Ile Glu Asp Gly Lys Val Asn  
 165 170 175

Asn Asp Lys Val Ile Ala Glu His Val Met Pro Glu Glu Lys Lys Asn  
 180 185 190

Val Gln Gln Leu Asn Gln Asn Glu Leu Gln Ser Pro Asp Ser Ile Asp  
 195 200 205

Glu Gln Glu Glu Asp Lys Ser Gly Thr Asp Gly Lys Glu Asn His Arg  
 210 215 220

333

Ala Val Ser Leu Pro Leu Pro His Leu Ser Ser Asn Asn Tyr Phe Gly			
225	230	235	240
Glu Ser Ser His Ser Ile Glu His Gln Lys Asp Gly Glu Thr Ser Pro			
	245	250	255
Ser Ser Ile Glu Thr Lys Leu Asn Ala Thr Ser Val Ile Asn Glu Glu			
	260	265	270
Gly Gln Ser Lys Val Thr Lys Glu Ala Asp Ile Asp Asp Leu Ser Ser			
275	280	285	
His Ser Gln Asn Leu Arg Ala Ser Leu Val Lys Ala Gly Asp Asn Ile			
290	295	300	
Ser Glu Ala Pro Tyr Asp Lys Glu Lys Lys Ile Leu Asp Val Gly Asn			
305	310	315	320
Thr Leu Ala Ala His Lys Ser Asn Gln Lys Pro Ser His Ser Asp Glu			
	325	330	335
Gln Phe Asp Gln Glu Asp His Ile Asp Ala Pro Arg Ser Asn Ser Ser			
	340	345	350
Arg Lys Ser Asp Ser Ser Phe Met Ser Leu Arg Arg Gln Ser Ser Lys			
	355	360	365
Gln His Lys Leu Leu Asn Glu Glu Glu Asp Leu Ile Lys Pro Asp Asp			
370	375	380	
Ile Ser Ser Ala Gly Thr Lys Asp Ile Glu Gly His Ser Leu Leu Glu			
385	390	395	400
Asn Tyr Ala Pro Asn Met Ile Leu Ser Gln Ser Thr Gly Val Glu Arg			
	405	410	415
Arg Phe Glu Asn Ser Ser Ser Ile Gln Asn Ser Leu Gly Asn Glu Ile			
	420	425	430
His Asp Ser Gly Glu His Met Ala Ser Gly Asp Thr Phe Asn Glu Leu			
	435	440	445
Asp Asp Gly Lys Leu Arg Lys Ser Lys Lys Asn Gly Gly Arg Ser Gln			
	450	455	460
Leu Gly Gln Asn Ile Pro Asn Ser Gln Ser Thr Phe Pro Thr Ile Ala			
465	470	475	480

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Asn Ile Gly Ser Lys Asp Asn Asn Val Pro Gln His Asn Phe Ser Thr
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Ser Ile Ser Ser Leu Thr Asn Asn Leu Arg Arg Ala Ala Pro Glu Ser
      500                      505                      510

Phe His Gly Ser Arg Met Asn Asn Ile Phe His Lys Lys Gly Asn Gln
      515                      520                      525

Asn Leu Leu Leu Arg Ser Asn Asp Leu Asn Lys Asn Ser Ala Ala Pro
      530                      535                      540
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Ala Ser Pro Leu Ser Asn Glu His Ile Thr Ser Ser Thr Asn Ser Gly
      545                      550                      555                      560

Ser Asp Ala Asn Arg Gln Ser Asn Ser Gly Ala Lys Phe Asn Ser Phe
      565                      570                      575

Ala Gln Phe Leu Lys Ser Asp Gly Ile Asp Ala Glu Ser Arg Thr Gln
      580                      585                      590

Arg Lys Leu Trp Leu Gln Arg Glu Asn Ser Ile Met Asp Leu Ser Ser
      595                      600                      605

Gln Asn Asp Gly Ser Asp Ser Ile Phe Met Ala Gly Asn Ile Asp Ala
      610                      615                      620

Lys Arg Glu Phe Glu Arg Ile Ser His Glu Tyr Ser Asn Val Lys Arg
      625                      630                      635                      640

Phe Tyr Asn Pro Leu Asp Glu Ala Leu Leu Arg Val Gln Pro Ile Ile
      645                      650                      655

Thr Gly Asn Ala Asn Asn Ile Arg Lys Lys Ser His Asn Asp Ala Gln
      660                      665                      670

Ser Ile Ala His Ser Ser Ser Asp Thr Asp His Lys Asp Glu Asp Asp
      675                      680                      685

Leu Leu Phe Thr Asn Tyr Asp Lys Lys Phe Asp Asp Leu Tyr Pro His
      690                      695                      700

Leu Ala Ser Ala Lys Ile Gln Ala Val Leu Ser Gly Ile Trp Lys Ser
      705                      710                      715                      720

Glu Ser Tyr Leu Phe Asn Lys Asp Val Asn Pro Ile Asn Lys Asn Arg
      725                      730                      735

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Thr Thr Ser Thr Asn His Ser Val Gly His Thr Ala Ser Gln Asn Ala  
 740 745 750  
 Arg Asn Leu Leu Arg Gly Pro Met Gly Ser Ser Thr Thr Leu His His  
 755 760 765  
 Gln Arg Val Ile Asn Ser Leu Gln Pro Thr Thr Arg Ala Val Asn Arg  
 770 775 780  
 Arg Met Glu Asn Val Gly Tyr Met His Thr Gln Pro Gln Gln Arg  
 785 790 795

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<210> 281  
 <211> 1212  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 281  
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 ggatttttatt ttattttcttt tttaatgcta agaaagtaat tccgcataat taaacgtgtg 180  
 ctggcctcga taggtaccta tagtatacag aagcttacga aaagctcctg caggatggca 240  
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 agagatcgca taaaaaacca aaaggaaacg aattacttgt caaatagtta ttgtaatgga 420  
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 aacaatatat aattggaata atggctggtt gggatatttt tgggttggtgt atgttatcac 540  
 cctgttcacg tttttcggat acttagtttt attcaatgtg gtaaaccattg aatgttttca 600  
 gcttaagatc tattttttttt tttctagaag aaattgcgtc ctttactaac tttattttac 660  
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 caatatattt aa 1212

<210> 282  
 <211> 190  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

&lt;400&gt; 282

Met Ala Gly Trp Asp Ile Phe Gly Trp Phe Arg Asp Val Leu Ala Ser  
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Leu Gly Leu Trp Asn Lys His Gly Lys Leu Leu Phe Leu Gly Leu Asp  
 20 25 30

Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asn Asp Arg Leu  
 35 40 45

~~Ala Thr Leu Gln Pro Thr Trp His Pro Thr Ser Glu Glu Leu Ala Ile~~  
 50 55 60

Gly Asn Ile Lys Phe Thr Thr Phe Asp Leu Gly Gly His Ile Gln Ala  
 65 70 75 80

Arg Arg Leu Trp Lys Asp Tyr Phe Pro Glu Val Asn Gly Ile Val Phe  
 85 90 95

Leu Val Asp Ala Ala Asp Pro Glu Arg Phe Asp Glu Ala Arg Val Glu  
 100 105 110

Leu Asp Ala Leu Phe Asn Ile Ala Glu Leu Lys Asp Val Pro Phe Val  
 115 120 125

Ile Leu Gly Asn Lys Ile Asp Ala Pro Asn Ala Val Ser Glu Ala Glu  
 130 135 140

Leu Arg Ser Ala Leu Gly Leu Leu Asn Thr Thr Gly Ser Gln Arg Ile  
 145 150 155 160

Glu Gly Gln Arg Pro Val Glu Val Phe Met Cys Ser Val Val Met Arg  
 165 170 175

Asn Gly Tyr Leu Glu Ala Phe Gln Trp Leu Ser Gln Tyr Ile  
 180 185 190

&lt;210&gt; 283

&lt;211&gt; 1025

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 283

ttctttacaa ttcaccttgc attattgaag gagtgtctatt cttcgttttg ccacctttt 60  
 gctgttttcc ctcatatcac ataatacccg gagaggctct ttcctgcgac agcgcaacat 120

```

ccaaccatcc taaaggtatg ggtgtactga cgatgcgatt atttcattaa gttctgtctt 180
ttttgtataa atgaaaaaag aacggtgaaa tccatagaaa tacagagagc gacgcaaaca 240
gcgcgcgagac tctacgggta atagactcac atccacgtga ccagtttcca atcgaacttt 300
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gcgaaagttt cattgtttga tacatcttga tagtaaccgc aggcttcttt cttagtctcat 420
attttattgt atttcaacta atattatttt tttttcagtga gaagggaagg tgaaccaaga 480
acatacaaac atagccaaag atgtctgcc aagctcaaaa ccctatgcgt gatttgaaga 540
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tcagaacttt cggatatcaga agaaacgaaa aaattgctgt tcacgttacc gtcagaggtc 720
caaaggctga agaaattttg gaaagagggt tgaagggtcaa ggaataccaa ttgagagaca 780
gaaacttctc tgctaccggt aacttcggtt tcggtattga cgaacacatt gacttgggta 840
tcaagtatga cccatccatc ggtattttcg gtatggattt ctatgtcgtc atgaacagac 900
caggtgctag agtcactaga agaaagagat gtaagggtac cggttggaac tcccacaaga 960
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aataa 1025

```

&lt;210&gt; 284

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 284

```

Met Ser Ala Lys Ala Gln Asn Pro Met Arg Asp Leu Lys Ile Glu Lys
  1              5              10              15

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Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg
      20              25              30

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Ala Ser Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser
      35              40              45

```

```

Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys
      50              55              60

```

```

Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu
      65              70              75              80

```

```

Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Asp Arg Asn Phe
      85              90              95

```

```

Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu
      100             105             110

```

```

Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Phe Gly Met Asp Phe Tyr
      115             120             125

```

338



Val Val Met Asn Arg Pro Gly Ala Arg Val Thr Arg Arg Lys Arg Cys  
 130 135 140

Lys Gly Thr Val Gly Asn Ser His Lys Thr Thr Lys Glu Asp Thr Val  
 145 150 155 160

Ser Trp Phe Lys Gln Lys Tyr Asp Ala Asp Val Leu Asp Lys  
 165 170

<210> 285  
 <211> 1229  
 <212> DNA  
 <213> Candida albicans

<400> 285  
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 aaaaatttga gtgtggtg cacaatcct tctcatacca ctgaaagaat gtttttaaat 180  
 ttacctttta acaattccct gttcaatgcc ccaccagtag aaattaattt taatgatctt 240  
 gaagtgttgg aattgtacac tcaattagta ttataccgag atgatattac caaatctact 300  
 tttgaattag ctatatcacc agcaatttg aatatttctc aacggaaaat catatcaatt 360  
 ttatgtaatt atttgaattt attagaattg tttgataatg ggttgataat aattagaaga 420  
 aaaccaggat acattgctca gtgtataact caacaatcta ttattcctaa ttctcaacag 480  
 gtgtctgggc caactcacc gcaacaacat caacagaatc aacttcaaca acagcaacag 540  
 caacaacatc aacatcaaca tccttcacat tcatcatcga tgatgaacct tcatcaattg 600  
 ggtggtacat tagctgttcc agcgaccct gaattattaa gatcccaatc gcaatcagca 660  
 ttaccgttgc caagattgag acagcaaacc tctacaccaa ttcaacaaa tcaacaagtt 720  
 cagcaccaaa atcaaccacc acaacaacaa cagcaacagc atgttcaacc acaatataat 780  
 tattacaatc agcaatctat tcaaagccaa ccacattctg cgagacctta ttctcaatca 840  
 tataatattt atcaacaaca acagcaacag cagcaacaac aagctcaaca acaagctcaa 900  
 caacaacaac aacaacaatt acaatatcaa caggacacc agtcacaagt ttcaacacct 960  
 acattgaatt cttctagtgc tgctgatta cttagatcaa gtagcagtag atcatttgtt 1020  
 gatgtgagat ccacacctcc cacaagtagt tttgctcaac agcaacaaca acaacaaca 1080  
 caacagcaac agccgccact aacttcatca atccatgatt ctccaacacc acatcatcat 1140  
 ttaccacttc aacagcagcc accacaacca aatcattacc tatccaatta ccatcagggg 1200  
 gttggtctc aacaaaaaac tccattggc 1229

<210> 286  
 <211> 409  
 <212> PRT  
 <213> Candida albicans

<400> 286  
 Arg Glu Arg Ile Glu Glu Glu Lys Arg Glu Lys Arg Gly Gln Leu Glu  
 1 5 10 15

Glu Gln His Arg Ser Ala Ser Asn Ala Ser Met Ala Ser Leu Leu Ser  
                   20                                  25                                  30  
 Ala Ala Ser Thr Thr Ala Ala Thr Lys Asn Leu Ser Val Ala Gly Thr  
                   35                                  40                                  45  
 Asn Pro Ser His Thr Thr Glu Arg Met Phe Leu Asn Leu Pro Phe Asn  
                   50                                  55                                  60  
 Asn Ser Ser Phe Asn Ala Pro Pro Val Glu Ile Asn Phe Asn Asp Leu  
                   65                                  70                                  75                                  80

---

Glu Val Leu Glu Leu Tyr Thr Gln Leu Val Leu Tyr Arg Asp Asp Ile  
                                   85                                  90                                  95  
 Thr Lys Ser Thr Phe Glu Leu Ala Ile Ser Pro Ala Asn Leu Asn Ile  
                   100                                  105                                  110  
 Ser Gln Arg Lys Ile Ile Ser Ile Leu Cys Asn Tyr Leu Asn Leu Leu  
                   115                                  120                                  125  
 Glu Leu Phe Asp Asn Gly Leu Ile Ile Ile Arg Arg Lys Pro Gly Tyr  
                   130                                  135                                  140  
 Ile Ala Gln Cys Ile Thr Gln Gln Ser Ile Ile Pro Asn Ser Gln Gln  
                   145                                  150                                  155                                  160  
 Val Ser Gly Pro Thr His Pro Gln Gln His Gln Gln Asn Gln Leu Gln  
                                   165                                  170                                  175  
 Gln Gln Gln Gln Gln Gln His Gln His Gln His Pro Ser His Ser Ser  
                   180                                  185                                  190  
 Ser Met Met Asn Leu His Gln Leu Gly Gly Thr Leu Ala Val Pro Ala  
                   195                                  200                                  205  
 His Pro Glu Leu Leu Arg Ser Gln Ser Gln Ser Ala Leu Pro Leu Pro  
                   210                                  215                                  220  
 Arg Leu Arg Gln Gln Thr Ser Thr Pro Ile Gln Gln Asn Gln Gln Val  
                   225                                  230                                  235                                  240  
 Gln His Gln Asn Gln Pro Pro Gln Gln Gln Gln Gln His Val Gln  
                   245                                  250                                  255  
 Pro Gln Tyr Asn Tyr Tyr Asn Gln Gln Ser Ile Gln Ser Gln Pro His  
                   260                                  265                                  270

340

Ser Ala Arg Pro Tyr Ser Gln Ser Tyr Asn Ile Tyr Gln Gln Gln Gln  
275 280 285

Gln Gln Gln Gln Gln Gln Ala Gln Gln Gln Ala Gln Gln Gln Gln Gln  
290 295 300

Gln Gln Leu Gln Tyr Gln Gln Gly His Gln Ser Gln Val Ser Thr Pro  
305 310 315 320

Thr Leu Asn Ser Ser Ser Ala Ala Ala Leu Leu Arg Ser Ser Ser Ser  
325 330 335

Arg Ser Phe Val Asp Val Arg Ser Thr Pro Pro Thr Ser Ser Phe Ala  
340 345 350

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Leu Thr  
355 360 365

Ser Ser Ile His Asp Ser Pro Thr Pro His His His Leu Pro Leu Gln  
370 375 380

Gln Gln Pro Pro Gln Pro Asn His Tyr Leu Ser Asn Tyr His Gln Gly  
385 390 395 400

Val Gly Ser Gln Pro Lys Thr Pro Leu  
405

<210> 287

<211> 2153

<212> DNA

<213> Candida albicans

<400> 287

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tattaacaga atactttttt gtattcaact ctctaactct ttctattttt tttttttttc 180  
tatatacact gttaaatcaa tcaacaatag caggatatcc attcatatac aaatagataa 240  
actgtttaat taattaatta actgatttga ttggggaaaa aacaaatttt atatttggag 300  
aattgaattt caatcatttt aacaaattca aagctttaat tcccacctat caaatttcat 360  
tattattttg ttttcattat tttttttttc cttttctttc tttctttctt tcttttttgg 420  
aacaaagtaa tagccgataa aataaataat tcacatagcc caattcatat tacattgact 480  
tttgacaaga ggtatatata atggatttta gaaatttatc aactacaccg aatcaaatgg 540  
gcactgtaat gcaacgtcgt ccctctctat catcattatc gtcagcctcg ggctattctt 600  
cttccaatta tgggtggaat cctacacca atcccaacaa ttccaatacc aataacaata 660  
gtagtggcaa tagtaataac aacactcatg gcaataacac tcccaaatta tcaactcaaa 720

gattgacaaa taataggaat ttacaatcct tgtggataaa ccaaccatct attgctcctt 780  
 ctaatgttgt tccttgggtg gaacagcaac aacaacaaac ccttgatctg ttggaaaata 840  
 atactaaaac agactccagt aatgatgctt ctgctactaa taataataat gttaatgtta 900  
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 acacaaatgt taatgcaaac acaacagcaa ctagtattaa tgcttccacg attttaaata 1020  
 ctacaccaag tattaatgac actaatgata atgccaaaaa aattaatggt tccatgatta 1080  
 gtaataacaa taacaataac agtaacaata ataacaacaa cactaacaat agtagtacag 1140  
 gaagttctaa cattgcaaac atgcttcctt ctgtttctaa tgcaacgaca atgaataaca 1200  
 gtaatagtat caatagcacc acaaacaata ctacaattaa cgaagctgat gatgacgagt 1260  
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 tagtaaacca attgaatgga agagaaatag gtggaagaaa attacgtgtt gaatacaaaa 1500  
 aaatgcttcc ggcacaagaa agagaacgta ttgaaagaga gaaaagggag aaaagaggtc 1560  
 aattggaaga acaacatcgt tctgcatcaa atgcttcttt ggcttcttta ttgtcagctg 1620  
 cttcaactac agcagcaact aaaaatttga gtgtggctgg cacaatcct tctcatacca 1680  
 ctgaaagaat gtttttaaat ttacctttta acaattcctt gttcaatgcc ccaccagtag 1740  
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 caacggaaaa tcatatcaat ttatgtaatt atttgaattt attagaattg tttgataatg 1920  
 ggttgctact aattagaaaa aaaccaggat ccattgctca gtgtataact caaaaatcta 1980  
 ttattcctaa ttctcaacag gtgtctgggc caactcacc gcaccaccat caaagaatc 2040  
 aacttcacca acagcaacag caacacacat caacatcaac atccttaaca ttcattcatg 2100  
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&lt;210&gt; 288

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 288

Met Asp Phe Arg Asn Leu Ser Thr Thr Pro Asn Gln Met Gly Thr Val  
 1 5 10 15

Met Gln Arg Arg Pro Ser Leu Ser Ser Leu Ser Ser Ala Ser Gly Tyr  
 20 25 30

Ser Ser Ser Asn Tyr Gly Gly Asn Pro Thr Pro Asn Pro Asn Asn Ser  
 35 40 45

Asn Thr Asn Asn Asn Ser Ser Gly Asn Ser Asn Asn Asn Thr His Gly  
 50 55 60

Asn Asn Thr Pro Lys Leu Ser Thr Gln Arg Leu Thr Asn Asn Arg Asn  
 65 70 75 80

Leu Gln Ser Leu Trp Ile Asn Gln Pro Ser Ile Ala Pro Ser Asn Val

85

90

.95

Val Pro Trp Val Glu Gln Gln Gln Gln Gln Thr Leu Asp Ser Leu Glu  
100 105 110

Asn Asn Thr Lys Thr Asp Ser Ser Asn Asp Ala Ser Ala Thr Asn Asn  
115 120 125

Asn Asn Val Asn Val Asn Val Asn Ala Asn Ala Asn Val Asn Ala Asn  
130 135 140

~~Ala Asn Ile His Ala Gln Thr His Val Asn Thr Asn Val Asn Ala Asn~~  
145 150 155 160

Thr Thr Ala Thr Ser Ile Asn Ala Ser Thr Ile Leu Asn Thr Thr Pro  
165 170 175

Ser Ile Asn Asp Thr Asn Asp Asn Ala Lys Lys Ile Asn Val Ser Met  
180 185 190

Ile Ser Asn Asn Asn Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Thr  
195 200 205

Asn Asn Ser Ser Thr Gly Ser Ser Asn Ile Ala Asn Met Leu Pro Ser  
210 215 220

Val Ser Asn Ala Thr Thr Met Asn Asn Ser Asn Ser Ile Asn Ser Thr  
225 230 235 240

Thr Asn Asn Thr Thr Ile Asn Glu Ala Asp Asp Asp Glu Leu Ile Pro  
245 250 255

Thr Ala Ile Val Ile Lys Asn Ile Pro Phe Ala Ile Lys Lys Glu Gln  
260 265 270

Leu Leu Asp Val Met Thr Lys Leu Asn Leu Pro Leu Pro Tyr Ala Phe  
275 280 285

Asn Tyr His Phe Asp Asn Gly Val Phe Arg Gly Leu Ala Phe Ala Asn  
290 295 300

Phe Thr Ser Thr Asp Glu Thr Ser Ala Val Val Asn Gln Leu Asn Gly  
305 310 315 320

Arg Glu Ile Gly Gly Arg Lys Leu Arg Val Glu Tyr Lys Lys Met Leu  
325 330 335

Pro Ala Gln Glu Arg Glu Arg Ile Glu Arg Glu Lys Arg Glu Lys Arg

343

	340		345		350
Gly Gln Leu Glu Glu Gln His Arg Ser Ala Ser Asn Ala Ser Leu Ala					
355		360		365	
Ser Leu Leu Ser Ala Ala Ser Thr Thr Ala Ala Thr Lys Asn Leu Ser					
370		375		380	
Val Ala Gly Thr Asn Pro Ser His Thr Thr Glu Arg Met Phe Leu Asn					
385		390		395	400

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Leu Pro Phe Asn Asn Ser Ser Phe Asn Ala Pro Pro Val Glu Ile Asn					
	405		410		415
Phe Asn Asp Leu Glu Val Leu Glu Leu Tyr Thr Gln Leu Val Leu Tyr					
	420		425		430
Arg Asp Asp Ile Thr Lys Ser Thr Phe Glu Leu Ala Ile Ser Pro Ser					
	435		440		445
Ile Phe Glu Tyr Phe Ser Thr Glu Asn His Ile Asn Leu Cys Asn Tyr					
	450		455		460
Leu Asn Leu Leu Glu Leu Phe Asp Asn Gly Leu Leu Leu Ile Arg Lys					
	465		470		475
Lys Pro Gly Ser Ile Ala Gln Cys Ile Thr Gln Lys Ser Ile Ile Pro					
	485		490		495
Asn Ser Gln Gln Val Ser Gly Pro Thr His Pro His His His Gln Lys					
	500		505		510
Asn Gln Leu His Gln Gln Gln Gln Gln His Thr Ser Thr Ser Thr Ser					
	515		520		525
Leu Thr Phe Ile Ile Asp Asp Glu Pro Ser Ser Ile Gly Trp Tyr Ile					
	530		535		540
Ser Cys Ser Ser Ala Pro					
545		550			

&lt;210&gt; 289

&lt;211&gt; 3254

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 289

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cctgacagta tattaataaa tattcttttt aacttatttt tcaatcaaga aggtactgaa 240
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tttattcatt ccaaggtata acaagaacgt taggaataat ataaaattat caccaaagct 420
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```

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gatggtttta taatgataac caagatgacg actttttggg ttggtttgat gttaatatga 3240
tgcaagagaa ataa 3254

```

&lt;210&gt; 290

&lt;211&gt; 917

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 290

```

Met Lys Phe Glu Lys Gly Lys Val Arg Ile Leu Pro Lys Pro Ser Pro
  1             5             10             15

```

```

Thr Pro Thr Asn Pro Gln Thr Pro Leu Pro Leu Leu Pro Ala Gln Thr
          20             25             30

```

```

Lys Pro Val Asn Ser Lys Arg Lys Ser Ala Ala Ser Thr Pro Gly Asn
          35             40             45

```

```

Glu Ser Lys Lys Ser Arg Lys Ser Asn Ser Thr Ala Ser Thr Pro Asn
          50             55             60

```

```

Ser Ala Thr Pro Thr Ser Val Gly Thr Pro Pro Gln Lys Thr Ser Lys
          65             70             75             80

```

```

Pro Thr Gly His Arg Pro Val Thr Ser Cys Thr Phe Cys Arg Gln His
          85             90             95

```

```

Lys Ile Lys Cys Asn Ala Ser Asp Asn Tyr Pro Asn Pro Cys Glu Arg
          100            105            110

```

```

Cys Lys Lys Met Gly Leu Lys Cys Glu Ile Asp Pro Glu Phe Arg Pro
          115            120            125

```

```

Arg Lys Gly Ser Gln Ile Gln Ser Leu Lys Ser Asp Val Asp Glu Leu
          130            135            140

```

```

Lys Ala Lys Ile Glu Met Leu Thr Lys Asn Glu Ser Leu Leu Thr Gln
          145            150            155            160

```

```

Ala Leu Asn Gln His Asn Leu Asn His Ala Ser Gln Gln Gln Gln Ser
          165            170            175

```

346



Ser Gly Ser Gln Ser Gln Gln Gln His Pro Pro Asn Pro Gln Arg Ala  
 180 185 190  
 Leu Ser Tyr Thr Ser Ala Asn Ser Ser Pro Gln Val Ala Phe Ser Asn  
 195 200 205  
 Ala Ser Pro Ile Pro Ser Val Thr Ser Ile Gln Gln Asn Ala Pro Leu  
 210 215 220  
 Thr His Glu Asn Ser Asp Asn Ser Pro Tyr Ala Leu Asn Thr Pro Glu  
 225 230 235 240

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Asn Ile Glu Glu Leu Gln Pro Ile Ser Glu Phe Ile Leu Gly Asp Val  
 245 250 255  
 Thr Leu Pro Leu Asn Arg Ala Asn Glu Leu His Asp Lys Phe Met Thr  
 260 265 270  
 Thr His Leu Pro Phe Leu Pro Ile Ile Ile Ser Arg Ser Ala Thr Glu  
 275 280 285  
 Leu Tyr His Lys Ser Gln Leu Leu Phe Trp Ala Val Ile Leu Thr Ala  
 290 295 300  
 Ser Leu Ser Glu Pro Glu Pro Lys Leu Tyr Met Ser Leu Ala Ser Leu  
 305 310 315 320  
 Ile Lys Gln Leu Ala Ile Glu Thr Cys Trp Ile Lys Thr Pro Arg Ser  
 325 330 335  
 Thr His Val Ile Gln Ala Leu Ile Ile Leu Ser Ile Trp Pro Leu Pro  
 340 345 350  
 Asn Glu Lys Val Leu Asp Asp Cys Ser Tyr Arg Phe Val Gly Leu Ala  
 355 360 365  
 Lys Asn Leu Ser Leu Gln Leu Gly Leu His Arg Gly Gly Glu Phe Ile  
 370 375 380  
 Gln Glu Phe Ser Arg Asn Gln Val Ser Leu Gly Pro Asp Ala Glu Arg  
 385 390 395 400  
 Trp Arg Thr Arg Ser Trp Leu Ala Val Phe Phe Cys Glu Gln Phe Trp  
 405 410 415  
 Ser Ser Leu Leu Gly Leu Pro Pro Ser Ile Asn Thr Thr Asp Tyr Leu  
 420 425 430

347

Leu Glu Asn Ala Arg Val Asp Lys Ser Leu Pro Lys Asn Phe Arg Cys  
 435 440 445  
 Leu Ile Ser Leu Ser Ile Phe Gln Cys Lys Leu Val Asn Ile Met Gly  
 450 455 460  
 Ile Ser Val Thr Arg Pro Asp Gly Leu Leu Glu Pro Ser Asn Arg Ala  
 465 470 475 480  
 Gly Ser Leu Ser Leu Leu Asp Arg Glu Leu Glu Arg Leu Arg Phe Lys  
 485 490 495  
 Leu Gln Phe Glu Glu Gly Gly Pro Ile Glu Val Tyr Tyr Leu Tyr Ile  
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 Lys Leu Met Ile Cys Cys Phe Ala Phe Leu Pro Gly Thr Pro Ile Glu  
 515 520 525  
 Asp Gln Val Lys Tyr Val Ser Phe Ala Tyr Leu Ser Ala Thr Arg Ile  
 530 535 540  
 Val Thr Ile Val Ser Lys Met Val Asn Asp Ile Ser Leu Ile Glu Leu  
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 Pro Ile Tyr Ile Arg Gln Ala Val Thr Tyr Ser Val Phe Met Leu Phe  
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 Lys Leu His Leu Ser Arg Tyr Leu Ile Asp Lys Tyr Val Asp Ser Ala  
 580 585 590  
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 595 600 605  
 Ser Trp Lys Asp Leu Gln Asn Asp Ile Ser Arg Thr Ala Lys Val Leu  
 610 615 620  
 Glu Asn Leu Asn Met Val Leu Tyr Asn Tyr Pro Glu Ile Phe Leu Asn  
 625 630 635 640  
 Asp Ser Glu Asn Glu Asp Ser Ser Ile Ile Thr Arg Met Arg Ser His  
 645 650 655  
 Leu Thr Ala Ser Leu Phe Tyr Asp Leu Val Trp Cys Val His Glu Ala  
 660 665 670  
 Arg Arg Arg Ser Val Leu Asp Lys Gly Lys Arg Gln Ala Gln Pro Asn  
 675 680 685

348

Lys Lys Ile Leu Pro Leu Pro Phe Tyr Asn Gln Ile Thr Lys Asp Asp  
 690 695 700

Phe Lys Thr Ile Thr Thr Thr Ser Pro Asn Gly Thr Thr Ile Thr Thr  
 705 710 715 720

Leu Val Pro Thr Asp Gln Ala Met Asn Gln Ala Lys Ser Lys Ser Phe  
 725 730 735

Asp Ser Ser Lys Pro Leu Glu Ile Asn Gly Ile Pro Leu Pro Met Leu  
 740 745 750

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Glu Ala Thr Gly Ser Thr Arg Glu Val Leu Asp Ser Leu Pro Ser Gln  
 755 760 765

Ser Leu Pro Ser Gln Ala Pro Thr Leu Gln Gln Tyr Pro Met Gln Gln  
 770 775 780

Asp Gln Gln Gln Gln Glu Pro Ser Gln Gln Gln Gln Lys His Ser  
 785 790 795 800

Gln Gln Ser Gln Gln Tyr Gln Gln Gln Gln Gln Ser Asn Gln Gln Gln  
 805 810 815

Pro His Leu Gln His Gln Arg Gln Phe Gln Gln Ser Pro Pro Pro Gln  
 820 825 830

Phe Ser Met Ile Ser Ser Thr Pro Pro Leu Gln Gln Pro Pro Phe Ile  
 835 840 845

Leu Ala Asn Ser Pro Leu Pro Gln Thr Tyr Leu Pro Lys Ile Asp Glu  
 850 855 860

Met Asn Met Ser Pro Glu Val Lys Gln Glu Asn Ser Val Ala Pro Phe  
 865 870 875 880

Ala Ser Gln Ile Thr Asn Phe Phe Asp Gln Gln Thr Ser Gly Trp Phe  
 885 890 895

Asn Asn Asp Asn Gln Asp Asp Asp Phe Leu Gly Trp Phe Asp Val Asn  
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Met Met Gln Glu Lys  
 915

<210> 291  
 <211> 908  
 <212> DNA  
 <213> Candida albicans

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 atacagaggg aaaatcaccc tttttattat taccaaggtc tcaatgatta gtgtggctag 300  
 cgtctgttac tacttaccce gtgtttgtag ataattgccca ctcaatcttt aattgaccat 360  
 cgaccacaaa aataatatgg aaataatact aacagaactt agaaacatca ctcataatga 420  
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 atttgactgt tgggtcaattt gtttacgtta ttagaaaaag aatcaagtta ccaagcgaaa 720  
 aagccatttt catctttgtc aatgacatat taccccaac cgctgcatta atcagtacaa 780  
 tctacgaaga acacaaggac gaagatgggt tcttatacgt tttatactct ggagagaata 840  
 cttttggcga gaaactagca attgacattt catcattaga ttacagtgat atccctgatt 900  
 atgtttaa 908

<210> 292  
 <211> 135  
 <212> PRT  
 <213> Candida albicans

<400> 292  
 Met Arg Ser Gln Phe Lys Asp Glu His Pro Phe Glu Lys Arg Gln Ala  
 1 5 10 15  
 Glu Ala Ala Arg Ile Ala Gln Arg Phe Lys Asp Arg Val Pro Val Ile  
 20 25 30  
 Cys Glu Lys Val Glu Asn Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys  
 35 40 45  
 Tyr Leu Val Pro Val Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile  
 50 55 60  
 Arg Lys Arg Ile Lys Leu Pro Ser Glu Lys Ala Ile Phe Ile Phe Val  
 65 70 75 80  
 Asn Asp Ile Leu Pro Pro Thr Ala Ala Leu Ile Ser Thr Ile Tyr Glu  
 85 90 95

350

02-07-1999

SEQL

EP99870141.1

Glu His Lys Asp Gly Phe Leu Tyr Val Leu Tyr Ser Gly Glu  
100  
Asn Thr Phe Gly Glu Lys Leu Ala Ile Asp Ile Ser Ser Leu Asp Phe  
115  
Ser Asp Ile Pro Asp Tyr Val  
130

<210> 293  
<211> 2891  
<212> DNA  
<213> Candida albicans

<400> 293

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gattgtatc tacgtttgta ttgatgttg ccttattgt ccctatggg atctacgctt 240  
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agataatgt aacacgaaac atgtttacc caccataaa ggggggtgtt aagatttga 660  
gttcaactc aactccccc gatgtggac cctatgaat agattatgt actgacgac 720  
ctcccacgc tagtagtcg gaagtgtga agttatgt atgacgact gcgcatgac 780  
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351

Printed: 17-08-2000

351

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cgttggtggc cgacgacgag ttatttaaaa agattgttga agaaaagttt aatttgggga 2040
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taactaatta a 2891

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&lt;210&gt; 294

&lt;211&gt; 796

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 294

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Met Phe Thr Leu Phe Phe Phe Thr Thr Asp Gln Met Asn Val Arg Pro
  1             5             10             15

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Asn Ala Pro Phe Arg Pro Pro Arg Pro Ile Lys Gly Gly Val Ala Val
          20             25             30

```

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Val Gln Lys Val Val Lys Arg Lys Leu Pro Thr Thr Thr Asn Pro Lys
      35             40             45

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Pro Ala Lys Ile Leu Thr Thr Asp Pro Gly Ser Thr Lys Tyr Val Ile
      50             55             60

```

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Gln Trp Arg Lys Lys Thr Ser Lys Lys Asn Lys Thr Trp Asp Gly Asp
      65             70             75             80

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Gly Tyr Ala Val Ile Lys Gln Leu Glu Asn Gly Ala Cys Glu Ile Ser
          85             90             95

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Ile Lys Asn Ser Asp Gly Lys Pro Met Gly Lys Arg Val Phe Thr Ala
      100            105            110

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Thr Pro Asn Leu Asp Asp Val Ile Ser Val Gly Pro Tyr Glu Leu Glu

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352

115	120	125
Leu Asp Glu Lys Val Gly Ser Asn Ser Thr Pro Gln Thr Val Thr Arg		
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Val Thr His Gln Phe Lys Lys Val Ala Pro Pro Thr Ala Ser Ser Arg		
145	150	155 160
Lys Pro Leu Tyr Asp Asp Cys Ala Asp Ala Ile Ala Leu Pro Pro Pro		
165	170	175
<hr/>		
Pro Lys Ala Lys Asp Tyr Val Lys Val Asn Ile Asp Pro His Leu Ala		
180	185	190
Lys Val Leu Arg Pro His Gln Val Glu Gly Val Lys Phe Met Tyr Glu		
195	200	205
Cys Leu Met Gly Tyr Arg Gly Phe Gly Gly His Gly Cys Leu Leu Ala		
210	215	220
Asp Glu Met Gly Leu Gly Lys Thr Leu Met Thr Ile Thr Thr Ile Trp		
225	230	235 240
Thr Leu Leu Lys Gln Asn Pro Phe Met Glu Lys Gly Ala Val Val Asn		
245	250	255
Lys Val Leu Val Val Cys Pro Val Thr Leu Ile Ser Asn Trp Arg Gln		
260	265	270
Glu Phe Arg Lys Trp Leu Gly Ala Asn Lys Leu Asn Val Leu Thr Leu		
275	280	285
Asn Asn Pro Met Ser Asn Glu Lys Gln Asp Ile Leu Asn Phe Gly Lys		
290	295	300
Leu Asn Val Tyr Gln Val Leu Val Val Asn Tyr Glu Lys Leu Val Ala		
305	310	315 320
His Phe Asp Glu Leu Ser Ala Val Lys Phe Asp Leu Leu Val Cys Asp		
325	330	335
Glu Gly His Arg Leu Lys Asn Ser Ala Asn Lys Val Leu Asn Asn Leu		
340	345	350
Ile Lys Leu Asn Ile Pro Lys Lys Ile Val Leu Thr Gly Thr Pro Ile		
355	360	365
Gln Asn Glu Leu Val Glu Phe His Thr Leu Ile Ser Phe Leu Asn Pro		

353

370	375	380
Gly Val Leu Pro Glu Leu Lys Leu Phe Gln Arg Asn Phe Ile Thr Pro		
385	390	395 400
Ile Ser Arg Ala Arg Asp Ile Asn Cys Phe Asp Pro Glu Val Lys Lys		
	405 410	415
Arg Gly Glu Glu Ile Ser Gln Gln Leu Ile Glu Leu Thr Gln Ser Phe		
	420 425	430

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Ile Leu Arg Arg Thr Gln Ala Ile Leu Ala Asn Tyr Leu Thr Gln Lys		
	435 440	445
Thr Asp Ile Leu Leu Phe Val Pro Pro Thr Ser Leu Gln Leu Lys Leu		
	450 455	460
Phe Asp Tyr Ile Thr Asn Leu Lys Lys Phe Asn Gln Phe Glu Ala Phe		
	465 470	475 480
Thr Met Ile Asn Leu Phe Lys Lys Ile Cys Asn Ser Pro Ser Leu Leu		
	485 490	495
Ala Asp Asp Glu Leu Phe Lys Lys Ile Val Glu Glu Lys Phe Asn Leu		
	500 505	510
Gly Met Ala Ser Gly Lys Ile Asn Ile Leu Val Pro Leu Leu Leu Glu		
	515 520	525
Ile Ala Ser Leu Gly Glu Lys Ile Val Leu Ile Ser Asn Tyr Thr Lys		
	530 535	540
Thr Leu Asp Leu Leu Glu Gln Val Leu Arg Lys Val Ser Leu Thr Phe		
	545 550	555 560
Ser Arg Leu Asp Gly Ser Thr Pro Asn Asn Val Arg Ser Lys Leu Val		
	565 570	575
Asn Gln Phe Asn Thr Asn Pro Asp Ile Asn Val Phe Leu Leu Ser Ser		
	580 585	590
Lys Ser Gly Gly Met Gly Ile Asn Leu Val Gly Ala Ser Arg Leu Ile		
	595 600	605
Leu Phe Asp Asn Asp Trp Asn Pro Ala Thr Asp Leu Gln Ser Met Ser		
	610 615	620
Arg Ile His Arg Asp Gly Gln Leu Lys Pro Cys Phe Ile Tyr Arg Leu		





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ctt 2643

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&lt;210&gt; 296

&lt;211&gt; 714

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 296

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Met Thr Leu Pro Ile Gln Asp Leu Glu Pro Asp Tyr Tyr Ile Ser Val
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Asn Tyr Pro Thr Thr Asp Asn Gly Ser Pro Thr Pro Gln Ala Glu Lys
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Ser Leu Lys Thr Leu Ile Asp Leu Leu Tyr Asp Lys Gly Phe Ala Ala
      35                      40                      45

Gln Ile Arg Pro Gly Asp Leu Asp His Leu Leu Val Phe Val Lys Leu
      50                      55                      60

Ser Ser Tyr Lys Phe Ser Glu Glu Ala Glu Lys Asp Leu Ile Lys Asn
      65                      70                      75                      80

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Tyr Glu Phe Gly Val Thr Gly Lys Asp Asp Val Leu Ala Ser Lys Leu
      85                      90                      95

Arg Ile Ile Tyr Gln Tyr Leu Thr Tyr Pro Gln Ser Val Gly Gly Cys
      100                     105                     110

Gly Ile Thr Pro Asn Ser Gly Asp Trp Lys Phe Val Thr Ser Ile Val
      115                     120                     125

Pro Ile Thr Asn Ala Phe Asn Glu Thr Thr Leu Val Glu Asp Leu Lys
      130                     135                     140

Ile Asn Val Thr Gln Pro Asn Leu Ser Ile Ala Thr Ile Lys Lys Thr
      145                     150                     155                     160

Tyr Gly Val Glu Val Ala Leu Tyr Phe Glu Tyr Ile Lys His Tyr Thr
      165                     170                     175

Phe Trp Leu Leu Leu Leu Ser Ile Ile Gly Leu Val Ser His Phe Arg
      180                     185                     190

Lys Asp Lys Arg Phe Ser Leu Thr Phe Ala Phe Ile Asn Leu Leu Trp
      195                     200                     205

Gly Val Leu Phe Leu Ala Ser Trp His Arg Arg Glu Gln His Leu Val
      210                     215                     220

Asn Val Trp Gly Val Gln Asn Ser His Leu Ile Glu Glu His Asn Ser
      225                     230                     235                     240

Glu Leu Ala Lys Val Asn Glu Arg Tyr Glu Glu Lys Ser Thr Tyr Phe
      245                     250                     255

His Ala Asn Asn Thr Asn Gly Phe Arg Phe Leu Lys Gln Leu Ala Phe
      260                     265                     270

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357

Ile Pro Ile Ala Leu Val Phe Val Gly Val Leu Ile Ser Tyr Gln Leu  
 275 280 285  
 Ser Cys Phe Cys Ile Glu Ile Phe Leu Thr Asp Ile Tyr Asp Gly Pro  
 290 295 300  
 Gly Lys Ser Leu Leu Thr Leu Leu Pro Thr Val Leu Ile Ser Val Phe  
 305 310 315 320  
 Val Pro Ile Leu Thr Ile Val Tyr Asn Ala Val Thr Asp Ile Ile Ile  
 325 330 335

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Lys Trp Glu Asn His Asp Asn Gln Tyr Ser Lys Asn Asn Ser Ile Leu  
 340 345 350  
 Val Lys Thr Phe Val Leu Asn Phe Leu Thr Gly Tyr Val Pro Leu Ile  
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 Ile Thr Ser Phe Ile Tyr Leu Pro Phe Ala His Leu Val Gln Pro His  
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 385 390 395 400  
 Phe Tyr Thr Lys Tyr Leu Leu Lys Leu Lys Ser Gln Glu Glu Phe Lys  
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 Ile Asn Gln Gly Arg Leu Asp Ala Gln Phe Phe Tyr Phe Ile Val Thr  
 420 425 430  
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 435 440 445  
 Arg Phe Val Phe Asn Phe Ile Glu Thr Lys Ile Gln Lys Lys Pro Gln  
 450 455 460  
 Leu Gln Thr Lys Asp Asp Asn Pro Asp Glu Ser Ile Trp Leu His Asn  
 465 470 475 480  
 Val Arg Leu Ser Leu Lys Leu Pro Glu Tyr Asn Val Asp Asp Asp Phe  
 485 490 495  
 Arg Gly Leu Val Leu Gln Phe Gly Tyr Leu Ile Met Phe Gly Pro Val  
 500 505 510  
 Trp Pro Leu Ala Pro Leu Val Cys Ile Ile Phe Asn Leu Ile Phe Phe  
 515 520 525

Lys Leu Asp Asn Phe Lys Leu Leu Asn Gly Lys Tyr Phe Lys Pro Pro  
 530 535 540

Val Pro Arg Arg Val Asp Ser Ile His Pro Trp Asn Leu Ala Leu Phe  
 545 550 555 560

Leu Leu Ala Trp Ile Gly Ser Ile Ile Ser Pro Val Val Thr Ala Phe  
 565 570 575

Tyr Arg His Gly Thr Ala Pro Pro Lys Ser Met Gly Gln Phe Ala Leu  
 580 585 590

Asp Lys Ala Ser Val His Val Ser Ser Ser Val Phe Leu Val Leu Leu  
 595 600 605

Met Phe Val Ser Glu His Gly Phe Leu Ile Leu Ser Tyr Leu Leu Phe  
 610 615 620

Glu Phe Ser Ser Leu Phe Lys Ser Gln Val Glu Trp Glu Asn Asp Phe  
 625 630 635 640

Val Asp Asn Asp Ile Lys Leu Arg His Asp Tyr Tyr Ser Gly Lys Val  
 645 650 655

Lys Pro Thr Tyr Lys Val His Ser Asp Glu Leu Trp Glu Lys Phe Thr  
 660 665 670

Pro Gln Ser Thr Leu Asn Phe Thr Gly Pro Lys Pro Thr Ala Glu Thr  
 675 680 685

Asp Asp Lys Val Glu Lys Ile Ala Ser Thr Glu Asp Ala Tyr Ser Thr  
 690 695 700

Ser Ala Glu Lys Ser Thr Thr Thr Ala Thr  
 705 710

<210> 297

<211> 1784

<212> DNA

<213> Candida albicans

<400> 297

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```

&lt;210&gt; 298

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 298

```

Met Val Ser Val Ser Lys Leu Ile Asn Asn Gly Leu Leu Leu Thr Ser
  1             5             10             15

```

```

Gln Ser Val Phe Gln Asp Val Ala Thr Pro Gln Gln Ala Ser Val Gln
      20             25             30

```

```

Gln Tyr Asn Ile Leu Asn Phe Leu Gly Gly Ser Ala Pro Tyr Ile Gln
      35             40             45

```

```

Arg Asn Gly Tyr Gly Ile Ser Thr Asp Ile Pro Ala Gly Cys Glu Ile
      50             55             60

```

```

Ala Gln Ile Gln Leu Tyr Ser Arg His Gly Glu Arg Tyr Pro Ser Lys
      65             70             75             80

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360

361

Asp Leu Glu Ile Phe His Ser Ala Leu Gly Leu Leu Glu Pro Ala Glu  
340 345 350

Asp Leu Pro Thr Ser Tyr Ile Pro Phe Pro Asn Pro Tyr Val His Ser  
355 360 365

Ser Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Leu Gln Cys  
370 375 380

Gly Asn Asp Ala Tyr Val Arg Tyr Ile Ile Asn Asp Ala Val Val Pro  
385 390 395 400

Ile Pro Lys Cys Ala Thr Gly Pro Gly Phe Ser Cys Lys Leu Asp Asp  
405 410 415

Phe Glu Asn Phe Val Lys Glu Arg Ile Gly Asp Val Asp Phe Val Lys  
420 425 430

Gln Cys Gly Val Asn Ser Thr Tyr Pro Ser Glu Leu Thr Phe Tyr Trp  
435 440 445

Asp Tyr Lys Asn Val Thr Tyr Ser Ala Pro Leu Glu Leu  
450 455 460

<210> 299

<211> 1871

<212> DNA

<213> Candida albicans

<400> 299

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atagccagac tataaaaaatt acgggggattt aattcgcgac tcaccacagt tctcacacag 420
tatgtgcttt tttcataagt atgatttgaa ccctaaaata tcaactttca taataaacat 480
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gaccagcgga attgacattt tattgggatt ataaagacag aaagtataat gcgccgttaa 1860
tagatcagta a 1871

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&lt;210&gt; 300

&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 300

Met Val Gly Leu Ser Arg Val Leu Asn Ala Gly Phe Ile Leu Ser Gly  
1 5 10 15

Gln Ser Val Phe Gln Asp Val Ala Ala Pro His Gln Ala Ser Ile Glu  
20 25 30

Gln Tyr Asn Ile Val Lys Tyr Leu Gly Gly Ser Gly Pro Tyr Ile Gln  
35 40 45

Asn Ser Gly Tyr Gly Ile Ser Thr Asp Ile Pro Glu Lys Cys Thr Ile  
50 55 60

Glu Gln Val Gln Met Ile Ser Arg His Gly Glu Arg Phe Pro Ser Lys  
65 70 75 80

Gly Asp Gly Lys Tyr Phe Asn Ser Val Met Glu Val Phe Lys Arg Tyr  
85 90 95

Gly Glu Phe His Gly Asp Leu Ser Phe Leu Asn Asp Tyr Glu Tyr Phe  
100 105 110

Val Thr Asn Pro Asp Tyr Tyr Glu Lys Glu Thr Thr Pro Lys Asn Ser  
115 120 125

363

Lys Gly Pro Tyr Phe Gly Thr Thr Asn Leu Leu Arg His Gly Ala Tyr  
 130 135 140  
 Phe Arg Lys Arg Tyr Gln Ser Leu Phe Asp Gln Lys Glu Lys Leu Val  
 145 150 155 160  
 Val Phe Thr Ser Asn Ser Gly Arg Cys Tyr Gln Ser Gly Val Tyr Phe  
 165 170 175  
 Ala Arg Gly Phe Leu Gly Asp Asp Tyr Ser Glu Asp Thr Val Glu Phe  
 180 185 190

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Val Val Val Asp Glu Asp Lys Lys Met Gly Gly Asn Ser Leu Thr Pro  
 195 200 205  
 Arg Tyr Ala Cys Lys Thr Leu Asn Gln Asp Leu His Lys Asp Leu Val  
 210 215 220  
 Asn Gln Tyr Asp Lys Thr Tyr Leu Asp Asp Ile Leu Ser Arg Trp Leu  
 225 230 235 240  
 Val Asp Asn Pro Gly Leu Asp Leu Ser Ala Asp Gln Val Ser Ser Leu  
 245 250 255  
 Phe Leu Trp Cys Ala Phe Glu Ile Asn Val Arg Gly Tyr Ser Pro Phe  
 260 265 270  
 Cys Asn Leu Phe Thr Lys Asp Glu Phe Ile Arg Ser Gly Tyr Arg Asn  
 275 280 285  
 Asp Val Gly Asn Tyr Tyr Gln Thr Gly Pro Gly Asn Asn Met Thr Lys  
 290 295 300  
 Val Ile Gly Ser Pro Met Val Glu Ala Ser Leu Lys Met Leu Gln Glu  
 305 310 315 320  
 Asp Ser Lys Ile Trp Leu Thr Phe Thr His Asp Thr Asp Ile Glu Met  
 325 330 335  
 Tyr Leu Thr Ser Leu Gly Leu Ile Val Pro Pro Gly Asp Leu Pro Val  
 340 345 350  
 Asp Arg Val Pro Phe Pro Asn Pro Tyr Asn Ala Ala Glu Phe Phe Pro  
 355 360 365  
 Gln Gly Ala Arg Thr Tyr Thr Glu Lys Leu Lys Cys Gly Glu Lys Gln  
 370 375 380

364

Tyr Val Arg Phe Ile Val Asn Asp Ala Val Tyr Pro Tyr Pro Asp Cys  
 385 390 395 400

Ser Gly Gly Pro Gly Phe Thr Cys Glu Leu Asn Asp Phe Ile Lys Leu  
 405 410 415

Val Lys Ser Arg Leu His Asp Val Asp Tyr Lys Leu Gln Cys Glu Val  
 420 425 430

Asp Gly Pro Ala Glu Leu Thr Phe Tyr Trp Asp Tyr Lys Asp Arg Lys  
 435 440 445

Tyr Asn Ala Pro Leu Ile Asp Gln  
 450 455

<210> 301

<211> 1888

<212> DNA

<213> Candida, albicans

<400> 301

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 acgtgtacac gctcaatctc aggtaaagaa agtttatatt ccatcactat ataacaacaa 180  
 tcaggctttg caaaaaaaca tttaaaacta atactggtaa tatggaaata taacgcctcg 240  
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 agcttaataa gagcagtcaa attaacacgg ctcaattaat agtacttaat aatatgaagc 360  
 cgatcaatta accgatcctt tgaataattt gaaaataaaa taaagtaata taaataggta 420  
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 taacatcgtc aattctcttg gcggtagtgc cccttatatt caaagaaacg gatatgggat 660  
 ttctactgat atccctgctg gttgtgaaat tgctcaaatt caattgtatt caagacatgg 720  
 tgaaagatac ccaagtaaaa gtaatggtaa aagtttagaa gcaatttatg ctaaatttga 780  
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 aagatatattt gctagaggat ttttaggtga tgactttaaa gaaggtaaaa ctgtcaagtt 1080  
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 tgatttatcc accaatgaag agtttatcaa atattcttat ggtaatgacc tttccaacta 1380  
 ttattctaatt ggtgctggta acaattacac cagaatcatt gggtcagtga ttttaaattc 1440

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tggtgtcaat agtacctacc catctgagct tactttctac tgggattata aaaatgtcac 1860
ttacaatgct cctttaggtg atttttaa 1888

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&lt;210&gt; 302

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 302

```

Met Val Ser Val Ser Lys Leu Leu Asn Asn Gly Leu Leu Leu Ala Gly
  1              5              10              15

Gln Ser Val Phe Gln Asp Val Ala Thr Pro Gln Gln Ala Ser Val Gln
      20              25              30

Gln Tyr Asn Ile Val Asn Ser Leu Gly Gly Ser Ala Pro Tyr Ile Gln
      35              40              45

Arg Asn Gly Tyr Gly Ile Ser Thr Asp Ile Pro Ala Gly Cys Glu Ile
      50              55              60

Ala Gln Ile Gln Leu Tyr Ser Arg His Gly Glu Arg Tyr Pro Ser Lys
      65              70              75              80

Ser Asn Gly Lys Ser Leu Glu Ala Ile Tyr Ala Lys Phe Glu Asn Tyr
      85              90              95

Lys Gly Thr Phe Lys Gly Asp Leu Ala Phe Leu Asn Asp Tyr Thr Tyr
      100              105              110

Phe Val Thr Asp Lys Asn Asn Tyr Glu Lys Glu Thr Ser Pro Lys Asn
      115              120              125

Ser Glu Gly Thr Tyr Ala Gly Thr Thr Asn Ala Leu Arg His Gly Ala
      130              135              140

Ala Phe Arg Ala Lys Tyr Gly Ser Leu Tyr Lys Glu Asn Ser Thr Leu
      145              150              155              160

Pro Val Phe Ser Ser Asn Ser Gly Arg Cys Tyr Gln Thr Ser Arg Tyr
      165              170              175

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366

Phe Ala Arg Gly Phe Leu Gly Asp Asp Phe Lys Glu Gly Lys Thr Val  
 180 185 190  
 Lys Phe Asn Ile Ile Ser Glu Asp Ala Asp Val Gly Ala Asn Ser Leu  
 195 200 205  
 Thr Pro Arg Ser Ala Cys Ser Lys Asn Lys Glu Arg Ser Ser Ser Thr  
 210 215 220  
 Ala Lys Lys Tyr Asn Thr Thr Tyr Leu Asn Ala Ile Thr Glu Arg Leu  
 225 230 235 240  
 Val Lys Pro Asn Pro Gly Leu Asn Leu Thr Thr Ser Asp Val Asn Asn  
 245 250 255  
 Leu Phe Ser Trp Cys Ala Tyr Glu Ile Asn Val Arg Gly Ser Ser Pro  
 260 265 270  
 Phe Cys Asp Leu Phe Thr Asn Glu Glu Phe Ile Lys Tyr Ser Tyr Gly  
 275 280 285  
 Asn Asp Leu Ser Asn Tyr Tyr Ser Asn Gly Ala Gly Asn Asn Tyr Thr  
 290 295 300  
 Arg Ile Ile Gly Ser Val Ile Leu Asn Ser Ser Leu Glu Leu Leu Lys  
 305 310 315 320  
 Asp Thr Lys Asn Ser Asn Gln Val Trp Leu Ser Phe Ala His Asp Thr  
 325 330 335  
 Asp Leu Glu Ile Phe His Ser Ala Leu Gly Leu Leu Glu Pro Ala Glu  
 340 345 350  
 Asp Leu Pro Thr Ser Tyr Ile Pro Phe Pro Asn Pro Tyr Val His Ser  
 355 360 365  
 Ser Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Leu Gln Cys  
 370 375 380  
 Gly Asn Asp Ala Tyr Val Arg Tyr Ile Ile Asn Asp Ala Val Val Pro  
 385 390 395 400  
 Ile Pro Lys Cys Ala Thr Gly Pro Gly Phe Ser Cys Lys Leu Asp Asp  
 405 410 415  
 Phe Glu Asn Phe Val Lys Glu Arg Ile Gly Asp Val Asp Phe Val Lys  
 420 425 430

367

Gln Cys Gly Val Asn Ser Thr Tyr Pro Ser Glu Leu Thr Phe Tyr Trp  
 435 440 445

Asp Tyr Lys Asn Val Thr Tyr Asn Ala Pro Leu Gly Asp Phe  
 450 455 460

<210> 303

<211> 1886

<212> DNA

<213> *Candida albicans*

<400> 303

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aacaacaat caacatatta aatcgttatc ccaactttgt cagttttact aacacctttt 180
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<210> 304  
 <211> 461  
 <212> PRT  
 <213> Candida albicans

<400> 304

Met Val Ser Val Ser Lys Leu Ile Asn Asn Gly Leu Leu Leu Thr Ser  
 1 5 10 15

Gln Ser Val Phe Gln Asp Val Ala Thr Pro Gln Gln Ala Ser Val Gln  
 20 25 30

Gln Tyr Asn Ile Leu Asn Phe Leu Gly Gly Ser Ala Pro Tyr Ile Gln  
 35 40 45

Arg Asn Gly Tyr Gly Ile Ser Thr Asp Ile Pro Ala Gly Cys Glu Ile  
 50 55 60

Ala Gln Ile Gln Leu Tyr Ser Arg His Gly Glu Arg Phe Pro Thr Ala  
 65 70 75 80

Ser Ser Gly Lys Asp Tyr Glu Lys Ile Tyr Ala Lys Phe Lys Asn Tyr  
 85 90 95

Asn Gly Thr Phe Lys Gly Asp Leu Ser Phe Leu Asn Asp Tyr Thr Tyr  
 100 105 110

Phe Val Lys Asp Gln Ser Asn Tyr Ala Lys Glu Thr Ser Pro Lys Asn  
 115 120 125

Ser Glu Gly Thr Tyr Ala Gly Thr Thr Asn Ala Leu Arg His Gly Ala  
 130 135 140

Ala Phe Arg Ala Lys Tyr Gly Ser Leu Tyr Lys Glu Asn Ser Thr Leu  
 145 150 155 160

Pro Ile Phe Thr Ser Asn Ser Asn Arg Val His Glu Thr Ser Lys Tyr  
 165 170 175

Phe Ala Arg Gly Phe Leu Gly Asp Asp Tyr Glu Glu Gly Lys Thr Val  
 180 185 190

Lys Phe Asn Ile Ile Ser Glu Asp Ala Asp Leu Gly Ala Asn Ser Leu  
 195 200 205

Thr Pro Arg Ser Ala Cys Ser Lys Asn Lys Glu Ser Ser Ser Ser Thr  
 210 215 220

369

Ala Lys Lys Tyr Asn Thr Thr Tyr Leu Asn Ala Ile Ala Glu Arg Leu  
225 230 235 240

Val Lys Pro Asn Pro Gly Leu Asn Leu Thr Thr Ser Asp Val Asn Asn  
245 250 255

Leu Phe Ser Trp Cys Ala Tyr Glu Ile Asn Val Arg Gly Ser Ser Pro  
260 265 270

Phe Cys Asp Leu Phe Thr Asn Glu Glu Phe Ile Lys Asn Ser Tyr Gly  
275 280 285

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Asn Asp Leu Ser Lys Tyr Tyr Ser Asn Gly Ala Gly Asn Asn Tyr Thr  
290 295 300

Arg Ile Ile Gly Ser Val Ile Leu Asn Ser Ser Leu Glu Leu Leu Lys  
305 310 315 320

Asp Thr Glu Asn Ser Asn Gln Val Trp Leu Ser Phe Ala His Asp Thr  
325 330 335

Asp Leu Glu Ile Phe His Ser Ala Leu Gly Leu Leu Glu Pro Ala Glu  
340 345 350

Asp Leu Pro Thr Ser Tyr Ile Pro Phe Pro Asn Pro Tyr Val His Ser  
355 360 365

Ser Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Leu Gln Cys  
370 375 380

Gly Asn Asp Ala Tyr Val Arg Tyr Ile Ile Asn Asp Ala Val Val Pro  
385 390 395 400

Ile Pro Lys Cys Ala Thr Gly Pro Gly Phe Ser Cys Lys Leu Asp Asp  
405 410 415

Phe Glu Asn Phe Val Lys Glu Arg Ile Gly Asp Val Asp Phe Ile Lys  
420 425 430

Gln Cys Gly Val Asn Ser Thr Tyr Pro Ser Glu Leu Thr Phe Tyr Trp  
435 440 445

Asp Tyr Lys Asn Val Thr Tyr Asn Ala Pro Leu Glu Leu  
450 455 460



<210> 305  
 <211> 1635  
 <212> DNA  
 <213> Candida albicans

<400> 305  
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~~cttcaacaat actaaceaat ttttgeaege tgtggaagga gaaacttaca ctgtacacta 360~~  
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 caciaaggaa ttaatcacca tgaaggatg tgattgaata taacctatat cagtgattat 540  
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 aaaagaaaat ccggttagagg ttgtattgtt gctcaagatt tgtcagtttt ggctttgtct 1260  
 attgttaaac aaggtgacaa tgaaattgaa ggattaactg acaccactgt tccaaaaaga 1320  
 ttaggtccaa agagagctaa ccacattaga aaattctttg gtttaactaa agaagatgat 1380  
 gttagagatt tcggttggttag aagagaaggt actaaagggtg acaaaaactta caccaaagct 1440  
 ccaaagattc aaagattagt tactccacaa actttacaaa gaaagagagc tttgaaagct 1500  
 aaaaaagtca agaatgctca acaacaaaga gatgctgctg ctgaatacgc tcaattgttg 1560  
 gctaagagat tgcataaaag aaaagaagaa agagctgaaa ttaaaaagaa gagagctgaa 1620  
 tctttaaaga actaa 1635

<210> 306  
 <211> 236  
 <212> PRT  
 <213> Candida albicans

<400> 306  
 Met Lys Leu Asn Ile Ser Tyr Pro Ala Asn Gly Thr Gln Lys Ser Met  
 1 5 10 15  
 Asp Ile Asp Asp Asp Thr Lys Leu Arg Val Ser Thr Glu Lys Arg Met  
 20 25 30

Gly Gln Glu Val Glu Gly Asp Ser Val Gly Asp Glu Phe Lys Gly Tyr  
                   35                                  40                                  45  
 Ile Phe Lys Ile Thr Gly Gly Asn Asp Lys Gln Gly Val Pro Met Lys  
                   50                                  55                                  60  
 Gln Gly Val Met His Pro Thr Arg Val Arg Leu Leu Leu Ser Lys Gly  
                   65                                  70                                  75                                  80  
 His Ser Cys Tyr Arg Pro Arg Arg Thr Gly Glu Arg Lys Arg Lys Ser  
                                   85                                  90                                  95

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Val Arg Gly Cys Ile Val Ala Gln Asp Leu Ser Val Leu Ala Leu Ser  
                   100                                  105                                  110  
 Ile Val Lys Gln Gly Asp Asn Glu Ile Glu Gly Leu Thr Asp Thr Thr  
                   115                                  120                                  125  
 Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn His Ile Arg Lys Phe  
                   130                                  135                                  140  
 Phe Gly Leu Thr Lys Glu Asp Asp Val Arg Asp Phe Val Val Arg Arg  
                   145                                  150                                  155                                  160  
 Glu Val Thr Lys Gly Asp Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln  
                                   165                                  170                                  175  
 Arg Leu Val Thr Pro Gln Thr Leu Gln Arg Lys Arg Ala Leu Lys Ala  
                                   180                                  185                                  190  
 Lys Lys Val Lys Asn Ala Gln Gln Gln Arg Asp Ala Ala Ala Glu Tyr  
                   195                                  200                                  205  
 Ala Gln Leu Leu Ala Lys Arg Leu His Glu Arg Lys Glu Glu Arg Ala  
                   210                                  215                                  220  
 Glu Ile Lys Lys Lys Arg Ala Glu Ser Leu Lys Asn  
                   225                                  230                                  235

&lt;210&gt; 307

&lt;211&gt; 1520

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 307

gtgacgagaa cttctgtcat ctcgagtctg ccaactgcct ctaacagcaa caacaataag 60

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aacaatgata acggaggagg attatcccat acaaacagaa tagttgttgg tgtagttggt 120
gggggttggtg gttctatatt aattggtttg ttggccgttt tattttactt gagaaagaga 180
aacaaccgtg attatgaagg tggatggact ttctggagaa agaatgagaa attgggaagt 240
gatgagttct tcaatggtga attgggtgtc agagacagaa atattaatca aggatcaa 300
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ttgaatccaa gtcaactaac ttgtatataa aatctgatat caattcccta gcattatgca 660
ctgattcaga aactttcaag ttacgacaaa tgaaccattc caatacagtc ttgctattga 720
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ttatagtctg tcctagataa
1520

```

&lt;210&gt; 308

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 308

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Met Ser Glu Tyr Ser Val Tyr Gln Gln Leu Asn Glu Asp Thr Asn Ala
  1             5             10             15

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Thr Lys Tyr Thr Tyr Lys Leu Leu Gln Leu Pro Ser Lys Ile Leu Asn
      20             25             30

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Gln Leu Glu Ser Lys Ser Thr Asn Leu Tyr Ile Lys Ser Asp Ile Asn
      35             40             45

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Ser Leu Ala Leu Cys Thr Asp Ser Glu Thr Phe Lys Leu Arg Gln Met
      50             55             60

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Asn His Ser Asn Thr Val Leu Leu Leu Asn Lys Glu Pro Asp Asn Lys
      65             70             75             80

```

Leu Ile Gly Phe Gln Lys Thr Ser Tyr Glu Tyr Glu Leu Thr Glu Ile  
                                   85                                  90                                  95

Lys Gly Ser Ile Asp Thr Ser Asp Ile Pro Ile Phe Asn Gly Gln Thr  
                                   100                                  105                                  110

Ala Gln Gln Pro Ile Asp Leu Ile Ala Leu Glu Asp Asn Ser Ile Cys  
                                   115                                  120                                  125

Ser His Gln Glu Phe Leu Ser Asn Trp Tyr Glu Leu Gly Gly Cys Glu  
                                   130                                  135                                  140

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Ile Asp Asn Gly Ala Tyr Ile Met Ser Ala Asp Ile Ile Thr Glu Leu  
 145                                  150                                  155                                  160

Leu Tyr Leu Leu Ile Thr Lys Leu Met Ser Leu Gln Val His Glu Phe  
                                   165                                  170                                  175

Ser Pro Glu Asp Val Ser Ser Ile Ile Thr Pro Pro Tyr Asn Asp Ser  
                                   180                                  185                                  190

Met Val Thr Ser Ile Ile His Lys Phe Cys Thr Ile Glu Ser Glu Lys  
                                   195                                  200                                  205

Tyr Gln Leu Asn Asp Leu Lys Ile Thr Gln Trp Phe Gly Ile Val Glu  
                                   210                                  215                                  220

Met Ser Lys Ile Asn His Lys Met Thr Asp Ile Ser Glu Phe Leu Leu  
 225                                  230                                  235                                  240

Asn Trp Lys Thr Ser Leu Pro Ser Phe Tyr Asn Pro Pro Leu Asp Ile  
                                   245                                  250                                  255

Ser Gln Leu Ala Gly Tyr Tyr Cys Ser Pro Ile Glu Asn Lys Ile Leu  
                                   260                                  265                                  270

Tyr Val Asp Pro Glu Ser Leu Ser Glu Asn Leu Ser Gln Arg Phe Lys  
                                   275                                  280                                  285

Glu Leu Phe Glu Leu Asp Lys Ser Trp Asn Tyr Asp Glu Phe Ile Pro  
                                   290                                  295                                  300

Phe Ile Lys Lys Phe Val Pro Ala Gly Lys Lys Val Asp Ser Ile Ile  
 305                                  310                                  315                                  320

Leu Lys Tyr Gly Lys Lys Lys Lys Val Gly Arg Asp Arg Phe Ile Val  
                                   325                                  330                                  335

Cys Pro Arg

&lt;210&gt; 309

&lt;211&gt; 710

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 309

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ggggtgggttc ccattttaat ttaaaaaaat tttttaccat ccaaaggatt ttatttaccc 60
aaagaccaaa aaattattat ttgaaatggg gattaaaatg gggataattt tattttgcct 120
gatgaaaaga ttagtaccog tttgaaagtc ctgattcaaa ttatgggtcaa gctaaaagag 180
aaatatttga ttttaattact ggtgataaaa aaccaagaat tttccatggt gatgaatcat 240
taattgatga ttctcaagaa gctgctgatg aatatgaaaa acaattgatt aataattttg 300
ctaaaaaaga ttcggtgaaa ttacctttat ttgatttatt tttattaggt tgtgcaccgg 360
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gggttttacc agtatcaaat gctcctctgg gaccagaaaa tagaataact ttatctatcc 480
cagttatatg tcattccgca agagtacat ttgttggtga aggggttaact aaggcaccaa 540
ttattaaac cattatggaa agaccagaaa aagggtttacc aagttcaatt gttaatgaag 600
gtgctgctgg tagagtgagt tgggttggtg atgatgatgc attgaatgat ttgtttgata 660
taactaaaaa gaaatacaaa tatttatcta tacctgaacc aagtcattaa 710

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&lt;210&gt; 310

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 310

```

Val Lys Leu Pro Leu Phe Asp Leu Phe Leu Leu Gly Cys Ala Pro Asp
  1             5             10             15

Gly His Ile Ala Ser Leu Phe Pro Asn His Gly Glu Gln Leu Arg Glu
      20             25             30

Lys Leu Ala Trp Val Leu Pro Val Ser Asn Ala Pro Ser Gly Pro Glu
      35             40             45

Asn Arg Ile Thr Leu Ser Ile Pro Val Ile Cys His Ser Ala Arg Val
      50             55             60

Thr Phe Val Val Glu Gly Leu Thr Lys Ala Pro Ile Ile Lys Thr Ile
      65             70             75             80

Met Glu Arg Pro Glu Lys Gly Leu Pro Ser Ser Ile Val Asn Glu Gly
      85             90             95

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375

Ala Ala Gly Arg Val Ser Trp Phe Val Asp Asp Asp Ala Leu Asn Asp  
 100 105 110

Leu Phe Asp Ile Thr Lys Lys Lys Tyr Lys Tyr Leu Ser Ile Pro Glu  
 115 120 125

Pro Ser His  
 130

<210> 311  
 <211> 1190  
 <212> DNA  
 <213> Candida albicans

<400> 311  
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 attcccggaa cgtcttggac tacttggata caacaatgga aaatgaggaa aatgaggaaa 180  
 atgaggaaaa cgaggaaaac gagggaaaata ttaccgaag agtaattata ttacaagcat 240  
 tgaaagagga gaagtgaacg ccccaaacag aaacaatacc gaacatcaca aaaaaaaaaa 300  
 aagacaacag ctaaaatttt ttggtcagaa cacaactttg gaagaaagaa aaaaaccgga 360  
 aaaaagaaat tcatctaaaa cacatacaca atatatatat atatataaa atatatccat 420  
 atacatatgc tttaatttaa ccttcccgcc tttcttttct tctttttgaa ttatatcgat 480  
 tttaaaaact acacttcacg atggctggag ttagacaatt aagaataata gcattaacgg 540  
 cctttgtcct tggtttaatt ttacttttac ataaagttag atccaacgct gcacaccttg 600  
 ttcatgcaca agcatcagac caacaaccaa acaaacataa caccaaaagt actacatata 660  
 ccgccactaa tgacgaatca gttgccaatc tcattgattc taaaaatgat cctcaaaactg 720  
 atgacaaaaa aaatcaaaaa atatcacaaag atcaagatga agccatcaat ggtaataaag 780  
 aactaataa agacaccacc aaagtcaaac cagataatgg tgaatatgat ccaatatctg 840  
 atttgataaa aattagatca ttatcaccaa tgacaatttt cagtaaatca tattgtccat 900  
 attcaaaaaa gattaaacaa ttgttattag aaaaatatga tataacacca gcaccaaagt 960  
 ttgttgaatt agatcgatat gaatatggag ctgaattaca aagttatttg acagagaaga 1020  
 gtgggagaag aactgtgcca aacgtattgg ttggtaaatc atttgaaagt aggggtgggt 1080  
 gtgatgaatt tgaaaaactt cataaagata atgatttgat taaattgtta gttgaatggg 1140  
 ggtctgggtc tttacaagtt gcaaagaaga ataccctac aaatgcctaa 1190

<210> 312  
 <211> 229  
 <212> PRT  
 <213> Candida albicans

<400> 312  
 Met Ala Gly Val Arg Gln Leu Arg Ile Ile Ala Leu Thr Ala Phe Val  
 1 5 10 15

Leu Gly Leu Ile Phe Thr Leu His Lys Val Gly Ser Asn Ala Ala Ser  
                     20                    25                    30

Leu Val His Ala Gln Ala Ser Asp Gln Gln Pro Asn Lys His Asn Thr  
                     35                    40                    45

Lys Ser Thr Thr Tyr Thr Ala Thr Asn Asp Glu Ser Val Ala Asn Leu  
                     50                    55                    60

Ile Asp Ser Lys Asn Asp Pro Gln Thr Asp Asp Lys Ile Asn Gln Lys  
                     65                    70                    75                    80

---

Ile Ser Gln Asp Gln Asp Glu Ala Ile Asn Gly Asn Lys Asp Thr Asn  
                     85                    90                    95

Lys Asp Thr Thr Lys Val Lys Pro Asp Asn Gly Glu Tyr Asp Pro Ile  
                     100                    105                    110

Ser Asp Leu Ile Lys Ile Arg Ser Leu Ser Pro Met Thr Ile Phe Ser  
                     115                    120                    125

Lys Ser Tyr Cys Pro Tyr Ser Lys Lys Ile Lys Gln Leu Leu Leu Glu  
                     130                    135                    140

Lys Tyr Asp Ile Thr Pro Ala Pro Asn Val Val Glu Leu Asp Arg Tyr  
                     145                    150                    155                    160

Glu Tyr Gly Ala Glu Leu Gln Ser Tyr Leu Thr Glu Lys Ser Gly Arg  
                     165                    170                    175

Arg Thr Val Pro Asn Val Leu Val Gly Lys Ser Phe Glu Ser Arg Gly  
                     180                    185                    190

Gly Cys Asp Glu Phe Glu Lys Leu His Lys Asp Asn Asp Leu Ile Lys  
                     195                    200                    205

Leu Leu Val Glu Trp Gly Ser Gly Arg Leu Gln Val Ala Lys Lys Asn  
                     210                    215                    220

Thr Pro Ser Asn Ala  
 225

<210> 313  
 <211> 1256  
 <212> DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 313

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agtgcgtgaa gccagtcctg aatgtgcgag gaagcccagt cagttagtag tgtccttccc 180
tccactgtct gtaatacaaaa atttccctta gtgaaaatgc gaaatataatc tgtactggga 240
accccccgga aaaaaaaaaa cctatgctca aaactatatg tactgtacac aatctagggc 300
tatagcccta atattgtaca ggaagaactt taactatggt gcgaagagcg tttccaattt 360
tttttttttc aggtgtagtc tgttctatgg caatactggt gttagtagag agtgtctcgc 420
actaacagaa catttttttc agaacaggaa aatttttgaa atctaacatc ttttactgaa 480
agccaageat caacacaata atgtcaaccc aatctgttca agtatgtaaa cgaattgaaa 540
taaagagata gagagatggt ttattatcaa aatacgaaag gaaaggcaat taaaaaagga 600
aatcaaaaag tccaacctt gcagtagaag aattgaggta tatgaatttg atagatagcc 660
agaacggtgt tacataaatg ggatatagaa caaaactata cgaggagttt gtttcaacga 720
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caaagaaatt cggtggtcgt ggtgccagag caagattcca aaaatcttac cgtaa 1256

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&lt;210&gt; 314

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 314

```

Met Ser Thr Gln Ser Val Gln Thr Phe Gly Lys Lys Lys Thr Ala Thr
  1              5              10              15

Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Ile Asn Gly
          20              25              30

Ser Pro Ile Thr Leu Val Gln Pro Glu Ile Leu Arg Phe Lys Val Tyr
  35              40              45

Glu Pro Leu Thr Leu Val Gly Leu Asp Lys Phe Gln Gly Ile Asp Ile
  50              55              60

Arg Val Lys Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala Ile
  65              70              75              80

Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr Val

```



90

95

Asp Glu Ala Ser Lys Asn Glu Leu Lys Lys Ile Phe Ala Ser Tyr Asp  
                   100                  105                  110

Lys Thr Leu Leu Val Ala Asp Ser Arg Arg Met Glu Pro Lys Lys Phe  
                   115                  120                  125

Gly Gly Arg Gly Ala Arg Ala Arg Phe Gln Lys Ser Tyr Arg  
                   130                  135                  140

<210> 315  
 <211> 959  
 <212> DNA  
 <213> Candida albicans

<400> 315  
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 tagatatgat ggatagggtta gaatcgtctt taaagagaag gtataatata taactgattt 180  
 ggcgaggtgt tggaaaagtc actccactgt atatatctc ggagtttaac gtactacagt 240  
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 ttcaaccaat tgctgaagcc cacgttttaa ttatccctaa acaccatggg gcaaagttgc 660  
 acaacattcc agacgactac cttagtgaac ttttaccagt tgtcaaaaaa ttgacaaaag 720  
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 acggaagaat tgctcatcaa gttgttgatc acgttcactt ccatttgatt cctaaaaagg 840  
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<210> 316  
 <211> 152  
 <212> PRT  
 <213> Candida albicans

<400> 316  
 Met Ala Ser His Ala Ser Cys Ile Phe Cys Lys Ile Ile Lys Gly Glu  
           1                  5                  10                  15

Ile Pro Ser Phe Lys Leu Ile Glu Thr Ala Lys Thr Tyr Ser Phe Leu  
                   20                  25                  30

379

Asp Ile Gln Pro Ile Ala Glu Ala His Val Leu Ile Ile Pro Lys His  
           35                          40                          45  
 His Gly Ala Lys Leu His Asn Ile Pro Asp Asp Tyr Leu Ser Asp Ile  
           50                          55                          60  
 Leu Pro Val Val Lys Lys Leu Thr Lys Val Leu Lys Leu Asp Glu Asn  
           65                          70                          75                          80  
 Asn Thr Pro Glu Gly Glu Gly Tyr Asn Val Leu Gln Asn Asn Gly Arg  
                           85                          90                          95

---

Ile Ala His Gln Val Val Asp His Val His Phe His Leu Ile Pro Lys  
                           100                          105                          110  
 Lys Asp Glu Ala Thr Gly Leu Gly Val Gly Trp Pro Ala Glu Ala Thr  
           115                          120                          125  
 Asp Phe Asp Lys Leu Gly Lys Leu His Glu Lys Leu Lys Glu Glu Leu  
           130                          135                          140  
 Ala Lys Val Asp Asn Glu Lys Leu  
           145                          150

&lt;210&gt; 317

&lt;211&gt; 297

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 317

cataattatt acatataaac tcgcactata attttttttt tttctattct gtgtgtgtgt 60  
 gtgtgtgaga gccagagaaa ccaaactgac tgagtgatcg tctctcaaca atttatttct 120  
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 ttcttctttt cttctttacc aaaacactag tatttcaaca tgagagataa gtggagaaaa 240  
 aagagagtta gaagattaaa gagaaagaga cggaagggtta gagctagatc caagtaa 297

&lt;210&gt; 318

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 318

Met Arg Asp Lys Trp Arg Lys Lys Arg Val Arg Arg Leu Lys Arg Lys  
           1                          5                          10                          15

Arg Arg Lys Val Arg Ala Arg Ser Lys

20

25

&lt;210&gt; 319

&lt;211&gt; 1303

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 319

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tattgtctga tgctatacgg aatgggcggtt acaaatac aaacttatat ttgaaagtaa 60
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gattagggct ttagccctat cacgtgaaat actgtatata aaaaattctt tatagcgcga 240
taaaacatat tttttttccg tattaacaaa tatgtgtgaa gttttgtcct ggtgttttct 300
cactgttttt cttttttttt ctggtagtat caattaacgc ttagatccaa tacagttttg 360
gtaacttgta cacgaacaaa atctcaaatt tggtactgtg tgaaccaaca aggaagagaa 420
aaaaaaaccc atacaaaaat ttttcagtat caaggaatta gaagagacgt ttaaatcaac 480
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taccctaata gggtttcatta tttggaaagt tatgtttatg ggagttctat ttattaagat 600
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cttttcagat agccaaataa ctaagcaact caagataaca taggatcatg catcaatcac 900
aatgaaaca ttaatactaa ctaacttttt ttttatttat taggccggtg ttaaaacttt 960
cgaattaaga actaaatcta aggaacaatt agaattctaa ttggttgaat tgaacaaga 1020
attggccact ttaaaagttc aaaaattaca aagaccaagt ttaccaagaa ttcacactgt 1080
tcgtaaaaac attgctagag tattgactgt tattaacttg aatcaaagag aaaatgttcg 1140
tgccttttac gctggtaaaa aatacattcc aaaagattta agagctaaaa agactagagc 1200
ttaagaaga aaattgacta aatttgaagc ttctcaagaa actgaaaaag ctagaaaaca 1260
aagaattgct tttccacaaa gaaaatttgc tattaaagct taa 1303

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&lt;210&gt; 320

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 320

Met Ala Gly Val Lys Thr Phe Glu Leu Arg Thr Lys Ser Lys Glu Gln

1

5

10

15

Leu Glu Ser Gln Leu Val Glu Leu Lys Gln Glu Leu Ala Thr Leu Lys

20

25

30

Val Gln Lys Leu Gln Arg Pro Ser Leu Pro Arg Ile His Thr Val Arg  
 35 40 45

Lys Asn Ile Ala Arg Val Leu Thr Val Ile Asn Leu Asn Gln Arg Glu  
 50 55 60

Asn Val Arg Ala Phe Tyr Ala Gly Lys Lys Tyr Ile Pro Lys Asp Leu  
 65 70 75 80

Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Lys Leu Thr Lys Phe Glu  
 85 90 95

Ala Ser Gln Glu Thr Glu Lys Ala Arg Lys Gln Arg Ile Ala Phe Pro  
 100 105 110

Gln Arg Lys Phe Ala Ile Lys Ala  
 115 120

<210> 321  
 <211> 2690  
 <212> DNA  
 <213> Candida albicans

<400> 321

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&lt;210&gt; 322

&lt;211&gt; 729

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 322

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Met Ser Asp Ile Tyr Ile Ile Ile His Ile Ser Thr Thr Cys Asp Asp
  1                   5                   10                   15

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Ser Pro Thr Phe Val Thr Lys Asp Ser Ser Glu Leu Ile Glu Phe Ala
      20                   25                   30

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Trp Glu Thr Val Asp Ser Val Thr Leu Glu Thr Leu Tyr Lys Gly Ser
      35                   40                   45

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Asn Leu Val Arg Pro Thr Asn Thr Pro Ile Thr Pro Tyr Cys Ser Lys
      50                   55                   60

```

```

Ile His Arg Ile Thr Trp Asp Asn Val Lys Asn Ala Gly Ser Phe Lys
      65                   70                   75                   80

```

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Asp Ala Ile Thr Asn Phe Asp Gln Tyr Val Gln Glu His Ile Ile Ser
      85                   90                   95

```

383

Lys Lys Lys Glu Phe Ser Ile Val Met Phe Asp Ile Ser Lys Leu Arg  
 100 105 110  
 Val Gln Leu Val Arg Glu Ala Arg Asp Lys Ser Val Val Leu Pro Ser  
 115 120 125  
 Tyr Leu Gln His Pro Arg Ile Phe Asp Leu Pro Arg Glu Tyr Leu Asn  
 130 135 140  
 Trp Gln Ser Ser His Pro Glu Thr Leu Ser Tyr Pro Pro Thr Ser Leu  
 145 150 155 160  
 Thr Asn Ile Ile Thr Ala Leu Glu Val Glu Val Glu Asn Ile Ser Glu  
 165 170 175  
 Tyr Val Asp Leu Pro Asn Phe Ser Ser Thr Pro Ser Pro Ser Lys Ala  
 180 185 190  
 Ser Ala Thr Thr Thr Thr Thr Thr Ala Asn Val Thr Ala Ile Asp Val  
 195 200 205  
 Leu Ser Ser Glu Thr Glu Pro Asn Gly Lys Val Ile Ala Asn Leu His  
 210 215 220  
 Ala Lys Ile Ala Lys Gln Leu Ile Lys Lys Ser Ile Pro Val Glu Asn  
 225 230 235 240  
 His Pro Asn Val Phe Thr Arg Pro Phe Asp Ser Ala Gln Asp Ile Thr  
 245 250 255  
 Ala Phe Thr Ser Glu Arg Ser Lys Val Leu Tyr Leu Ser Asn Leu Pro  
 260 265 270  
 Asn Asp Thr Thr Gln Ser Glu Leu Glu Ser Trp Phe Thr Gln Tyr Gly  
 275 280 285  
 Gly Arg Pro Gly Gly Phe Trp Thr Phe Lys Ser Ala Asp Asp Asn Asn  
 290 295 300  
 Asn Asn Asn Asn Asn Asn Ser Asn Gly Gly Lys Gly Tyr Gln Asn Ala  
 305 310 315 320  
 Arg Lys Tyr Gly Ile Ser Gly Phe Val Ala Phe Asn Thr His Glu Glu  
 325 330 335  
 Ala Val Asp Cys Leu Ala Leu Asn Gly Arg Val Leu Asn Asp Arg Pro  
 340 345 350

384

Ile Glu Val Gln Ala Ser Ser Ser Lys Val Phe Asp Met Ala Met Asp  
 355 360 365

Lys Leu Leu Leu Thr Ser Phe Pro Leu Ser Lys Asn Arg Pro Arg Pro  
 370 375 380

Gly Asp Trp Thr Cys Leu Ser Cys Gly Phe Ser Asn Phe Gln Arg Arg  
 385 390 395 400

Thr His Cys Phe Arg Cys Ser Phe Ala Ala Val Ala Phe Gln Asp Val  
 405 410 415

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Phe Asn Ser Asn Thr Gly Asn Ala Asn Gly Asn Gly Asn Val Ser Gly  
 420 425 430

Asn His Asn His Asn His Asn Ser Gly Ala Arg Arg Gly Met Asn Leu  
 435 440 445

Gln Pro Ala Gln Ala Asn Glu Lys Ile Gly Thr Gly Asn Ile Ser Ile  
 450 455 460

Pro Ser Tyr Asn Asp Pro Ile Lys Gly Pro Thr Gly Asn Val Thr Asn  
 465 470 475 480

His Leu Asn Asn Ser Glu Thr Asn Leu Ser Asn Asn Thr Asn Leu Asn  
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Asn Asn Asn His His Ser Asn Asn Tyr His Asn Asn Tyr His His His  
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Asn Asn Asn Asn Asn Asn His Gly Asn Ser Asn Gly Asn Thr Ile His  
 515 520 525

Gly Arg Ser His Tyr Asn Asn Ser Val Pro Phe Arg Ala Gly Asp Trp  
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Lys Cys Glu Asn Cys Met Tyr His Asn Phe Ala Lys Asn Leu Cys Cys  
 545 550 555 560

Leu Lys Cys Gly Val Ala Lys Pro Ala Ile Asn Asn Gln Gln Asn Asn  
 565 570 575

Thr Ile His Ser Val Asn Ser Thr Ala Ala Ala Ile Ala Ala Ala Thr  
 580 585 590

Ala Ser Gly Gln Pro Leu Asn Leu Asn Asn Asn Ala Phe Leu Asn Leu  
 595 600 605

385

Gln Gln Gln Gln Ser Gln Ser Gln Pro Gln Gly Gln His His Tyr Asn  
 610 615 620

Gln His Ser Arg Asn Asn Asn Ala Ser Gly Ala Ser Lys Phe Asn Asn  
 625 630 635 640

Gly Tyr Asn Pro Lys Asn Gln Tyr Tyr Asn Asn Asn Ser Lys Asn Leu  
 645 650 655

Ser Asn Asn Phe Gly Leu Asn Gly Met His Gln Gln Asn Gln Asn Gln  
 660 665 670

Ile Leu Met Tyr Ser Gln Gln Leu Gln Gln Gln Gln Gln Gln Gln  
 675 680 685

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
 690 695 700

Gln Gln Gln Gln Gln Gln His Asp Leu Asn Gly Ser Ser Ser Ser His  
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Gln Ser Lys Leu Gln Leu Asn Asn Thr  
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<210> 323  
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 <212> DNA  
 <213> Candida albicans

<400> 323  
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&lt;210&gt; 324

&lt;211&gt; 952

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 324

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Met Ser Asp Ser Gly Tyr Thr Leu Ile Tyr Glu Pro Asn Thr Ala Thr
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Lys Val Ser Val Asn Glu Phe Lys Asn Leu Leu Glu Lys Gly Lys Asp
          20           25           30

Asp Val Lys Val Asp Thr Met Lys Lys Ile Leu Ile Thr Ile Leu Asn
          35           40           45

Gly Asp Pro Leu Pro Asp Leu Leu Met His Ile Ile Arg Phe Val Met
50           55           60
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Pro Ser Arg Asn Lys Glu Leu Lys Lys Leu Leu Tyr His Tyr Trp Glu
65           70           75           80

Val Cys Pro Lys Met Asp Glu Ser Gly Lys Met Arg His Glu Met Ile
          85           90           95

Leu Val Cys Asn Ala Ile Gln Arg Asp Leu Gln His Pro Asn Glu Tyr
          100          105          110

Ile Arg Gly Asn Thr Leu Arg Tyr Leu Thr Lys Leu Lys Glu Pro Glu
          115          120          125

Leu Leu Glu Thr Leu Val Pro Asn Val Arg Gln Cys Leu Glu His Arg
          130          135          140

His Ala Tyr Val Arg Lys Asn Ala Val Phe Ala Leu Trp Ser Ile His
          145          150          155          160

Lys Val Ser Asp His Leu Ala Pro Asp Ala Asp Glu Leu Ile Tyr Arg
          165          170          175

Phe Leu Tyr Glu Glu Asn Asp Ser Val Cys Lys Arg Asn Ala Phe Val
          180          185          190

Cys Leu Gly Asp Leu Asn Arg Glu Ala Ala Leu Gln Tyr Ile Gln Asp
          195          200          205

Asn Ile Ser Val Ile Glu Thr Leu Asp Pro Leu Ile Gln Leu Ala Phe
          210          215          220

Ile Glu Phe Ile Lys Lys Asp Ser Ile Gln Asn Pro Ala Leu Lys Gln
          225          230          235          240

Gln Tyr Ala Gln Leu Met Thr Glu Ile Ile Glu Ser Ser Ser Asn Val
          245          250          255

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388

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Val Met Tyr Glu Ala Ala Asn Thr Leu Thr Val Leu Thr Ser Asn Pro
      260                      265                      270

Gln Ser Ile Leu Leu Ala Gly Asn Lys Phe Val Glu Leu Ala Thr Arg
      275                      280                      285

Glu Ser Asp Asn Asn Val Lys Ile Ile Thr Leu Glu Arg Ile Asn Gln
      290                      295                      300

Leu His Lys Gln His Pro Gly Val Leu Gln Asp Leu Ser Leu Glu Ile
      305                      310                      315                      320

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Leu Arg Gly Leu Ser Ser Gln Asp Leu Asp Val Lys Lys Lys Ala Leu
      325                      330                      335

Asp Val Thr Leu Gln Phe Ile Thr Thr Arg Asn Val Glu Asp Val Val
      340                      345                      350

Lys Leu Leu Lys Lys Glu Leu Gln Ser Thr Ala Leu Ser Asn Asp Asp
      355                      360                      365

Lys Asn Ala Asp Tyr Arg Gln Leu Leu Ile Asn Ala Ile His Gln Leu
      370                      375                      380

Ala Ile Lys Phe Val Glu Val Ala Ala Asn Val Ile Asp Leu Leu Leu
      385                      390                      395                      400

Asp Ser Ile Ala Asp Leu Asn Thr Thr Ala Ala Tyr Glu Val Ile Thr
      405                      410                      415

Phe Val Lys Glu Val Val Glu Lys Phe Pro Asp Leu Arg Asp Ala Ile
      420                      425                      430

Leu Arg Arg Leu Ile Leu Ala Leu Pro His Val Lys Ser Gly Lys Val
      435                      440                      445

Phe Arg Gly Ala Leu Trp Val Ile Gly Glu Tyr Ala Leu Glu Glu Ser
      450                      455                      460

Leu Ile Gln Glu Ser Trp Lys Tyr Ile Arg Gly Ser Ile Gly Glu Val
      465                      470                      475                      480

Pro Ile Ile Ala Ser Glu Leu Lys Ser Lys Lys Arg Asp Asp Thr Glu
      485                      490                      495

Glu Ser Gln Glu Glu Glu Thr Glu Tyr Asp Gly Lys Pro Arg Arg Lys
      500                      505                      510

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389

Gly Pro Val Val Leu Pro Asp Gly Thr Tyr Ala Thr Glu Ser Ala Leu  
 515 520 525  
 Thr Ser Glu Thr Thr Asp Ser Leu Glu Ser Asp Ser Lys Thr Pro Ile  
 530 535 540  
 Arg Lys Gln Ile Leu Ala Gly Asp Phe Tyr Leu Gly Ala Val Leu Ala  
 545 550 555 560  
 Ser Thr Leu Val Lys Leu Ile Leu Arg Leu Gln Ser Leu Lys Gln Thr  
 565 570 575  
 Gln Glu Lys Ile Leu Asn Gly Leu Lys Ala Glu Ala Leu Leu Ile Met  
 580 585 590  
 Val Ser Ile Leu Arg Val Gly Glu Ser Ser Leu Val Ser Lys Lys Ile  
 595 600 605  
 Asp Glu Asp Ser Ala Asp Arg Ile Leu Ser Tyr Ile Lys Ile Leu Asn  
 610 615 620  
 Asp Glu Glu Asp Leu Gln Glu Ile Lys Thr Ser Phe Leu Glu Asp Thr  
 625 630 635 640  
 Lys Asp Ala Phe Lys Ala Gln Ile Asn Asn Ala Glu Leu Lys Lys Ala  
 645 650 655  
 Glu Ala Leu Ala Lys Asp Leu His Asp Asn Ala Glu Gln Ile Asp Asp  
 660 665 670  
 Ala Ile Val Phe Arg Gln Leu Asp Lys Asp Asn Lys Lys Ser Lys Ala  
 675 680 685  
 Ser Val Asp Asp Val Ala Ala Ala Ser Gly Ser Asn Glu Leu Lys Lys  
 690 695 700  
 Glu Asn Leu Ser Ser Arg Leu Asn Lys Ile Ile Gln Leu Thr Gly Phe  
 705 710 715 720  
 Ser Asp Pro Ile Tyr Ala Glu Ala Phe Val Lys Val His Gln Tyr Asp  
 725 730 735  
 Val Val Leu Asp Val Leu Leu Val Asn Gln Thr Thr Thr Thr Leu Arg  
 740 745 750  
 Asn Leu Ser Val Glu Phe Ala Thr Leu Gly Asp Leu Lys Val Val Asp  
 755 760 765

390

Lys Pro Thr Thr Ala Asn Ile Gly Pro His Gly Phe Tyr Lys Val Gln  
 770 775 780  
 Thr Thr Ile Lys Val Thr Ser Ala Asp Thr Gly Val Ile Phe Gly Asn  
 785 790 795 800  
 Ile Val Tyr Asp Gly Gln His Ser Asp Asp Ser Arg Ile Val Ile Leu  
 805 810 815  
 Asn Asp Val His Val Asp Ile Met Asp Tyr Ile Lys Pro Ala Thr Cys  
 820 825 830

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Ser Glu Ser Gln Phe Arg Lys Met Trp Asn Glu Phe Glu Trp Glu Asn  
 835 840 845  
 Lys Ile Thr Ile Lys Ser Pro Ile Glu Thr Leu Lys Glu Tyr Leu Asp  
 850 855 860  
 Glu Leu Met Lys Gly Thr Asn Met Gln Cys Leu Thr Pro Gly Ala Val  
 865 870 875 880  
 Ile Gly Glu Glu Cys Gln Phe Leu Ser Ala Asn Leu Tyr Ser Arg Ser  
 885 890 895  
 Ser Phe Gly Glu Asp Ala Leu Ala Asn Leu Cys Ile Glu Lys Gln Ser  
 900 905 910  
 Asp Gly Pro Ile Ile Gly His Val Arg Ile Arg Ser Lys Gly Gln Gly  
 915 920 925  
 Leu Ala Leu Ser Leu Gly Asp Arg Val Ala Ser Ile Ser Arg Lys Gly  
 930 935 940  
 Lys Lys Ala Thr Ile Ala Arg Val  
 945 950

&lt;210&gt; 325

&lt;211&gt; 2270

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 325

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 cgagacttcc atagcaaagt taacaagcac aattgtcatt ttaacttaat tgggtggatta 180

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&lt;210&gt; 326

&lt;211&gt; 589

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 326

Met Leu Glu Leu Asn Ser Ile Thr Ile Pro Arg Asn Phe Thr Glu Phe

1

5

10

15

Gln Leu Thr Ala Leu Lys Ile Tyr Tyr Gln Leu Lys Ile Leu Phe Leu

20

25

30

Ala Thr Tyr Cys Ala Gln Gly Ser Phe Gly Leu Asn Gly Ser Val Cys  
 35 40 45  
 Leu Ala Arg Asp Ile Phe Val Gly Tyr Val Val Tyr Thr Gln Leu Leu  
 50 55 60  
 Lys Leu Tyr Arg Val Leu Arg Gly Tyr Gly Ile Val Asp Ser Ile Arg  
 65 70 75 80  
 Arg Leu Tyr Leu Tyr Val Ser Ser Thr Val Ser Ser Gln Ile Phe Ser  
 85 90 95

---

Leu Pro Phe Ile Lys Ser Lys Ile Asp Lys Glu Leu Gln Ala Thr Ile  
 100 105 110  
 Gly Lys Val Glu Glu Glu Ile Met Lys Asn Asp Pro Gln Leu Leu Gln  
 115 120 125  
 Phe Pro Glu Leu Pro Glu Gln Gly Ile Asp Ala Asp Asn Val Ser Leu  
 130 135 140  
 Glu Leu Asp Lys Leu Gln Asn Leu Lys His Ser Asp Trp Ile Asn Gly  
 145 150 155 160  
 Arg Val Ser Gly Ala Val Tyr His Gly Gly Glu Asn Leu Leu Ser Leu  
 165 170 175  
 Gln Val Glu Ala Tyr Lys Lys Tyr Ser Val Ala Asn Gln Leu His Pro  
 180 185 190  
 Asp Val Phe Pro Gly Val Arg Lys Met Glu Ala Glu Val Val His Met  
 195 200 205  
 Val Leu Asp Ile Phe Asn Ala Pro Ser Asp Gly Cys Gly Ser Thr Thr  
 210 215 220  
 Ser Gly Gly Thr Glu Ser Leu Leu Leu Ala Gly Leu Ser Ala Arg Glu  
 225 230 235 240  
 Tyr Gly Lys Lys Tyr Arg Gly Ile Thr Glu Pro Glu Val Ile Ala Pro  
 245 250 255  
 Val Thr Ile His Ala Gly Ile Glu Lys Ala Cys Phe Tyr Phe Gly Met  
 260 265 270  
 Lys Leu His Lys Val Asp Leu Asp Pro Val Thr Phe Gln Val Asp Val  
 275 280 285

393

Lys Lys Val Glu Arg Leu Ile Asn Ser Asn Thr Val Leu Ile Cys Gly  
 290 295 300  
 Ser Ala Pro Asn Tyr Pro His Gly Ile Ile Asp Asp Ile Glu Ser Leu  
 305 310 315 320  
 Ser Lys Leu Ala Val Lys Tyr Asn Ile Pro Leu His Val Asp Ala Cys  
 325 330 335  
 Leu Gly Ser Phe Ile Val Ser Phe Leu Glu Lys Ser Lys Val His Gly  
 340 345 350

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Asp Arg Lys Leu Pro Ile Phe Asp Phe Arg Leu Pro Gly Val Thr Ser  
 355 360 365  
 Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala Pro Lys Gly Ser Ser  
 370 375 380  
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 385 390 395 400  
 Ala Ser Asp Trp Thr Gly Gly Met Tyr Gly Ser Pro Thr Leu Ala Gly  
 405 410 415  
 Ser Arg Pro Gly Ala Leu Val Val Gly Cys Trp Ala Thr Leu Ile Asn  
 420 425 430  
 Ile Gly Lys Gln Gly Tyr Thr Lys Phe Cys Tyr Asp Ile Val Ser Ala  
 435 440 445  
 Ser Met Lys Val Lys Arg Ala Ile Glu Thr Asp Pro Ile Leu Ser Lys  
 450 455 460  
 His Leu Gln Ile Ile Gly Asp Pro Ile Gly Ser Val Ile Ser Phe Gln  
 465 470 475 480  
 Leu Ala Pro Gln Gln Ser Gly Asn Leu Ser Ile Tyr Glu Ile Ser Asp  
 485 490 495  
 Leu Leu Thr Lys Lys Gly Trp His Phe Ala Thr Leu Gln Asn Pro Ser  
 500 505 510  
 Ala Leu His Phe Ala Phe Thr Arg Leu Thr Val Pro Val Val Asp Glu  
 515 520 525  
 Leu Ile Ala Asp Leu Val Glu Ala Thr Lys Glu Ala Val Ala Ile Ala  
 530 535 540



Glu Glu His Lys Lys Asn Gly Val Thr Lys Ala Pro Gly Asp Thr Ala  
 545 550 555 560

Ala Leu Tyr Gly Ile Ala Gly Ser Val His Thr Ala Gly Leu Ala Asp  
 565 570 575

Arg Leu Ile Val Ala Phe Leu Asp Thr Leu Tyr Lys Ile  
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<210> 327

<211> 3605

<212> DNA

<213> Candida albicans

<400> 327

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tatag 3605

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&lt;210&gt; 328

&lt;211&gt; 1034

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 328

Met Leu Lys Thr Arg Leu Lys Gln Ser Arg Ala Ile Ser Arg Val Val

1

5

10

15

Arg Arg Tyr Ala Cys Ser His Pro Ile Ser Pro Asn Leu Asp Lys Tyr

20

25

30

Pro Val Gly Leu Lys Leu His Gly Tyr Glu Val Thr Gln Thr Ser Pro

35

40

45

Ile Pro Glu Phe Ser Leu Thr Ala Val Ser Leu Lys His Thr Glu Ser  
 50 55 60  
 Gly Ala Thr His Leu His Leu Asp Ser Pro Asn Asp Ser Asn Asn Val  
 65 70 75 80  
 Phe Ser Ile Ala Phe Lys Thr Asn Pro Pro Asp Asn Thr Gly Val Pro  
 85 90 95  
 His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Lys Lys Phe Pro Val  
 100 105 110

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Arg Asp Pro Phe Phe Lys Met Thr Asn Arg Ser Leu Ser Asn Phe Met  
 115 120 125  
 Asn Ala Met Thr Gly His Asp Tyr Thr Phe Tyr Pro Phe Ala Thr Thr  
 130 135 140  
 Asn Ser Lys Asp Phe Glu Asn Leu Met Asp Val Tyr Leu Ser Ser Val  
 145 150 155 160  
 Phe Glu Pro Gln Leu Asn His Thr Asp Phe Leu Gln Glu Gly Trp Arg  
 165 170 175  
 Ile Glu Asn Gln Asn Val His Asp Ile Ser Ser Lys Leu Glu Phe Lys  
 180 185 190  
 Gly Val Val Tyr Asn Glu Met Lys Gly Gln Tyr Ser Asn Ser Ala Tyr  
 195 200 205  
 Tyr Phe Tyr Ile Lys Phe Leu Glu Ser Ile Tyr Pro Ser Leu Asn Asn  
 210 215 220  
 Ser Gly Gly Asp Pro Lys Lys Ile Val Asp Leu Ser Tyr Glu Gly Leu  
 225 230 235 240  
 Leu Glu Phe His Ser Lys Asn Tyr His Pro Ser Asn Ala Lys Thr Phe  
 245 250 255  
 Thr Tyr Gly Lys Leu Pro Leu Glu Asp Ser Leu Ser Lys Ile Ser Lys  
 260 265 270  
 Tyr Tyr Glu Ser Phe Glu Lys Lys Val Ser Ser Val Asp Val Lys Gln  
 275 280 285  
 Pro Ile Phe Ser Thr Asp Lys Ser Glu Ile Phe Asp Val Thr Ile Pro  
 290 295 300

397

Gly Pro Val Asp Thr Met Asn Gly Lys Glu Thr Ser Glu Gln Tyr Cys  
 305 310 315 320  
 Thr Ser Ile Thr Trp Asn Leu Gly Asn Pro Leu Asp Pro Asn Met Gln  
 325 330 335  
 Tyr Asp Ile Phe Lys Trp Lys Ile Leu Ser Ser Leu Leu Phe Asp Gly  
 340 345 350  
 His Asn Ser Pro Phe Tyr Gln Glu Leu Ile Glu Ser Gly Tyr Gly Asp  
 355 360 365

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Asp Phe Ser Ala Asn Thr Gly Leu Asp Ser Thr Thr Ala Leu Leu Ser  
 370 375 380  
 Phe Thr Val Gly Leu Asn Tyr Leu Thr Lys Gln Lys Val Asp Asn Phe  
 385 390 395 400  
 Asn Glu Lys Val Met Glu Ile Ile Asn Asn Lys Ile Ile Pro Glu Leu  
 405 410 415  
 Ser Asn Glu Glu Ser Ser Ser Tyr His Gly Arg Ile Asp Ala Ile Leu  
 420 425 430  
 His Gln Ile Glu Ile Gly Phe Lys Arg His Lys Pro Asp Phe Gly Phe  
 435 440 445  
 Gly Leu Leu Ser Ser Ile Val Pro Ser Trp Val Asn Gly Val Asp Pro  
 450 455 460  
 Ile Asp Thr Leu Gln Val Glu Lys Ile Leu Ser His Phe Lys Glu Asp  
 465 470 475 480  
 Tyr Lys Gln Asn Gly Leu Arg Ile Phe Lys Glu Leu Leu Glu Lys Thr  
 485 490 495  
 Leu Cys Asn Pro His Ser Gln Lys Phe Lys Phe Thr Met Glu Pro Arg  
 500 505 510  
 Glu Asp Phe Thr Lys Gln Leu Val Lys Asp Glu Asn Leu Met Ile Glu  
 515 520 525  
 Lys Arg Val Ser Glu Leu Thr Glu Asp Asn Lys Lys Ala Ile Tyr Glu  
 530 535 540  
 Gln Asn Leu Glu Leu Ala Lys Leu Gln Leu Glu Asp Gln Asn Thr Glu  
 545 550 555 560

Val Leu Pro Thr Leu Thr Ile Asp Asp Ile Pro Lys Arg Gly Asp Phe  
565 570 575

Tyr Ala Ile Asp Leu Gly Gln Val Asn Lys Lys Val Val His Glu Arg  
580 585 590

Val Val Asp Thr Asn Gly Leu Val Tyr Ala Asn Ala Leu Lys Asp Ile  
595 600 605

Ser Tyr Leu Pro Thr Lys Leu Tyr Lys Tyr Leu Pro Leu Phe Asn Asn  
610 615 620

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Cys Leu Thr Asn Leu Ala Gly Thr Glu Asn Thr Pro Ile Thr Glu Leu  
625 630 635 640

Glu Thr Lys Ile Gln Met Leu Thr Gly Gly Ile Thr Phe Ser Ser Lys  
645 650 655

Ile Ser Thr Asp Pro Tyr Asn Ile Glu Gln Leu Lys Leu Gln Tyr Val  
660 665 670

Leu Ser Gly Met Ala Leu Lys Glu Lys Ser Ser Ser Val Tyr Asp Leu  
675 680 685

Trp Leu Glu Ile Leu Thr Thr Thr Lys Phe Asp Thr Ser Asp Glu Val  
690 695 700

Leu Glu Lys Leu Ser Val Leu Ile Lys Asn Met Gly Gln Asn Gln Ile  
705 710 715 720

Asn Asn Ile Ala Asp Arg Gly His Ser Tyr Ala Ala Ala Val Ser Ser  
725 730 735

Ser Lys Leu Thr Pro Ser Lys Tyr Ile Ser Asp Ile Val Ser Gly Leu  
740 745 750

Ser Gln Val Gln Phe Val Met Glu Leu Asn Ser Lys Leu Glu Ser Glu  
755 760 765

Gly Lys Glu Tyr Leu Ala Lys Glu Ile Ile Pro Ile Leu Gln Glu Ile  
770 775 780

Gln Lys Tyr Val Leu Gln Gly Glu Phe Arg Tyr Arg Leu Val Gly Asn  
785 790 795 800

Gln Glu Ile Ile Val Glu Asn Glu Lys Leu Ile Glu Lys Phe Asp Lys  
805 810 815

Asp Ile Ser Ser Asn Arg Pro Thr Leu Ser Leu Thr Val Thr Asp Gly  
                   820                  825                  830

Leu Ser Ala Leu Leu Asn Ser Phe Asn Tyr Asn His Thr Ser Glu Asn  
                   835                  840                  845

Val Leu Val Asn Leu Pro Phe Gln Val Gly Tyr Ser Ser Leu Gly Lys  
                   850                  855                  860

Ile Gly Ser Ser Tyr Ser Ser Lys Asp Gly Ala Ser Leu Gln Ile Leu  
 865                  870                  875                  880

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Ser Gln Leu Tyr Ser Phe Lys Asn Leu His Ser Lys Ile Arg Glu Ser  
                   885                  890                  895

Asn Gly Ala Tyr Gly Gly Gly Leu Thr Tyr Asp Gly Leu Asn Gly Thr  
                   900                  905                  910

Leu Asn Phe Tyr Ser Tyr Arg Asp Pro Asn Pro Val Lys Ser Ile Gln  
                   915                  920                  925

Thr Phe Arg Asp Ser Leu Ser Tyr Gly Leu Asp Ala Asn Trp Asn Asp  
                   930                  935                  940

Lys Asp Leu Gln Glu Ala Lys Leu Arg Val Phe Gln Ser Val Asp Ala  
 945                  950                  955                  960

Pro Ile Asn Ile Ser Ser Gln Gly Ala Ser Ala Phe Phe Glu Asn Ile  
                   965                  970                  975

Asp Asp Tyr Leu Arg Gln Glu Arg Arg Glu Asn Phe Leu Gly Thr Thr  
                   980                  985                  990

Leu Lys Asp Leu Arg Asp Val Thr Glu Lys Tyr Leu Val Asp Asn Gln  
                   995                  1000                  1005

Asn Asn Leu Val Thr Val Ile Gly Asp Asn Glu Ile Leu Asn Val Asp  
 1010                  1015                  1020

Asn Lys Trp Gln Ile Arg Asn Phe Gln Val  
 1025                  1030

&lt;210&gt; 329

&lt;211&gt; 1366

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 329

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&lt;210&gt; 330

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 330

```

Met Pro Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg
  1              5              10              15

Leu Leu Asn Thr Asn Ile Asp Gly Arg Ile Lys Ile Met Tyr Ala Leu
      20              25              30

Thr Lys Ile Arg Gly Val Gly Arg Arg Tyr Ala Asn Leu Val Cys Lys
      35              40              45

Lys Ala Asp Val Glu Leu Thr Lys Arg Ala Gly Glu Leu Thr Gln Glu
      50              55              60

Glu Leu Glu Arg Ile Val Thr Ile Met Gln Asn Pro Thr Asn Tyr Lys
      65              70              75              80

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Ile Pro Ala Trp Phe Leu Asn Arg Gln Lys Asp Gln Val Asp Gly Lys
      85                      90                      95

Asp Tyr His Val Leu Ala Asn Asn Leu Glu S r Lys Leu Arg Asp Asp
      100                    105                    110

Leu Glu Arg Leu Lys Lys Ile Arg Ser His Arg Gly Ile Arg His Phe
      115                    120                    125

Trp Gly Leu Lys Val Arg Gly Gln His Thr Lys Thr Thr Ser Arg Gly
      130                    135                    140

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Arg  
145

<210> 331  
<211> 1327  
<212> DNA  
<213> Candida albicans

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<400> 331
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cttttaa

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<210> 332  
 <211> 136  
 <212> PRT  
 <213> Candida albicans

<400> 332  
 Met Ala Lys Phe Ile Lys Ser Gly Lys Val Ala Ile Val Val Arg Gly  
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 Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly  
                   20                  25                  30

Thr Lys Ser His Pro Phe Pro His Ala Ile Val Ala Gly Ile Glu Arg  
           35                  40                  45

Ala Pro Leu Lys Val Thr Lys Lys Met Asp Ala Lys Lys Val Thr Lys  
           50                  55                  60

Arg Thr Lys Val Lys Pro Phe Val Lys Leu Val Asn Tyr Asn His Leu  
           65                  70                  75                  80

Met Pro Thr Arg Tyr Ser Leu Asp Val Glu Ser Phe Lys Ser Ala Val  
                   85                  90                  95

Thr Ser Glu Ala Leu Glu Glu Pro Ser Gln Arg Glu Glu Ala Lys Lys  
           100                  105                  110

Val Val Lys Lys Ala Phe Glu Glu Lys His Gln Ala Gly Lys Asn Lys  
           115                  120                  125

Trp Phe Phe Gln Lys Leu His Phe  
           130                  135

<210> 333  
 <211> 1157  
 <212> DNA  
 <213> Candida albicans

<400> 333  
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 tcatcttatt caattctttt tcagcatcat tcgtatcttt aagcacaggg aatagcaatg 180  
 gatcatgtaa caaattcact ttcgtgattc gaaagcccaa aatgtttcgt tttacaacg 240  
 cacacacatg tgaaacctaa accgagttag tcgtcaagaa aataattcag tggttaaagtc 300  
 tgtaccttaa gcgtcaaacg tacttctgca acctctggca ttgagtgtaa tttaaatatt 360  
 catgataatc tggaactaca agctacgaaa aaaaaagaaa aagaaaaata gtacgagttc 420

```

ttggtgagat aaataatgga gaacactttt ttttttctct ttggagggtt tagaaggcaa 480
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catctttgaa tgatgcaatc aagggaatcg atgaaagagt ggggtctttg gatgttaaata 600
taagcaagat caactcggaa ttatccacat accaacaaaa gataagcaga atgagagacg 660
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tagaagctca aaaggatcag ttagagaatc aatcttgga tatgacacaa gcttccatga 780
caacagataa cttacaaaat accatggtca caataaatgc aatgaaaaca gccaataaac 840
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tggtggattt gattgataaa tcaaatgaac tacaggaggc acttctgacg agctatgatg 960
taccgatga catcagtgag ctggagttgg atgctgaatt agaagctctt ggcgaagaaa 1020
ttgattttga aaatgaaatg gcagagagtg ggatagggtc acctagttac ttaaatgata 1080
cagaacctac agcagcagat aaattgccta cattttattga cgaacaacca gaagaagctc 1140
aaaaaatcgc aaactag 1157

```

&lt;210&gt; 334

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 334

```

Met Asn Arg Leu Phe Gly Thr Lys Ser Thr Ala Pro Lys Pro Ser Leu
  1             5             10             15

```

```

Asn Asp Ala Ile Lys Gly Ile Asp Glu Arg Val Gly Ser Leu Asp Val
          20             25             30

```

```

Lys Leu Ser Lys Ile Asn Ser Glu Leu Ser Thr Tyr Gln Gln Lys Ile
      35             40             45

```

```

Ser Arg Met Arg Asp Gly Pro Gly Lys Ser Ala Leu Lys Gln Lys Ala
      50             55             60

```

```

Ile Lys Leu Leu Arg Gln Arg Lys Gln Ile Glu Ala Gln Lys Asp Gln
      65             70             75             80

```

```

Leu Glu Asn Gln Ser Trp Asn Met Thr Gln Ala Ser Met Thr Thr Asp
          85             90             95

```

```

Asn Leu Gln Asn Thr Met Val Thr Ile Asn Ala Met Lys Thr Ala Asn
          100             105             110

```

```

Lys Ser Leu Lys Gln Thr Tyr Gly Lys Ile Asn Ile Asp Glu Leu Glu
          115             120             125

```

```

Asp Leu Gln Asp Glu Met Leu Asp Leu Ile Asp Lys Ser Asn Glu Leu
          130             135             140

```

404

Gln Glu Ala Leu Ser Thr Ser Tyr Asp Val Pro Asp Asp Ile Ser Glu  
145 150 155 160

Ser Glu Leu Asp Ala Glu Leu Glu Ala Leu Gly Glu Glu Ile Asp Phe  
165 170 175

Glu Asn Glu Met Ala Glu Ser Gly Ile Gly Ala Pro Ser Tyr Leu Asn  
180 185 190

Asp Thr Glu Pro Thr Ala Ala Asp Lys Leu Pro Thr Phe Ile Asp Glu  
195 200 205

Gln Pro Glu Glu Ala Gln Lys Ile Ala Asn  
210 215

<210> 335

<211> 4550

<212> DNA

<213> Candida albicans

<400> 335

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tttatatttt tgggtttttt ttctttggtt tctttgaatt ttgcaaacca atccaaat 240
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tagggtcagt tagaaacatt gataaacaga ttttatcaaa cttgacaatt ttatggaatg 1500

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tgaaagattt acggaatgat caagttggat attatattac tgggtgctatt tctaaacata 4380

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attcttttaa ttttaaagt tgtaaattta gaattaagat taatcaaaga gattttaatc 4440  
 aaaaatcaga aattgtttgt gttagagtga aaggatctaa agttacaact gatactttat 4500  
 tttgtgaaat tgaaaaggtc ttactcaaag aagggtggtt agataaataa 4550

<210> 336

<211> 1349

<212> PRT

<213> Candida albicans

<400> 336

~~Met Pro His Ser Arg Gln Pro Ser Ile Ser Ser Ser Ile Met Ser Gln~~

1 5 10 15

Ser Asn His Asn His Pro Gln Lys Ile Gly Pro Trp Lys Leu Gly Lys  
 20 25 30

Thr Leu Gly Arg Gly Ala Thr Gly Arg Val Leu Leu Ala Thr His Gln  
 35 40 45

Thr Thr Gly Gln Lys Ala Ala Val Lys Val Val Ser Lys Ser Glu Leu  
 50 55 60

Gln Asp Glu Glu Thr Glu Lys Asn Gly Asp Gly Leu Pro Tyr Gly Ile  
 65 70 75 80

Glu Arg Glu Ile Ile Ile Met Lys Leu Leu Thr His Pro Asn Val Leu  
 85 90 95

Arg Leu Tyr Asp Val Trp Glu Thr Ser Lys Ala Leu Tyr Leu Val Leu  
 100 105 110

Glu Tyr Val Glu Gly Gly Glu Leu Phe Asp Leu Leu Val Glu Arg Gly  
 115 120 125

Pro Leu Pro Glu Val Glu Ala Ile Lys Tyr Phe Arg Gln Ile Ile Leu  
 130 135 140

Gly Thr Ala Tyr Cys His Ala Leu Gly Ile Cys His Arg Asp Leu Lys  
 145 150 155 160

Pro Glu Asn Leu Leu Leu Asp Ser Gln Leu Asn Val Lys Leu Ala Asp  
 165 170 175

Phe Gly Met Ala Ala Leu Glu Ser Asn Gly Lys Leu Leu Glu Thr Ser  
 180 185 190

Cys Gly Ser Pro His Tyr Ala Ala Pro Glu Ile Val Ser Gly Leu Lys

407

195	200	205
Tyr His Gly Ala Ala Ser Asp Val Trp Ser Cys Gly Val Ile Leu Phe 210	215	220
Ala Leu Leu Thr Gly Arg Leu Pro Phe Asp Asp Glu Asn Ile Arg Asn 225	230	235 240
Leu Leu Leu Lys Val Gln Ala Gly Asn Phe Glu Met Pro Val Asp Glu 245	250	255
<hr/>		
Val Ser Arg Glu Ala Arg Asp Leu Ile Ala Arg Met Leu Glu Val Asp 260	265	270
Pro Met Arg Arg Ile Ser Thr Glu Lys Ile Leu Arg His Pro Leu Leu 275	280	285
Thr Lys Tyr Pro Met Ser Asn Glu Asp Leu Ile Ser Glu Lys Ser Leu 290	295	300
Pro His Pro His Thr Gly Tyr Lys Ser Leu Gly Ser Val Arg Asn Ile 305	310	315 320
Asp Lys Gln Ile Leu Ser Asn Leu Thr Ile Leu Trp Asn Asp Arg Pro 325	330	335
Glu Glu Glu Ile Val Asp Cys Leu Leu Lys Asp Gly Ser Asn Pro Glu 340	345	350
Lys Thr Phe Tyr Ala Leu Leu Met Arg Tyr Lys His Asn Gln Asp Asp 355	360	365
Asn Thr Asn Asn Asn Ser Pro Lys Lys Ser Thr Ser Phe Asn Asn Lys 370	375	380
Val Val Arg Ser Gly Ser Lys Tyr Ser Leu Asn Gly Thr Pro Arg Arg 385	390	395 400
Lys Arg Ala Ser His Ile Ser Val Ser Arg Pro Thr Ser Phe Gln Tyr 405	410	415
Lys Ser Asn Pro Gly Ala Gly Ala Thr Ala Asn Arg Asn Ser Val Ala 420	425	430
Arg His Ser Val Ala Ser Ser Ala Asn Asn Ser Pro Arg Lys Ser Pro 435	440	445
Tyr Lys Ser Pro Tyr Arg Ser Pro Tyr Arg Ser Pro Tyr Lys Ser Pro		

450                      455                      460  
 Ser Lys Arg Tyr Ser Tyr Asn Gln Ser Pro Thr Lys Ser Pro Tyr Gly  
 465                      470                      475                      480  
 Arg Arg Ser Asn Ser Gln Arg Gln Phe Glu Asn Glu Pro Leu Lys Ala  
 485                      490                      495  
 Lys Pro Arg Asn Ile Tyr Asn Glu Ile Val Asp Ala Gln Ser Asn Phe  
 500                      505                      510  


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~~Ser Leu Pro Pro Ser Leu Pro Pro Ser Leu Pro Ser Lys Asp Ser Arg~~  
 515                      520                      525  
 Tyr Met Ile Asp Glu Pro Asn Gln Pro Gln Leu Gln Gln Pro Ala Leu  
 530                      535                      540  
 Ser Gln Val Pro Glu Asn Pro Ile Val Asp Glu Ser Pro Asp Leu Met  
 545                      550                      555                      560  
 Gln Ser Ala Lys Ile Ser Ser Gly Lys Arg Asn Ser Ile Ile Gly Lys  
 565                      570                      575  
 Asn Asn Asn Asn Ser Asn Ser Asn Lys Arg Met Ser Lys Arg Lys Ser  
 580                      585                      590  
 Ile Arg Ala Ser Met Thr Thr Gly Leu Lys Arg Asn Ser Ile Thr Met  
 595                      600                      605  
 Lys Leu Leu Ser Thr Tyr Ala Lys Leu Ser Gly Asp Asp Asp Trp Glu  
 610                      615                      620  
 Tyr Met Asp Lys Gln Thr Lys Arg Thr Ser Ala Thr Phe Ala Ala Leu  
 625                      630                      635                      640  
 Cys Asp Lys Ile Phe Asn Gln Glu Asp Tyr Asp Glu Glu Asp Glu Gln  
 645                      650                      655  
 Leu Val Asp Pro Glu Glu Lys Glu Ala Lys Glu Tyr Glu Arg Leu Met  
 660                      665                      670  
 Glu Leu Glu Arg Lys Lys His Glu Ala Glu Leu Lys Ala Arg Arg Glu  
 675                      680                      685  
 Leu Glu Lys Lys Lys Arg Arg Gln Lys Arg Arg Ser Ile Leu Ser Ser  
 690                      695                      700  
 Lys Lys Leu Ser Ile Ile Val Lys Asn Asp Ala Asp Pro Asn Asn Ser

409

705		710		715		720
Glu Gln Glu Leu Val Asp Glu Gly Ile Lys Gln Pro Lys Arg Gln Ser						
	725			730		735
Lys Asn Leu Thr Ala Leu Arg Ala Leu Ser Glu Gly Asn His Ala Ser						
	740			745		750
Glu Glu Leu Thr Leu Glu Asp Val Glu Asn Leu Lys Arg Arg Ser Ala						
	755			760		765

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Ser Gln Pro Val Pro Lys Arg Arg Gln Thr Pro Val Leu Thr Arg Arg						
	770			775		780
Pro Val Ser Arg Leu Asp Pro Leu Trp Gln Ala His Glu Asn Glu Gln						
	785			790		795
Leu Asp Arg Ala Lys Asp Ala Leu Glu Gln Glu Trp Arg Asp Ser Gln						
		805		810		815
Lys Arg Ser Ser Thr Val Ser Arg Lys Lys Val Asn Arg Glu Ser Met						
	820			825		830
Ile Ser Val Met Asp Asp Ile Val Glu Glu Asp Gln Gly Arg Val Asn						
	835			840		845
Arg Arg Ser Thr Arg Asn Thr Tyr Tyr Glu Arg Glu Arg Asp Tyr Glu						
	850			855		860
Leu Pro Glu Pro Thr Val Glu Asp Ser Asn Leu Thr Asp Asp Tyr Met						
	865			870		875
Thr Glu Ile Arg Lys Ser Arg Leu Leu Asn Ser Gln Leu Asn Val Arg						
		885		890		895
Asp Pro Leu Asn Glu Lys Arg Lys Ser Glu Pro Lys Thr Leu Ile Ser						
	900			905		910
Asn Val Gln Ile Pro Ser Val Thr Arg Lys Ser Arg Asn Phe Thr Thr						
	915			920		925
Ser Asn Lys Arg Leu Ser Val Leu Ser Met Tyr Ser Thr Lys Glu Ser						
	930			935		940
Tyr Arg Asp Leu Asn Ser Ile Ile Asn Ser Pro Asp Glu Asn Pro Glu						
	945			950		955
						960
Gln His Gln Asn Met Asn Lys Pro Ala Leu Arg Thr Ser Ile Ala Asp						

410



965

970

975

Arg Leu Asp Lys Ala Gly Leu Ala Glu Pro Glu Tyr Glu Thr Glu Thr  
 980 985 990

Asp Gly Glu Asp Lys Val Ser Val Ile Asp Leu Asp Asp His Leu Ala  
 995 1000 1005

Asp Arg Arg Thr Ser Tyr Tyr Asp Gly Ser Gly Lys Arg Ala Ser Arg  
 1010 1015 1020

~~Ala Ser Thr Thr Lys Arg Tyr Asn Val His Ser Ser Ser Glu Lys Arg~~  
 1025 1030 1035 1040

Pro Lys Ser Lys Val Pro Asp Leu Pro Lys Asn Asp Tyr Asp Asp Thr  
 1045 1050 1055

Phe Val Ser Asn Ser Asp Glu Val His Lys Arg Gln Tyr Lys Ser Met  
 1060 1065 1070

Val Ser Asp Glu Ser Ser Ala Ser Asp Asp Val Phe Asp Lys Ile Lys  
 1075 1080 1085

Leu Pro Asp Gly Lys Ser Thr Lys Ser Ser Ile Asp Glu Leu Ala Asn  
 1090 1095 1100

Gly Thr Ser Thr Ser Gly His Arg Lys Pro Lys Ile Arg His Ser Gln  
 1105 1110 1115 1120

Pro Gly Pro Glu Met Leu Ile Pro His Leu Asn Gly Gly Ile Glu Ser  
 1125 1130 1135

Ser Gln Pro Met Ser Lys Val Arg Gly Asn Asn Ser Ser Gly His Asp  
 1140 1145 1150

Asp Ser Val Pro Pro Pro Pro Pro Ala His Lys Val Asn Lys Lys Pro  
 1155 1160 1165

Leu Asp Asp Lys Thr Asn Phe Pro Pro Pro Glu Val Asp Pro Lys Arg  
 1170 1175 1180

Lys Gly Ser Phe Phe Arg Lys Leu Ser Trp Gly Ser Lys Lys Thr Ile  
 1185 1190 1195 1200

Glu Asn Asn Thr Asn Ala Ala Thr Asn Thr Thr Thr Gln Gln Gln Leu  
 1205 1210 1215

Pro Ser Pro Ala Glu Ser Lys Glu Glu Lys Pro Lys Ser Ser Phe Phe

411

1220

1225

1230

Arg Trp Phe Ser Ser Ser Asn Thr Pro Ser Ala Ala Glu Ile Arg Lys  
 1235 1240 1245

Phe Asn Thr Ile Leu Pro Lys His Glu Met Ser Thr Ala Leu Phe Ala  
 1250 1255 1260

Leu Leu Asn Ser Trp Ser Asn Phe Gly Leu Lys Asp Leu Arg Asn Asp  
 1265 1270 1275 1280

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Gln Val Gly Tyr Tyr Ile Thr Gly Ala Ile Ser Lys His Asn Ser Phe  
 1285 1290 1295

Asn Leu Lys Ser Cys Lys Phe Arg Ile Lys Ile Asn Gln Arg Asp Phe  
 1300 1305 1310

Asn Gln Lys Ser Glu Ile Val Cys Val Arg Val Lys Gly Ser Lys Val  
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Thr Thr Asp Thr Leu Phe Cys Glu Ile Glu Lys Val Leu Leu Lys Glu  
 1330 1335 1340

Gly Gly Leu Asp Lys  
 1345

<210> 337

<211> 1121

<212> DNA

<213> Candida albicans

<400> 337

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 gaaaaaccag aattgctggt gtcgtttacc atccatctaa taacgaattg gtagaacca 780  
 acaccttgac caaatctgct gttgttcaaa ttgatgtac tccattcaga caatgggtacg 840

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gtgctgctgc cattgaatcc gctgttgact ctcaattcgg ttctggtaga ttatacgctg 1020
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```

&lt;210&gt; 338

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 338

```

Met Gly Ile Ser Arg Asp Ser Arg His Lys Arg Ser Ala Thr Gly Ala
  1             5             10             15

```

```

Lys Arg Ala Gln Phe Arg Lys Lys Arg Lys Phe Glu Leu Gly Arg Gln
          20             25             30

```

```

Pro Ala Asn Thr Lys Ile Gly Pro Lys Arg Ile His Ser Val Arg Thr
      35             40             45

```

```

Arg Gly Gly Asn Gln Lys Phe Arg Ala Leu Arg Val Glu Thr Gly Asn
      50             55             60

```

```

Phe Ser Trp Gly Ser Glu Gly Val Ser Arg Lys Thr Arg Ile Ala Gly
      65             70             75             80

```

```

Val Val Tyr His Pro Ser Asn Asn Glu Leu Val Arg Thr Asn Thr Leu
          85             90             95

```

```

Thr Lys Ser Ala Val Val Gln Ile Asp Ala Thr Pro Phe Arg Gln Trp
      100             105             110

```

```

Tyr Glu Asn His Tyr Gly Ala Thr Leu Gly Lys Lys Lys Gly Gly Ala
      115             120             125

```

```

His Ala Ala His Ala Ala Glu Val Ala Asp Ala Lys Arg Ser Arg Lys
      130             135             140

```

```

Val Glu Arg Lys Leu Ala Ala Arg Ser Gly Ala Ala Ala Ile Glu Ser
      145             150             155             160

```

```

Ala Val Asp Ser Gln Phe Gly Ser Gly Arg Leu Tyr Ala Val Ile Ser
          165             170             175

```

```

Ser Arg Pro Gly Gln Ser Gly Arg Cys Asp Gly Tyr Ile Leu Glu Gly
      180             185             190

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413

Glu Glu Leu Ala Phe Tyr Leu Arg Arg Leu Thr Ala Lys Lys  
 195 200 205

<210> 339  
 <211> 819  
 <212> DNA  
 <213> Candida albicans

<400> 339  
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 agcattcgtc caaattgaga ccctcaatta cattttgtca aaaaaattgg tccctagtgt 180  
 tgctatcgat aacgaagggtg aaggcagttt agcttggaga catttagaga acttagttac 240  
 atctcatctt ccgtttcgag aaatcggtga tttaccgtgc agcgcttata ttgattgcta 300  
 cttgttccca gcaccacagc aatatagcaa tcataaataa attgccccgc ggttgacagt 360  
 gtatatcttc gaggaatggc aacctttgcc cccctctcga aaaacaatat aaatagagtc 420  
 aattttctcta gtagaggtaa attctttgaa tcttgttttt tttcgacata caccataaat 480  
 cccatagaaa actgcaaaat gtctgacgcc ggaagaaaaa acatttctac taaaatcaac 540  
 gaagctataa cccccgaatc cgaaaagtct accttggaaa agggcaagga acaagtcacc 600  
 agtacccttg acaaagctgt tggctcaaat gttccagata accaaaaatc tttcactcaa 660  
 actgttgcag acagcgtgca acaaggttcc gataatgcta aagctgattt gaagaaacaa 720  
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 ttgccaaaac tgaaattgga aaggctgctg aatactgta 819

<210> 340  
 <211> 106  
 <212> PRT  
 <213> Candida albicans

<400> 340  
 Met Ser Asp Ala Gly Arg Lys Asn Ile Ser Thr Lys Ile Asn Glu Ala  
 1 5 10 15  
 Ile Thr Pro Glu Ser Glu Lys Ser Thr Leu Glu Lys Gly Lys Glu Gln  
 20 25 30  
 Val Thr Ser Thr Leu Asp Lys Ala Val Gly Ser Asn Val Pro Asp Asn  
 35 40 45  
 Gln Lys Ser Phe Thr Gln Thr Val Ala Asp Ser Val Gln Gln Gly Ser  
 50 55 60  
 Asp Asn Ala Lys Ala Asp Leu Lys Lys Gln Ser Glu Gln Ala Glu Gly  
 65 70 75 80

414

Glu Gln Arg Pro Leu Ser Lys Gln Leu Lys Asn Met Ser Arg Leu Pro

85

90

95

Lys Ser Lys Leu Glu Arg Ser Ser Asn Thr

100

105

&lt;210&gt; 341

&lt;211&gt; 884

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 341

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ccttctcctg tgaaaagttt cgagatgtaa cgtttcgcag taatagagag ccagaatcca 60
tttttggtga ctacagacaa attcagaagt ttcaactgct gcatatcgcc ttaaatgact 120
gtagcattcg tccaaattga gacctcaat tacattttgt caaaaaaatt ggtccctagt 180
gttgctatcg ataacgaagg tgaaggcagt ttagcttgga ggcatctaga gaacttagtt 240
acatctcatc ttccgtttcg agaaatcggt gatttaccgt gcagcgctta tattgattgc 300
tacttggtcc cagcaccaca gcaatatagc aatcataaat aaattgcccc gcggttgaca 360
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&lt;210&gt; 342

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 342

Met Ser Asp Ala Gly Arg Lys Asn Ile Ser Thr Lys Ile Asn Glu Ala

1

5

10

15

Ile Thr Pro Glu Ser Glu Lys Ser Thr Leu Glu Lys Gly Lys Glu Gln

20

25

30

Val Thr Ser Thr Leu Asp Lys Ala Val Gly Ser Asn Val Pro Asp Asn

35

40

45

Gln Lys Ser Phe Thr Gln Thr Val Ala Asp Asn Val Gln Gln Gly Ser

415

50

55

60

Asp Asn Ala Lys Ala Asp Leu Lys Lys Gln Ser Glu Gln Ala Glu Gly  
65 70 75 80

Glu Ala Lys Thr Leu Ala Glu Thr Ala Gln Glu Tyr Val Glu Val Ala  
85 90 95

Lys Thr Glu Ile Gly Lys Ala Ala Glu Tyr Val Ser Gly Val Val Thr  
100 105 110

Gly Ala Thr Glu Gly Ala Lys Thr Gly Ala Asp Ser Thr Lys Lys  
115 120 125

&lt;210&gt; 343

&lt;211&gt; 1244

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 343

gaagggcacc ataatgaaat cgactcactt caggattata atggtatgaa acattgtact 60  
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cggttgtaaa cgtatctggt tcacttatca gtatcgatcat ttatattaac tacttttctc 180  
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aaattgtcaa taaaagaaac aaagaatgaa agaatgattg aatgaaagaa aaaaaaata 300  
tgaaagttag tgcgacataa ttagaataaa tgcgaatgt cttgaacttt acccattgag 360  
tagttgttgt agtgtaggag gaagaaaaca acagaaagaa agagagaaag aaaaatttcg 420  
ccactacaaa tattcaacaa gtttcatata gtaataataat cccaattgat cattacttta 480  
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aagaaataga cgaaagattg atttcaatag ctgaacaaga ttag 1244

&lt;210&gt; 344

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 344

Met Ser Asn Ser Ala Gly Phe Asp Arg His Ile Thr Ile Phe Ser Pro  
 1 5 10 15

Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Phe Lys Ala Ile Asn Ser  
 20 25 30

Ala Asn Ile Thr Ser Leu Gly Ile Thr Gly Gln Asp Ser Ala Val Ile  
 35 40 45

Ile Ser Gln Lys Lys Ile Pro Asp Lys Leu Leu Asp Pro Lys Thr Val  
 50 55 60

Ser Tyr Ile Phe Lys Ile Thr Pro Ser Ile Gly Met Val Ala Thr Gly  
 65 70 75 80

Ser Ile Ala Asp Ala Arg Ala Gln Ala Met Arg Ala Arg Ser Glu Ala  
 85 90 95

Thr Glu Phe Arg Tyr Lys Tyr Gly Tyr Glu Met Pro Val Glu Ser Leu  
 100 105 110

Ser Arg Arg Met Ala Asn Ile Ser Gln Leu Tyr Thr Gln Arg Ala Tyr  
 115 120 125

Met Arg Pro Leu Gly Val Ala Leu Thr Phe Ile Gln Val Asp Phe Ala  
 130 135 140

Asp Glu Gly Arg Gly Pro Gln Ile Phe Lys Cys Asp Pro Ala Gly Tyr  
 145 150 155 160

Phe Thr Gly Val Lys Ala Val Ala Thr Gly Pro Lys Gln Gln Glu Ala  
 165 170 175

Thr Thr Tyr Leu Glu Lys Lys Phe Lys Lys Thr Asp Ala Val Lys Gly  
 180 185 190

Asp Trp Gln Lys Thr Val Glu Phe Ala Ile Ile Ala Leu Ser Ser Val  
 195 200 205

Ile Gly Thr Glu Phe Arg Lys Asn Asp Ile Glu Ile Gly Val Ala Thr  
 210 215 220

Glu Gly Glu Phe Arg Ile Leu Thr Pro Glu Glu Ile Asp Glu Arg Leu  
 225 230 235 240

Ile Ser Ile Ala Glu Gln Asp  
245

<210> 345

<211> 968

<212> DNA

<213> Candida albicans

<400> 345

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<210> 346

<211> 155

<212> PRT

<213> Candida albicans

<400> 346

Met Lys Ile Glu Val Asp Ser Phe Ser Gly Ser Lys Ile Tyr Pro Gly  
1 5 10 15

Arg Gly Thr Leu Phe Val Arg Gly Asp Ser Lys Ile Phe Arg Phe Gln  
20 25 30

Ser Ser Lys Ser Ala Ser Leu Phe Gln Gln Arg Lys Asn Pro Arg Arg  
35 40 45

Ile Ser Trp Thr Val Leu Tyr Arg Arg His His Lys Lys Gly Ile Ser  
50 55 60



Glu Glu Ala Ala Lys Lys Arg Thr Arg Lys Thr Val Lys His Gln Arg  
65 70 75 80

Ala Ile Val Gly Ala Ser Leu Glu Leu Ile Lys Glu Arg Arg Ser Gln  
85 90 95

Lys Pro Ser Asp Arg Lys Ala Ala Arg Asp Ser Lys Leu Ala Lys Asp  
100 105 110

Lys Glu Ala Lys Lys Ala Ala Lys Ala Ala Arg Lys Ala Glu Lys Ala  
115 120 125

Lys Ala Val Ala Ser Gly Ala Ser Val Val Ser Lys Gln Gln Ala Lys  
130 135 140

Gly Ser Phe Gln Lys Val Lys Ala Thr Ser Arg  
145 150 155

<210> 347

<211> 1418

<212> DNA

<213> Candida albicans

<400> 347

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aacttcacat ctaatactgg tccaactgat cttgcaatat cccgcacctg ttcttcagtg 180  
taatcaaagt gaaatttacc tattgaaaca caagtgcctt tactatccat atttagtttg 240  
agctgcctag ttttctgat tcttggtaac aaaaaactat aattatttaa caaattatcg 300  
atagaatctc ttccaaagta caaccaattt cgatacattt ttttctatga gatgtttttt 360  
tcccctttgt ctttaactaa tgtatttggg tacactacct gaacctacca gttcagttca 420  
gtctaaaaaa ttttttattt attgtgtttg tttatactac cctttgcata tattactaat 480  
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aaaaagcagt agatgacacc accattttta agttgttgaa tatcttgaat gatgggggta 600  
aaccatccga aaaactcttg agagaaacca aagtaggtgt agctgtcaac aaattcagaa 660  
gtcacgacag tgccgaaatc aacggtttag ttaaaaaaat gatcagaaat tggagagatg 720  
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aaccatcaga gtcaaccaca ccatcggctg cccgtaaagg tccaagaaat ccaaaaactg 900  
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<210> 348

<211> 305

<212> PRT

<213> Candida albicans

<400> 348

Met Asp Thr Lys Glu Ile Arg Ser Thr Val Ser Asn Leu Glu Lys Ala

1

5

10

15

Val Asp Asp Thr Thr Ile Leu Lys Leu Leu Asn Ile Leu Asn Asp Gly  
 20 25 30

Val Lys Pro Ser Glu Lys Leu Leu Arg Glu Thr Lys Val Gly Val Ala  
 35 40 45

Val Asn Lys Phe Arg Ser His Asp Ser Ala Glu Ile Asn Gly Leu Val  
 50 55 60

Lys Lys Met Ile Arg Asn Trp Arg Asp Ala Val Gln Ala Glu Lys Asn  
 65 70 75 80

Asn Lys Lys Lys Leu Ala Ile Ala Ala Gly Thr Gly Thr Gly Thr Pro  
 85 90 95

Ser Ser Ser Ala Ile Ser Pro Ser Ser Ser Gly Ser Gly Ser Thr Thr  
 100 105 110

Pro Lys Pro Ser Glu Ser Thr Thr Pro Ser Ala Ala Arg Lys Gly Pro  
 115 120 125

Arg Asn Pro Lys Thr Asp Gly Val Asn Thr Gln Leu Tyr Glu Asn Asp  
 130 135 140

Thr Arg Asn Ala Ser Val Ser Ala Leu Tyr Thr Ser Leu Ala Val Asp  
 145 150 155 160

Arg Asp Asp Ser Pro Lys His Ile Leu Arg Ile Ala Ile Glu Ile Glu  
 165 170 175

Ala Glu Val Tyr Lys Ser Glu Tyr Ser Lys Val Ser Asp Ser Tyr Arg  
 180 185 190

Asn Arg Leu Arg Ser Phe Thr Met Asn Leu Arg Asn Lys Lys Asn Pro  
 195 200 205

420

Glu Leu Arg Glu Arg Ile Leu Ser Lys Gln Ile Leu Pro Ala Ala Phe  
210 215 220

Ile Lys Met Thr Pro Asn Glu Met Ala Pro Glu Ala Leu Lys Lys Glu  
225 230 235 240

Ile Glu Lys Leu His Lys Gln Asn Leu Phe Asp Ala Gln Gly Ala Thr  
245 250 255

Glu Lys Arg Ala Val Thr Asp Arg Phe Thr Cys Gly Lys Cys Lys His  
260 265 270

Lys Lys Val Ser Tyr Tyr Gln Met Gln Thr Arg Ser Ala Asp Glu Pro  
275 280 285

Leu Thr Thr Phe Cys Thr Cys Glu Asn Cys Gly Asn Arg Trp Lys Phe  
290 295 300

Ser  
305

<210> 349

<211> 1301

<212> DNA

<213> Candida albicans

<400> 349

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acaaagggtta agcattcgta ccaggaagtc tggaattaaa cggtagttac ttccagtata 180  
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gaatgaaaat gaaaaaaaaa agaataattt tgtagatcgc atagtgtgag cgcgcacaca 360  
cacacaaact ttgtagtgtt acagtttctc tctttcccat acactctcgc agtcgcacgc 420  
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<210> 350

<211> 149

<212> PRT

<213> Candida albicans

<400> 350

Met Pro Thr Arg Leu Thr Lys Thr Arg Lys His Arg Gly Asn Val Ser  
 1 5 10 15

Ala Gly Lys Gly Arg Ile Gly Lys His Arg Lys His Pro Gly Gly Arg  
 20 25 30

Gly Lys Ala Gly Gly Gln His His His Arg Thr Asn Leu Asp Lys Tyr  
 35 40 45

His Pro Gly Tyr Phe Gly Lys Val Gly Met Arg Tyr Phe His Lys Gln  
 50 55 60

Gln Asn His Phe Trp Arg Pro Glu Ile Asn Leu Asp Lys Leu Trp Thr  
 65 70 75 80

Leu Val Asp Ser Glu Lys Lys Asp Glu Tyr Leu Ser Lys Ser Ser Ala  
 85 90 95

Ser Ala Ala Pro Val Ile Asp Thr Leu Ala His Gly Tyr Gly Lys Val  
 100 105 110

Leu Gly Lys Gly Arg Leu Pro Glu Val Pro Val Ile Val Lys Ala Arg  
 115 120 125

Phe Val Ser Lys Leu Ala Glu Glu Lys Ile Arg Ala Val Gly Gly Val  
 130 135 140

Val Glu Leu Val Ala  
 145

<210> 351

<211> 423

<212> DNA

<213> Candida albicans

&lt;400&gt; 351

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 gttgaaatta gaaatttctt gggtgaaaaa agagtttagag aagttaaaat ccatgaaggt 240  
 gtcaccatgg aaatttcttc tactcaaaag gatgaattga ttgtttctgg taactccttg 300  
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 atccgtaaat tcttggatgg tatttatgtt tctgaaagag gtaccattgt tgaagaaatc 420  
 taa 423

&lt;210&gt; 352

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 352

Ala Ile Lys Ile Thr Val His Asn Gly Asp Arg Lys His Val Ala Ala  
 1 5 10 15

Leu Arg Thr Val Lys Ser Leu Ile Ala Asn Leu Ile Thr Gly Val Thr  
 20 25 30

Lys Gly Tyr Lys Tyr Lys Met Arg Phe Val Tyr Ala His Phe Pro Ile  
 35 40 45

Asn Val Asn Ile Ile Lys Lys Asp Gly Gln Asp Tyr Val Glu Ile Arg  
 50 55 60

Asn Phe Leu Gly Glu Lys Arg Val Arg Glu Val Lys Ile His Glu Gly  
 65 70 75 80

Val Thr Met Glu Ile Ser Ser Thr Gln Lys Asp Glu Leu Ile Val Ser  
 85 90 95

Gly Asn Ser Leu Glu Ala Val Ser Gln Asn Ala Ala Asp Ile Gln Gln  
 100 105 110

Ile Cys Arg Val Arg Asn Lys Asp Ile Arg Lys Phe Leu Asp Gly Ile  
 115 120 125

Tyr Val Ser Glu Arg Gly Thr Ile Val Glu Glu Ile  
 130 135 140

&lt;210&gt; 353

423

&lt;211&gt; 1655

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 353

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ttagagggtg ctctggtggt gacagcaatg aaggattatg tgctgtgagt ttcgatagag 1620
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&lt;210&gt; 354

&lt;211&gt; 384

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 354

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Met Gly Lys Gln Tyr Ile Ser Thr Val Ser Ala Ser Gln Ala His Lys
  1                      5                      10                     15

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```

Ser Asp Ile Leu Gly Val Ala Ile Thr Asn Lys Phe Thr Val Ser Val
      20                      25                      30

```

```

Ser Ser Asp Gly Tyr Ala Lys Phe Trp Asp Asn Lys Gln Asp Glu Val

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35	40	45
His Ser Pro Lys Glu Phe Val Gln Ser Val Phe Ile Asp Lys Ser Gly		
50	55	60
Ile His Ala Val Ala Ala Tyr Glu Asn Val Leu Pro Ser Ser Thr Leu		
65	70	75 80
Lys Val Thr Leu Leu Ala Phe Ala Cys Phe Asn Gly Ser Ile Ile Phe		
85	90	95
<hr/>		
Arg Tyr Tyr Ile Asn Asp Asp Phe Ser Thr Ile Glu Ser Leu Thr Asp		
100	105	110
Asp Ile Lys Ser Phe Glu Ser Asn Cys Trp Thr Pro Gly Phe Tyr Arg		
115	120	125
Asp Pro Glu Ser Lys Gln Asp Tyr Phe Ile Thr Thr Lys Thr Asn Gly		
130	135	140
Thr Thr Glu Val His Leu Leu Asn Ile Val Asp Glu Asn Glu Lys Ala		
145	150	155 160
Val Ile Thr Phe Glu Lys Phe Gly Gln Leu Lys Gly Asn Ser Ser Ser		
165	170	175
Phe Pro Asn Ser Leu Ala Ile Cys Pro Thr Glu Asn Lys Lys Cys Ala		
180	185	190
Val Gly Tyr Ile Asn Gly Asp Val Leu Leu Tyr Asp Phe Val Ser Leu		
195	200	205
Lys Leu Ile Tyr Thr Phe Arg Ser Ser Asp Leu Val Thr Ser Arg Asn		
210	215	220
Ser Gln Ser Thr Ser Ile Pro Arg Val Leu Ala Phe Ser Pro Gly Gly		
225	230	235 240
Thr Leu Leu Ala Val Ala Arg Asp Asn Gln Ala Ala Gly Ser Ile Thr		
245	250	255
Leu Tyr Asp Val Glu His Gly Glu Asn Val Gly Ser Leu Ala Thr Pro		
260	265	270
Ser His Ser Ala Lys Ser Val Val Gly Gly Phe Ala His Gln Gly Trp		
275	280	285
Ile Leu Gly Leu Ser Phe Asp Glu Glu Gly Lys His Leu Ala Ser Cys		

425

290                      295                      300  
 Gly Phe Asp Lys Cys Ile Arg Val Trp Asn Leu Glu Thr Ser Glu Arg  
 305                      310                      315                      320  
 Glu Ala Thr Ile Ser Ile Ser Ile Ser Asp Leu Asp Asp Thr Thr His  
                     325                      330                      335  
 Asn Asp Gln Asp Glu Ser Val Ala Ser Gly Val Ala Phe Ile Lys Lys  
                     340                      345                      350

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Gly Val Arg Gly Gly Ser Gly Gly Asp Ser Asn Glu Gly Leu Cys Val  
                     355                      360                      365  
 Val Ser Phe Asp Arg Gly Ile Arg Trp Tyr Arg Glu Ala Gly Gly Ile  
                     370                      375                      380

&lt;210&gt; 355

&lt;211&gt; 1418

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 355

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 catttgtaaa tgtagatgga taaagtaagt tgattgtata aaaaaagaat ggattcatta 180  
 atataaattt acaaatctga taataaacta cagtaactat tatgcaacaa ttgaaagtat 240  
 cctgtgtcac gtgattaggg ctcaaaagcc ctaacagggt gcacgtgatg ttgatttatt 300  
 tatccctgca cacattgagt tttttttcta tggtgaaaat tattagttag acgatgttgt 360  
 tcgcatttta ccacacactc tcacactgag tgtagtcata ctaacaatct tctcacacta 420  
 tacacaaaaa aaatctttcg tttgaaaagt tttgaaaggt tcgttttctc aatagtatat 480  
 ccatacaata actgccaaag atggtatggt caagtgttta aagagatcga aatgttttgt 540  
 ttttaattgga agtgatatca taatgagaaa atatgggaaa tagagatagg accgaattaa 600  
 ttgaaagagt tttcttttgg ggaaatgggt tcaataagat ttttcaagat tggaatcaaa 660  
 ttatgtcaga tgtgaagaag agtaaatata acaagaagtt caaatcatta aaaattttat 720  
 gtaaatacaa cgattatcaa ttacagtcaa cgaatagaat aaaacaaaag ccagcatata 780  
 acagatacca gtgattcatc ccagtgatat aaataatgat attcaattaa aaacaatatt 840  
 aagacatttt ttatttatgt atcaacaaaa tactaactta tctttctttt aattagtctg 900  
 acaaatccca aaatgttatg cgtgaattac gtattgaaaa attagtttta aacatttgtg 960  
 ttggtgaatc cgggtgataga ttaaccagag ccgccaaagt tttagaacaa ttatctggtc 1020  
 aaaccccagt tcaatctaaa gctagataca ctgtcagaac tttcggtatt agaagaaatg 1080  
 aaaaaattgc cgtccacgtt actgtcagag gtccaaaagc tgaagaaatc ttggaaagag 1140  
 gtttgaaagt taaagaatat caattaagat ctaaaaactt ctctgctacc ggtaactttg 1200



gtttcggtat tgatgaacat attgatttag gstatcaaata tgatccatct attgggtattt 1260  
 acggtatgga tttctacgtt gttatgggta gagccgggtgc tagagtcacc agaagaaaga 1320  
 gagctagatc cactattggt aactctcaca aaaccaacaa agaagatacc atccaatggt 1380  
 tcaagaccag atacgatgct gaagttttgg ataaataa 1418

<210> 356

<211> 174

<212> PRT

<213> Candida albicans

<400> 356

Met Ser Asp Lys Ser Gln Asn Val Met Arg Glu Leu Arg Ile Glu Lys  
 1 5 10 15

Leu Val Leu Asn Ile Cys Val Gly Glu Ser Gly Asp Arg Leu Thr Arg  
 20 25 30

Ala Ala Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser  
 35 40 45

Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys  
 50 55 60

Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu  
 65 70 75 80

Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Ser Lys Asn Phe  
 85 90 95

Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu  
 100 105 110

Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Tyr Gly Met Asp Phe Tyr  
 115 120 125

Val Val Met Gly Arg Ala Gly Ala Arg Val Thr Arg Arg Lys Arg Ala  
 130 135 140

Arg Ser Thr Ile Gly Asn Ser His Lys Thr Asn Lys Glu Asp Thr Ile  
 145 150 155 160

Gln Trp Phe Lys Thr Arg Tyr Asp Ala Glu Val Leu Asp Lys  
 165 170

<210> 357

<211> 919  
 <212> DNA  
 <213> Candida albicans

<400> 357

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tcataattgac atgataagga tttatcaata ctgttaggtc tatagcccta actttaatca 180
tttacacgtg atacaaaaaa gttgtttgat cccgcacgac tatgagtacg cactcactaa 240
ttatagcctg aaaaaaaaaa tttccacata gtaaggggat tttgtatggt ggtgcgctcg 300
cctaagacgt ctgcatacat tttctaaagt cacactgata tagggatggt gtggtagtga 360
ttgtgtgttc ccaccaaata actttgcgga cactctcata tactcaattt ttttcttaca 420
aaaatttttt ttcttctact tttttcaaga attcttcttt tacaattcaa caacatcaat 480
catgggtaaa ggtaaaccac gagggcttaa ctctgctaga aaattaagag ttcacagaag 540
aaacaacaga tgggctgata aagcttataa agctagatta ttaggtaccg ctttcaaadc 600
ttctccattt ggtggttcat ctacgcacaa aggtatcggt ttggaaaaaa ttggtattga 660
atctaaacaa ccaaactctg ctatcagaaa atgtgtcaga gtccaattaa tcaaaaacgg 720
taagaaagtc actgctttcg ttccaaacga tgggtgtttg aactttgttg acgaaaatga 780
cgaagtcttg ttggctgggt tcggtagaag aggtaaagct aagggggata ttccaggggt 840
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agaaaagcca agatcatag                                     919
```

<210> 358  
 <211> 145  
 <212> PRT  
 <213> Candida albicans

<400> 358

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Met Gly Lys Gly Lys Pro Arg Gly Leu Asn Ser Ala Arg Lys Leu Arg
  1              5              10              15

Val His Arg Arg Asn Asn Arg Trp Ala Asp Gln Ala Tyr Lys Ala Arg
          20              25              30

Leu Leu Gly Thr Ala Phe Lys Ser Ser Pro Phe Gly Gly Ser Ser His
          35              40              45

Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ser Lys Gln Pro
          50              55              60

Asn Ser Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly
          65              70              75              80

Lys Lys Val Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Val
          85              90              95

Asp Glu Asn Asp Glu Val Leu Leu Ala Gly Phe Gly Arg Arg Gly Lys
```

428

100

105

110

Ala Lys Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser  
 115 120 125

Gly Val Ser Leu Leu Ala Leu Trp Lys Glu Lys Lys Glu Lys Pro Arg  
 130 135 140

Ser  
 145

<210> 359  
 <211> 1164  
 <212> DNA  
 <213> Candida albicans

<400> 359  
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 cacgaaatgt gggttgaaaa acttgagtc tcaaaaaggt tctctcgtaa aaggccagag 120  
 aaagaaaaaa ccaccaaacc cccaccacca acctaacctt ttccttccat ccattcctct 180  
 ttccttactt tgcaaagtgt gaatccagtt atattcatta aagatcctat aaaatacgat 240  
 tattcacaat ttattatatt tttactcccg aaattcatta attgtaatcg tattgattta 300  
 gttatacttt gtcaaatcac cgaatcaaat caattgaatg aaattttatg tttttattat 360  
 caattaattc gtaatcataa gaataatgga gatactgatg gagataccga cagtttgcct 420  
 atgtttgatt atcgatttga aattaatata ttatttaatt tatcaacaaa aaaattgaat 480  
 caattatgtt taaataattg gaatcatgga tatattgagg aagggtgataa tgataacagt 540  
 actaacttgt catctttgcc attgtcaata acacaaatat caaacattga aattccaaca 600  
 atccaatcaa gagcaaatag tagtagtgct tataatgatg aggatgataa aattactact 660  
 agtcggcaat atcaacaatt taaaactact gctgtaggtg gaacatttga tcatttacat 720  
 gatggtcata aaattttatt atcaatggca atttttttaa cttcaaataa attaattatt 780  
 ggtataactg gttctaattt attaatattt aaaaaattta aatctcaatt acaaactttt 840  
 aatcaaagac aaaatttagt tattcaattc ataaatttat tattattgag tgaaaccagt 900  
 gttatttttt ttgaaattta tgaaattaat gatgtttgtg gtccaactgg ttatattaat 960  
 gatattgata atttaataat atctcaagaa actaaatctg gtggtgaatt tgtaacaaa 1020  
 tttcgtaaag atcatggatt taaattatta gatattacaa taattaaagt gattggtggg 1080  
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<210> 360  
 <211> 322  
 <212> PRT  
 <213> Candida albicans

<400> 360  
 Met Leu Asn Pro Val Ile Phe Ile Lys Asp Pro Ile Lys Tyr Asp Tyr

429

1	5	10	15
Ser Gln Phe Ile Ile Ser Leu Leu Pro Lys Phe Ile Asn Cys Asn Arg			
20	25	30	
Ile Asp Leu Val Ile Leu Cys Gln Ile Thr Glu Ser Asn Gln Leu Asn			
35	40	45	
Glu Ile Leu Cys Phe Tyr Tyr Gln Leu Ile Arg Asn His Lys Asn Asn			
50	55	60	

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Gly Asp Thr Asp Gly Asp Thr Asp Ser Leu Pro Met Phe Asp Tyr Arg			
65	70	75	80
Phe Glu Ile Asn Ile Leu Phe Asn Leu Ser Thr Lys Lys Leu Asn Gln			
85	90	95	
Leu Cys Leu Asn Asn Trp Asn His Gly Tyr Ile Ala Glu Gly Asp Asn			
100	105	110	
Asp Asn Ser Thr Asn Leu Ser Ser Leu Pro Leu Ser Ile Thr Gln Ile			
115	120	125	
Ser Asn Ile Glu Ile Pro Thr Ile Gln Ser Arg Ala Asn Ser Ser Ser			
130	135	140	
Ala Tyr Asn Asp Glu Asp Asp Lys Ile Thr Thr Ser Arg Gln Tyr Gln			
145	150	155	160
Gln Phe Lys Thr Thr Ala Val Gly Gly Thr Phe Asp His Leu His Asp			
165	170	175	
Gly His Lys Ile Leu Leu Ser Met Ala Ile Phe Leu Thr Ser Asn Lys			
180	185	190	
Leu Ile Ile Gly Ile Thr Gly Ser Asn Leu Leu Ile Asn Lys Lys Phe			
195	200	205	
Lys Ser Gln Leu Gln Thr Phe Asn Gln Arg Gln Asn Leu Val Ile Gln			
210	215	220	
Phe Ile Asn Leu Leu Leu Leu Ser Glu Thr Ser Val Ile Phe Phe Glu			
225	230	235	240
Ile Tyr Glu Ile Asn Asp Val Cys Gly Pro Thr Gly Tyr Ile Asn Asp			
245	250	255	
Ile Asp Asn Leu Ile Ile Ser Gln Glu Thr Lys Ser Gly Gly Glu Phe			

430

260

265

270

Val Asn Lys Phe Arg Lys Asp His Gly Phe Lys Leu Leu Asp Ile Thr  
 275 280 285

Ile Ile Lys Val Ile Gly Gly Asn Ile Glu Glu Asn Ser Trp Lys Gly  
 290 295 300

Lys Leu Ser Ser Thr Asp Ile Arg Glu Gln Glu Tyr Asn Arg Leu Leu  
 305 310 315 320

Asn Gln

<210> 361  
 <211> 1427  
 <212> DNA  
 <213> Candida albicans

<400> 361  
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 gttataaaag aagggttgtga tttttttttt ccactgggtg tgggtggtgct gattgtactg 180  
 ctgttcactt tattgtttcg tttcgttttt cctttgtttt gttgacgttg acattttttt 240  
 tgctgttggt gttgtatggg aatttttgta ttagttgttc ttttttggtt ttttttactt 300  
 gttcaaagtt tcatataata ataatatctt tgttttcata tttttttttt cagaacaaga 360  
 acaaatataa cttatataat ttgatcttac tcttatcccc aggtttttct atttgttttt 420  
 gggtttgcca ttcatatata tatatctatt attcaaataa atttgaggag tatcattaat 480  
 ttaaatataa tcagttaaca atgtcgtatc gtggctctaa tcaatttggg aatcaacctc 540  
 cacatcatgg aataccttct caacctcaac cacatattgg tccaatatct tccagcaaaa 600  
 gtcccttaga acaatttgaa gatgttgcta aaaaagttga agattggatc gatgattatt 660  
 ttaaagtctt gaaaccatac gtcccagcaa ttggtagagc atttttggtg gccactttct 720  
 atgaggatac ttttaagaatc ttactcaat ggaatgaaca agtttattac ttgcacaact 780  
 atagacacta ttggcggttg ttgaccgttt tattcttgat caataatatg gtggttatga 840  
 cagttgcac cacttttaga attgccagaa aaaagaataa cattgctact attgcattga 900  
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 ataaaagatc cttaaacaatg ccagggtttac cgatgttgaa caatcaagac aacaaaaagt 1080  
 atttcctttt agctggtaga attttggttag tattattatt tttgggattc gtcttttctt 1140  
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 ttgttggttg ttacaagaca aagttttcag ctgctatcat gcttattggt ttattcttat 1260  
 acaatgtgtt cactaaccaa ttctgggctt atgcatctca agatgctaga cgtgactttt 1320  
 tgagatatga attcttccaa gttttgtcaa ttgtgggagg attattgtta gtgggttaatg 1380  
 caggtgctgg tgaattctcc atcgatgaaa agaaaaagat ttattaa 1427

431

<210> 362  
 <211> 308  
 <212> PRT  
 <213> Candida albicans

<400> 362

Met Ser Tyr Arg Gly Pro Asn Gln Phe Gly Asn Gln Pro Pro His His  
 1 5 10 15

Gly Ile Pro Ser Gln Pro Gln Pro His Ile Gly Pro Ile Ser Ser Ser  
 20 25 30

Lys Ser Pro Leu Glu Gln Phe Glu Asp Val Ala Lys Lys Val Glu Asp  
 35 40 45

Trp Ile Asp Asp Tyr Phe Lys Val Leu Lys Pro Tyr Val Pro Ala Ile  
 50 55 60

Gly Arg Ala Phe Leu Val Ala Thr Phe Tyr Glu Asp Thr Leu Arg Ile  
 65 70 75 80

Phe Thr Gln Trp Asn Glu Gln Val Tyr Tyr Leu His Asn Tyr Arg His  
 85 90 95

Tyr Trp Arg Trp Leu Thr Val Leu Phe Leu Ile Asn Asn Met Val Val  
 100 105 110

Met Thr Val Ala Ser Thr Leu Val Ile Ala Arg Lys Lys Asn Asn Ile  
 115 120 125

Ala Thr Ile Ala Leu Ile Val Val Val Ile Ile Gln Gly Ile Gly Tyr  
 130 135 140

Gly Leu Leu Phe Asp Ala Gln Phe Val Leu Arg Asn Leu Ser Val Val  
 145 150 155 160

Gly Gly Leu Val Leu Ala Phe Ser Asp Ser Ile Val Arg Asp Lys Arg  
 165 170 175

Ser Leu Asn Met Pro Gly Leu Pro Met Leu Asn Asn Gln Asp Asn Lys  
 180 185 190

Lys Tyr Phe Leu Leu Ala Gly Arg Ile Leu Leu Val Leu Leu Phe Leu  
 195 200 205

Gly Phe Val Phe Ser Ser Asp Trp Ser Leu Gly Arg Val Phe Ile Ile  
 210 215 220

432

Ile Ile Gly Leu Thr Ser Cys Ala Ser Ile Val Val Gly Tyr Lys Thr  
 225 230 235 240

Lys Phe Ser Ala Ala Ile Met Leu Ile Val Leu Phe Leu Tyr Asn Val  
 245 250 255

Phe Thr Asn Gln Phe Trp Ala Tyr Ala Ser Gln Asp Ala Arg Arg Asp  
 260 265 270

Phe Leu Arg Tyr Glu Phe Phe Gln Val Leu Ser Ile Val Gly Gly Leu  
 275 280 285

Leu Leu Val Val Asn Ala Gly Ala Gly Glu Phe Ser Ile Asp Glu Lys  
 290 295 300

Lys Lys Ile Tyr  
 305

<210> 363  
 <211> 1876  
 <212> DNA  
 <213> Candida albicans

<400> 363  
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 aaattgtgga ggaagataac aatgggaaac aatatgagat tggtgggatt atagatccta 180  
 taaattatag agtcttggtc acattaattg aaaatacaga tggaagcaac aaagtcgcta 240  
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 gacaagtgtg tagaatcttt tttattaata gatgcttctc ttagttatgt tccagaacaa 360  
 ttcatgttag gagagagaga aacgcaatca ctcaattttt gcacaaacaa aaaacgagaa 420  
 gatgaagaag caaaaaagaa aatttttttt tctcaaccat cttaaactct cctacaatta 480  
 atttcatacc aataaagaac atgtctattg tattaccatc aggaactact gacggattta 540  
 aagccgtctc caaatactct gccccagtgc gtcgtccaat tgaaccagt ggtcgttact 600  
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 aagctgaaaa gaatgttaa caaatcgaag tcaacgaaga tgaggatttg ggagatgaag 720  
 aacaaagtga agagttatta gaacacgatc caagagaatg gaagactgcc aatttatatg 780  
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 agaaagaaat tgaagcaaga agatcacaag agattatcga attggtcgaa agagctcatg 1320

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aagactaaac agcaag                                     1876

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&lt;210&gt; 364

&lt;211&gt; 427

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 364

```

Met Ser Ile Val Leu Pro Ser Gly Thr Thr Asp Gly Phe Lys Ala Val
  1             5             10             15

```

```

Ser Lys Tyr Ser Ala Pro Val Arg Arg Pro Ile Glu Pro Val Gly Arg
      20             25             30

```

```

Tyr Phe Leu Ala His Ala Ser Arg Thr Leu Arg Gly His Thr Trp Ser
      35             40             45

```

```

Glu Phe Glu Lys Leu Glu Ala Glu Lys Asn Val Lys Gln Ile Glu Val
      50             55             60

```

```

Asn Glu Asp Glu Asp Leu Gly Asp Glu Glu Gln Ser Glu Glu Leu Leu
      65             70             75             80

```

```

Glu His Asp Pro Arg Glu Trp Lys Thr Ala Asn Leu Tyr Ala Val Leu
      85             90             95

```

```

Gly Leu Ser His Leu Arg Ser Lys Ala Thr Glu Asp Gln Ile Arg Arg
      100            105            110

```

```

Ala His Arg Lys Gln Val Leu Lys His His Pro Asp Lys Lys Ser Ala
      115            120            125

```

```

Ser Gly Gly Leu Glu Asn Asp Gly Phe Phe Lys Ile Ile Gln Lys Ala
      130            135            140

```

```

Phe Glu Val Met Leu Asp Pro Val Lys Arg Arg Gln Tyr Asp Ser Ile
      145            150            155            160

```



Asp Val Glu Asn Asp Pro Lys Pro Pro Ala Pro Lys Ser Lys Tyr Asp  
 165 170 175  
 Phe Phe Glu Ala Trp Gly Pro Val Phe Glu Ser Glu Ala Arg Phe Ser  
 180 185 190  
 Thr Lys Gln Pro Val Pro Leu Leu Gly Asn Leu Glu Ser Thr Lys Glu  
 195 200 205  
 Glu Val Asp Ala Phe Tyr Ser Phe Trp Gly Arg Phe Asp Ser Trp Lys  
 210 215 220

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Thr Phe Glu Phe Lys Asp Glu Asp Val Pro Asp Asp Thr Ala Asn Arg  
 225 230 235 240  
 Asp His Lys Arg Tyr Ile Glu Arg Lys Asn Ile Ala Gln Gln Lys Glu  
 245 250 255  
 Ile Glu Ala Arg Arg Ser Gln Glu Ile Ile Glu Leu Val Glu Arg Ala  
 260 265 270  
 His Ala Glu Asp Pro Arg Ile Lys Leu Phe Lys Glu Lys Ala Lys Lys  
 275 280 285  
 Glu Lys Ala Ala Lys Lys Trp Glu Lys Glu Ser Gly Ser Arg Lys Ala  
 290 295 300  
 Ala Glu Glu Ala Ala Ala Lys Lys Ala Ala Glu Glu Ala Ala Lys  
 305 310 315 320  
 Lys Ala Ala Glu Glu Ala Ala Ala Leu Lys Ala Asn Ser Lys Lys Ala  
 325 330 335  
 Lys Glu Ala Ala Lys Ala Ala Lys Lys Lys Asn Lys Arg Asn Ile Arg  
 340 345 350  
 Ala Ala Val Lys Asp Asn Asn Tyr Phe Gly Asp Ser Ala Lys Ser Ala  
 355 360 365  
 Asp Ile Asp Ala Asp Val Asp Leu Leu Ile Glu Lys Phe Asp Asp Val  
 370 375 380  
 Lys Leu Gly Glu Val Ala Asp Lys Val Lys Asp Ala Asp Ala Lys Ser  
 385 390 395 400  
 Val Lys Ser Thr Phe Val Glu Val Ala Lys Glu Leu Val Gly Ala Gly  
 405 410 415

435

Ser Leu Asp Ala Ser Tyr Leu Lys Tyr Phe Asn  
420 425

<210> 365

<211> 1178

<212> DNA

<213> Candida albicans

<400> 365

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gccctaattg tttgcacgtg atgtattgct ttgagtgaag agtgtacatt tgtacacaca 300
caaacaaaaa aaaactaact tcttccccca atatgctgcg tatagtgaga aatcttcttc 360
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<210> 366

<211> 82

<212> PRT

<213> Candida albicans

<400> 366

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Met Val Leu Val Gln Asp Leu Leu His Pro Ser Pro Ala Thr Glu Ala
  1             5             10             15

Lys Gln His Lys Leu Lys Thr Leu Val Gln Gln Pro Arg Ser Phe Phe
          20             25             30

Met Asp Val Lys Cys Gln Gly Cys Leu Asn Ile Thr Thr Val Phe Ser
    35             40             45

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His Ala Gln Thr Ala Val Thr Cys Asp Ser Cys Ser Thr Val Leu Cys

50

55

60

Thr Pro Thr Gly Gly Lys Ala Lys Leu Thr Glu Gly Cys Ser Phe Arg

65

70

75

80

Arg Lys

<210> 367

<211> 1179

<212> DNA

<213> Candida albicans

<400> 367

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<210> 368

<211> 106

<212> PRT

<213> Candida albicans

<400> 368

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15

Cys Arg Lys His Thr Gln His Lys Val Thr Gln Tyr Lys Ala Gly Lys  
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 Ala Ser Leu Phe Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser  
                   35                  40                  45  
 Gly Tyr Gly Gly Gln Thr Lys Gln Ile Phe His Lys Lys Ala Lys Thr  
                   50                  55                  60  
 Thr Lys Lys Val Val Leu Arg Leu Glu Cys Val Val Cys Lys Thr Lys  
                   65                  70                  75                  80

Ala Gln Leu Pro Leu Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp  
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<210> 369  
 <211> 3583  
 <212> DNA  
 <213> Candida albicans

<400> 369  
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&lt;210&gt; 370

&lt;211&gt; 1072

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 370

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Met Thr Leu Ser Ser Glu Ser Thr Lys Pro Ser Val Glu Glu Val Ser
  1             5             10             15

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Lys Ser Leu Lys Pro Thr Ile Thr Lys Lys Thr Ser Phe Thr Asp Tyr  
                     20                    25                    30

Leu Lys Ser Ala Lys Thr Lys Ala Lys Glu Glu Lys Val Thr Ile Glu  
                     35                    40                    45

Lys Ser Asp Lys Thr Ile Asn Ser Glu Glu Arg Lys Thr Glu Pro Ile  
                     50                    55                    60

Gln Gln Ser Glu Gln Leu Leu Thr Asp Lys Lys Asp Asn Lys Ser Glu  
                     65                    70                    75                    80

Pro Asn Ser Glu Val Asn Leu Lys Asp Asn Asn Asp Asp Ser Lys Ala  
                     85                    90                    95

Thr Ala Gly Cys Ala Leu Gly Pro Asp Lys Asn Thr Gly Lys Asn Asp  
                     100                    105                    110

Ser Asp Lys Ser Glu Thr Thr Gln Pro Lys Leu Ala Arg Ser Glu Ser  
                     115                    120                    125

Phe Ala Asp Thr Ser Leu Leu Ser Pro Val Asn Glu Ser Asp Thr Asp  
                     130                    135                    140

Phe Asn Phe Asn Glu Leu Ala Glu Ile Pro Glu Ala Lys Asp Gly Ser  
                     145                    150                    155                    160

Val Val Ala Ala Asn Val Ser Glu Asn Ile Asp Glu Asn Glu Asn Ile  
                     165                    170                    175

Ser Glu Ala Glu Thr Val Ile Ala Asp Asp Leu Pro Arg Leu Asp Glu  
                     180                    185                    190

Gly Lys Lys Leu Leu Arg Glu Gln Thr Ala Asp Val Lys Arg His Lys  
                     195                    200                    205

Leu Lys Lys Thr Lys Leu Asn Thr Ile Phe Ser Ser Asp Glu Glu Glu  
                     210                    215                    220

Glu Glu Ile Gln Glu Pro Asp Phe Lys Leu Gln Glu Pro Glu Lys Leu  
                     225                    230                    235                    240

Pro Glu Asp Asp Gln His Pro Asp Phe Gln Asn Ser Lys Ala Thr Thr  
                     245                    250                    255

Glu Ile Ser Asn Asp Lys Thr Glu Val Asn Lys Pro Glu Val Lys Glu  
                     260                    265                    270

440

Val Gly Glu Lys Glu Arg Asn His Gln Leu Glu Asp Arg Leu Pro Ile  
275 280 285

Lys Lys Glu Lys Met Arg Ser Glu Asn Ala Lys Thr Ser Glu Asn Gly  
290 295 300

Val Ser Ser Lys Ser Glu Ser Lys Ile Ser Lys Ser Lys Lys Leu Pro  
305 310 315 320

Tyr Lys Val Lys Arg Asp Ser Ser Gly Arg Ser Leu Leu Gln Arg Ala  
325 330 335

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Cys Lys Lys Gly Asn Phe Ala Asp Val Gln Asp Tyr Ile Glu Arg Gly  
340 345 350

Ala Ser Ala Asn Glu Lys Asp Phe Cys Gly Phe Thr Cys Leu His Glu  
355 360 365

Ala Ala Leu Glu Gly His Thr Gln Ile Val Lys Tyr Leu Ile Glu Asn  
370 375 380

Gly Ala Asn Val Asn Ala Lys Ala Asp Glu Ala Gly Asp Ser Glu Thr  
385 390 395 400

Pro Leu Ile Asp Ala Ala Glu Asn Lys His Leu Asp Cys Val Lys Val  
405 410 415

Leu Leu Glu Asn Asp Ala Asp Pro Thr Ile Phe Asn Ile Asp Gly Phe  
420 425 430

Thr Ala Leu Thr Lys Ile Tyr Asn Glu His Glu Gly Glu Gly Tyr  
435 440 445

Asp Glu Ile Ile Gln Val Leu Glu Glu Ala Thr Ala Asn Tyr Asn Ser  
450 455 460

Arg Leu Pro Arg Glu Val Gln Phe Val Ser Asp Ala Pro Ile Gly Ser  
465 470 475 480

Gly Pro Ile Met Glu Asp Pro Asn Asp Asn Tyr Phe Ala Glu Leu Ile  
485 490 495

Lys Gly Lys Gly Ile Tyr Lys Tyr Ala Ala Glu Asn Ser Lys Glu Lys  
500 505 510

Thr Ala Glu Tyr Phe Val Ala Gly His Asn Leu Glu Gly Lys Pro Asp  
515 520 525

441

Ile Leu Ile Leu Ala Ala Arg Asn Gly His Thr Glu Leu Val Asp Ile  
530 535 540

Ile Leu Gly Leu Asn Pro Thr Pro Phe Asn Ile Asp Thr Glu Ser Ser  
545 550 555 560

Cys Gly Val Thr Ala Leu Leu Ala Ser Ile Gly Arg Gly His Phe Glu  
565 570 575

Val Val Asp Ser Leu Leu Ser Lys Gly Ala Asp Pro Phe Lys Thr Arg  
580 585 590

Lys Lys Asp Gly Leu Asn Ala Leu Glu Ile Ala Gln His Ser Pro His  
595 600 605

Phe Asp Ser Arg Glu Val Ser Val Ile Met Lys Phe Met Glu Lys Lys  
610 615 620

Ser Gly Thr Lys Ile Leu Ser Gly Ile Pro Ser Arg Val Val Ser Arg  
625 630 635 640

Ala Thr Ser Arg Ala Pro Ser Val Pro Val Ser Ser Asp Glu Asp Asp  
645 650 655

Val Val Glu Glu Lys Glu Ile Thr Ala His Thr Glu Asn Lys Ser Ala  
660 665 670

Glu Lys Lys Ser Glu Asp Lys Ile Thr Lys Thr Val Asn Glu His Val  
675 680 685

Ser Asn Arg Lys Pro His Glu Ser Thr Gly Arg Lys Leu Glu Lys Thr  
690 695 700

His Ser Asn Glu Glu Arg Lys Arg Lys Arg Glu Trp Ser Asp Asp Glu  
705 710 715 720

Pro Lys Glu Pro His Leu Leu Lys Lys Ser Lys Ser Asp Leu Lys Leu  
725 730 735

Lys Ser Leu His Arg Glu Phe Thr Ser Asp Asp His His Thr Ser Glu  
740 745 750

Ser His Ser Asp Ser Phe Ala Glu Lys Arg Lys His Leu Ser Ala Thr  
755 760 765

Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Pro Ser Gln Ala Val  
770 775 780



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Ile Lys Ala Gln Glu Glu Gln Lys Ile Lys Asp Ala Glu Glu Ala Arg
785                      790                      795                      800

Leu Trp Gln Glu Lys Val Glu Ala Lys Lys Arg Ala Arg Arg Glu Met
                        805                      810                      815

Phe Leu Lys Ser Glu Lys Glu Lys Glu Gln Lys Arg Lys Glu Glu Glu
                        820                      825                      830

Glu Leu Arg Ala Gln Glu Glu Lys Arg Ile Ala Lys Ala Lys Gln Glu
835                      840                      845
-----
Glu Gln Glu Arg Leu Ala Arg Glu Ala Glu Glu Lys Ser Lys Glu Leu
850                      855                      860

Glu Glu Lys Lys Val Gly Leu Arg Gln Gln Leu Thr Leu Asp His Tyr
865                      870                      875                      880

Pro Val Gly Leu Arg Tyr Cys Lys Phe Asp Gly Asn Pro Asn Ile Ser
                        885                      890                      895

Ala Val Asp Lys Phe Leu Pro Phe Tyr Val Phe Val Ile Asp Asp Lys
                        900                      905                      910

Lys Tyr Ala Val Asp Leu Gln Val Ser Leu Ile Thr Ser Thr Val Val
                        915                      920                      925

Ser Lys Val Ile Asn Thr Val Gln Pro His Gln Lys Arg Glu Ile Asn
                        930                      935                      940

Ala Thr Glu Lys Ser Lys Leu Trp Lys Leu Phe Phe Lys Phe Ile Gly
945                      950                      955                      960

Ile Asp Pro Arg Asn Pro Asn Cys Asp Gln Arg Ser Ser Ile Thr Asn
                        965                      970                      975

Gly Gln Lys Gln Phe Gln Asn Leu Leu Leu His Phe Val Glu Val Asp
                        980                      985                      990

Leu Ala Glu Glu Phe Leu Lys Glu Phe Pro Glu Val His Ser Lys Ala
                        995                      1000                      1005

Lys Asp Asn Gln Ile Asp Val Ser Leu Glu Ser Leu Ser Gly Phe Ser
1010                      1015                      1020

Asp Cys Val Lys Asp Asp Ile Ile Val Asp Gly Asn Leu Glu Ile Asp
1025                      1030                      1035                      1040

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443

Ile Asp Ser Lys Lys Ile Glu Lys Phe Ile Pro Pro His Leu Asn Thr  
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Arg Lys Asp Ile Ile Arg Thr Val Ser Thr Leu Ala His Pro Leu Trp  
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 <211> 659  
 <212> DNA  
 <213> Candida albicans

<400> 371  
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<210> 372  
 <211> 52  
 <212> PRT  
 <213> Candida albicans

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Lys Ser Ile Cys Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr  
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Asn Cys Arg Lys Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys  
 35 40 45

Lys Lys Leu Lys  
 50

444

&lt;210&gt; 373

&lt;211&gt; 2297

&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 373

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&lt;210&gt; 374

&lt;211&gt; 598

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 374

Met Asn Asp Pro Arg Asp Glu Gln Ile Asp Ser Asp Asp Val Leu Thr  
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Glu Asp Ser Ser Asp Glu Leu Lys Asp Leu Val Gln Glu Phe Glu Leu  
 20 25 30

Lys Tyr Ala Glu Leu Lys Lys Asn Lys Ala Leu Lys Lys Arg Arg Ser  
 35 40 45

Gln Ser Pro Ser Glu Asp Met Ser Asn Lys Gln Lys Pro His Gln Pro  
 50 55 60

Glu Val Pro Arg Thr Pro Glu Lys Ala Lys Val His Leu Asp Lys Val  
 65 70 75 80

Val Glu Glu Pro Lys Gln Arg Ile Phe Thr Lys Lys Glu Pro Arg Asp  
 85 90 95

Ser Lys Ile Lys Glu Ser Asn Phe Leu Asn Lys Leu Tyr Glu Thr Ser  
 100 105 110

Asn Lys His Asp Lys Glu Asp Ala His Lys Ile Asp Phe Ser Lys Arg  
 115 120 125

Arg Phe Glu Phe Gln Leu Asp Lys Tyr Thr Phe Thr Pro Lys Asp Val  
 130 135 140

Val Asp Asp Leu Glu Pro Ile Ser Lys Leu Tyr Leu Arg Arg Arg Tyr  
 145 150 155 160

Leu Ala Gln Ser Gln Ile Ala Asp Ile Ile Ala Glu Thr Asp Ser Asn  
 165 170 175

Met Lys Phe Leu Lys Ile Asp Lys Phe Leu Ala Lys Thr His Lys Ser  
 180 185 190

Asn Asn Tyr Ala Glu Pro Lys Tyr Cys Asn Trp Cys Leu Val Ala Phe  
 195 200 205

Val Val Arg Lys Asp Pro Val Gln Val Ala Ala Asn Asn Ser Lys Tyr

446

210 215 220  
Ile Lys Leu Lys Val Gly Asn Phe Met Asn Ser Val Asp Leu Met Leu  
225 230 235 240  
Phe Asp Lys Ala Phe Gln Lys Asn Gly Lys Ile Gln Pro Gly Asp Leu  
245 250 255  
Leu Phe Ile Leu Asn Pro Leu Ile Asn Lys Tyr Glu Ile Gln Val Gly  
260 265 270  
Lys Gly Gln Phe Gln Ser Gly Phe Asn Leu Lys Val Glu Asn Thr Asn  
275 280 285  
Val Ser Ser Ile Leu Glu Ile Gly Ser Leu Arg Asp Phe Gly Phe Cys  
290 295 300  
Lys Phe Thr Arg Lys Leu Asp Asn Ser Arg Cys Lys Arg Ala Ile Asn  
305 310 315 320  
Thr Arg Thr Gln Glu Phe Cys Asp Ile His Leu Asp Met Lys Phe Lys  
325 330 335  
Ser Ser Thr Arg Met Glu Leu Asn Gly Ser Val Ser Ile Arg Ser Pro  
340 345 350  
Gln Lys Asn Lys Lys Lys Met Tyr Met Asn Lys Asn Gly Ser Gly Phe  
355 360 365  
Ile Lys Gln Tyr Asn Glu Glu Ser Thr Val Ile Gly Thr Ser Tyr Gly  
370 375 380  
Ser Pro Leu Asp Pro Lys Arg Tyr Gln Asp Pro Lys Val Leu Gln Asn  
385 390 395 400  
Gln Ile Lys Arg Arg Lys Leu Ile Asp Asp Lys Ala Lys Glu Met Leu  
405 410 415  
Glu Gln Lys Leu Ser Lys Leu Gly Ser Ala Ser Leu Leu Asn Asn Leu  
420 425 430  
Gln Leu Ser Lys Lys Glu Ala Thr Asp Lys Leu Ala Ser Asp Arg Ser  
435 440 445  
Lys Ser Lys Gly Phe Thr Asn Thr Met Ile Ser His Ile Gly Phe Asp  
450 455 460  
Pro Thr Gly Thr Ser Leu Asn Gln Asn Ser Thr Ser Leu Gly Ser Lys

447

465                                      470                                      475                                      480

Ser Met Glu Lys Ser Arg Ala Arg Glu Leu His Asp Leu Ser Val Glu

   485                                      490                                      495

Thr Ser Gly His Lys Ser Leu Ser Ser Ser Lys Gln Asp Arg Gln Ser

   500                                      505                                      510

Lys Val Ala Lys Trp Asn Thr Asn Ile Arg Thr Leu Gln Asn Tyr Asp

   515                                      520                                      525

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Arg Arg Val Ala Ser His Ser Leu Ser Thr Ser Arg Arg Leu Gln Asn

   530                                      535                                      540

Leu Val Gly Lys Gln Thr His Ala Thr Leu Val Asp Lys Arg Lys Arg

545                                      550                                      555                                      560

Val Val Val Ser Asp Asp Glu Gln Pro Gly Met Glu Glu Asp Glu Glu

   565                                      570                                      575

Asp Ile Glu Ile Gln Phe Asp Asp Glu Lys Ser Lys Met Ser Tyr Met

   580                                      585                                      590

Lys Met Thr Gly Ala Arg

   595

<210> 375

<211> 1499

<212> DNA

<213> Candida albicans

<400> 375

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tttttgagta gatataacag aactaccaa agtgagccca catctgttaa tcttgaaaag 180

caaaattgag aaaaccattt atgcaagtcg tgtactggtg atattcttgg tcaattgcta 240

cacttttgta atgaatactg taatgtagcc gacgtgggtt gaanaatata tatttaagta 300

tatagaatca ggtcaatata aaatgtttga aatataacaa aatgtttcaa tgtaaaactga 360

tggttaaggg attataaatc aaactgagta gtgcttttgt tcctaaaaaa cccatcgtgg 420

tggtaacgtc aggagaccgc gacatcaaat ggaattcaca caatcagtct ccgaatttat 480

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cagacaaact tcctacaaag cctccgtgca ggggtgtttt caagaatgag tatgagcagc 600

cctccggcag tgtcaaatta agaggcatgg gacacttggt tggccagtct atagatgtgg 660

ccagaaaact tggcaaactg aacgtagcag ttttttcgtc atctggtggt aatgcaggat 720

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 gggtcatttg ttcggtagga ggggggtggct tatacaacgg aatagttgaa ggtttggaaa 1080  
 atcataagga gataccagtg ttggcaattg aaactaaaca agcggccacg tttcacgagg 1140  
 cggtcaaaga aggtaaagtt gttcatttac aaaaagtgc aactttggcc acttctttgg 1200  
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 tgaataaatt tggtacatta agtccagatg atattatcat tgttgtcata tgtggtggat 1440  
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<210> 376

<211> 332

<212> PRT

<213> Candida albicans

<400> 376

Met Lys Glu Pro Ser Ile Thr Thr Thr Phe Val Glu Val Thr Asp Lys  
 1 5 10 15

Leu Pro Thr Lys Pro Pro Cys Arg Val Phe Phe Lys Asn Glu Tyr Glu  
 20 25 30

Gln Pro Ser Gly Ser Val Lys Leu Arg Gly Met Gly His Leu Val Gly  
 35 40 45

Gln Ser Ile Asp Val Ala Arg Lys Leu Gly Lys Ser Asn Val Ala Val  
 50 55 60

Phe Ser Ser Ser Gly Gly Asn Ala Gly Leu Ala Ala Ala Tyr Ala Ser  
 65 70 75 80

Gln Phe Phe Gly Val Ser Cys Thr Val Val Leu Pro Glu Ser Ser Lys  
 85 90 95

Pro Thr Val Ile Glu Lys Leu Lys Ser Leu Gly Ala Asp Val Ile Ile  
 100 105 110

His Gly Lys His Trp Gly Glu Ala Asp Asn Tyr Leu Thr Asp Phe Val  
 115 120 125

Ile Lys Asn Leu Asp Lys Thr Val Tyr Pro Val Tyr Cys His Pro Phe  
 130 135 140

Asp Asp Pro Leu Leu Trp Glu Gly His Ser Lys Ile Ile Thr Glu Ile  
 145 150 155 160

449

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Ile Asp Gln Lys Gln Leu Pro Asn Phe Asp Lys Val Lys Gly Val Ile
      165                      170                      175

Cys Ser Val Gly Gly Gly Gly Leu Tyr Asn Gly Ile Val Glu Gly Leu
      180                      185                      190

Glu Asn His Lys Glu Ile Pro Val Leu Ala Ile Glu Thr Lys Gln Ala
      195                      200                      205

Ala Thr Phe His Glu Ala Val Lys Glu Gly Lys Val Val His Leu Gln
      210                      215                      220
-----
Lys Val Gln Thr Leu Ala Thr Ser Leu Ala Ser Pro Tyr Leu Ser Ser
      225                      230                      235                      240

Lys Ala Leu Ala Asn Tyr Ile Glu Arg Pro Thr Val Leu Ala Glu Ile
      245                      250                      255

Asp Asp Leu Asp Ala Val Lys Gly Val Val Asp Val Tyr Asp His Phe
      260                      265                      270

Gly Tyr Met Val Glu Pro Ala Cys Gly Ala Ser Val Ala Ser Val Met
      275                      280                      285

His Arg Gln Asp Leu Leu Asn Lys Phe Gly Thr Leu Ser Pro Asp Asp
      290                      295                      300

Ile Ile Ile Val Val Ile Cys Gly Gly Ser Ala Ile Asn Lys Tyr Ile
      305                      310                      315                      320

Ile Asp Glu Tyr Arg Ser Leu Leu Glu Lys Asp Ser
      325                      330

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&lt;210&gt; 377

&lt;211&gt; 2564

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 377

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atctcaaagt tgccacgtaa gcacaattaa tctttttatg gttgtaacta tttctagtat 240
attctacgta ataggtgagg tcctatatgc agtacacaca ggtttttttc acagatggtg 300
acacagtgtt gaaaattatt cacgttgatt tataaatata caacttacct tccacgggtt 360

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tatagaatca tttcaatata atgagatcat cacaatcttc ttggttacca cgtattgggt 540
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acaacaacag attgggcaaa ttcgaattga ctggtattcc accagctcca agaggtgtcc 2040
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gtgatgatga ttcagatgat gaattcgatc acgatgaatt gtag 2564

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&lt;210&gt; 378

&lt;211&gt; 687

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 378

Met Arg Ser Ser Gln Ser Ser Trp Leu Pro Arg Ile Gly Leu Leu Tyr

1

5

10

15

Val Ala Leu Val Ile Leu Ile Pro Phe Leu Val Ser Pro Lys His Ala  
 20 25 30

Phe Ala Val Ala Ala Val Ser Asp Asp Glu Ser Ser Thr Asp Asn Tyr  
 35 40 45

Gly Thr Val Ile Gly Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val Gly  
 50 55 60

Val Met Lys Asn Gly Lys Val Glu Ile Leu Ala Asn Asp Gln Gly Asn  
 65 70 75 80

Arg Ile Thr Pro Ser Tyr Val Ser Phe Asn Gly Asp Glu Arg Leu Val  
 85 90 95

Gly Asp Ala Ala Lys Asn Gln Ala Ser Ser Asn Val Asn Asn Thr Val  
 100 105 110

Phe Asp Ile Lys Arg Leu Ile Gly Leu Lys Tyr Asn Asp Asp Thr Val  
 115 120 125

Gln Lys Glu Leu Lys His Leu Pro Tyr Lys Ile Glu Asn Lys Gly Asn  
 130 135 140

Lys Pro Val Val Lys Val Glu Tyr Gln Gly Glu Glu Lys Thr Phe Ser  
 145 150 155 160

Pro Glu Glu Ile Ser Ser Met Val Leu Gly Lys Met Lys Ser Ile Ala  
 165 170 175

Glu Asp Tyr Leu Gly Lys Lys Val Thr His Ala Val Val Thr Val Pro  
 180 185 190

Ala Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr  
 195 200 205

Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr Ala Ala  
 210 215 220

Ala Ile Ala Tyr Gly Leu Asp Lys Gly Asp Gln Glu Lys Gln Ile Ile  
 225 230 235 240

Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Ser Ile  
 245 250 255

Glu Gly Gly Val Phe Glu Val Leu Ala Thr Ala Gly Asp Thr His Leu  
 260 265 270

Gly Gly Glu Asp Phe Asp Phe Lys Ile Val Arg Tyr Leu Ala Lys Gln  
 275 280 285  
 Phe Lys Lys Lys His Asn Ile Asp Ile Thr Ala Asn Ser Lys Ala Ile  
 290 295 300  
 Ser Lys Leu Lys Arg Glu Ala Glu Lys Ala Lys Arg Thr Leu Ser Ser  
 305 310 315 320  
 Gln Met Ser Thr Arg Val Glu Ile Asp Ser Phe Val Asp Gly Ile Asp  
 325 330 335

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Phe Ser Glu Thr Leu Ser Arg Ala Lys Phe Glu Glu Leu Asn Ile Ala  
 340 345 350  
 Ala Phe Arg Lys Thr Leu Lys Pro Val Glu Gln Val Leu Lys Asp Gly  
 355 360 365  
 Gly Val Lys Lys Ser Asp Ile Asp Asp Ile Val Leu Val Gly Gly Ser  
 370 375 380  
 Thr Arg Ile Pro Lys Val Gln Glu Leu Leu Glu Gly Phe Phe Asp Gly  
 385 390 395 400  
 Lys Lys Ala Ser Lys Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly  
 405 410 415  
 Ala Ala Val Gln Ala Gly Val Leu Ser Gly Glu Glu Gly Val Asp Asp  
 420 425 430  
 Ile Val Leu Leu Asp Val Asn Pro Leu Thr Leu Gly Ile Glu Thr Ser  
 435 440 445  
 Gly Gly Val Met Thr Thr Leu Ile Lys Arg Asn Thr Ala Ile Pro Thr  
 450 455 460  
 Lys Lys Ser Gln Ile Phe Ser Thr Ala Ala Asp Asn Gln Pro Thr Val  
 465 470 475 480  
 Leu Ile Gln Val Tyr Glu Gly Glu Arg Thr Met Ala Lys Asp Asn Asn  
 485 490 495  
 Arg Leu Gly Lys Phe Glu Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly  
 500 505 510  
 Val Pro Gln Ile Glu Val Thr Phe Ser Leu Asp Ala Asn Gly Ile Leu  
 515 520 525

453

Lys Val Glu Ala Ala Asp Lys Gly Thr Gly Lys Ser Glu Ser Ile Thr  
530 535 540

Ile Thr Asn Glu Lys Gly Arg Leu Ser Lys Asp Glu Ile Asp Arg Met  
545 550 555 560

Val Glu Glu Ala Glu Lys Tyr Ala Gln Gln Asp Gln Glu Leu Lys Glu  
565 570 575

Lys Ile Glu Ala Arg Asn Ser Leu Glu Asn Tyr Ala His Val Leu Arg  
580 585 590

Gly Gln Leu Ser Asp Thr Ser Glu Thr Gly Leu Gly Ser Lys Leu Asp  
595 600 605

Asp Asp Asp Lys Glu Thr Leu Asp Asp Ala Ile Lys Glu Thr Leu Glu  
610 615 620

Phe Ile Glu Asp Asn Phe Asp Thr Ala Thr Ala Glu Glu Phe Glu Glu  
625 630 635 640

Gln Lys Gln Lys Leu Ile Asp Val Ala Asn Pro Ile Thr Ala Lys Leu  
645 650 655

Tyr Gly Gly Ala Ala Gly Glu Gly Ala Gly Gly Ala Gly Asp Ala Lys  
660 665 670

Phe Gly Asp Asp Asp Ser Asp Asp Glu Phe Asp His Asp Glu Leu  
675 680 685

<210> 379

<211> 1346

<212> DNA

<213> Candida albicans

<400> 379

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gccgtctctt gttcttttat tcttctaagg aatgctttat gtagttctga cattcttgcg 300  
taaaaggaag tacagtatta aagctcgaaa ctcaattgca acaaaagtct taattttttc 360  
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ttaggctgac agaaaaaaaa aatttagtac ctgccacacc agtagctcca aacccatata 480  
tgatttgata gagttgaagt atgctgacag atcttacttc acactttcag tacatgggcta 540  
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aataccacga gaatcagttt tgtagcattt caaaggatga atttatagag ttttacggaa 1080
atgaaagagt gcatattttac gatgggaaga tttttgaaat cactccatta caaaacaagg 1140
gttatgatat aaaagaattg atatcgttgg atatgatgca aaaagttcca tttctagagg 1200
atgagttggg acaaattaca gatgagcaaa taattgaatt tcacaactta tttttcaaca 1260
taaattgatga tggaacgggt aattataaaa aaccaatagg caaatataac agtaaaaaaga 1320
gacactttgc aaacgatgaa gaatag                                     1346

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&lt;210&gt; 380

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 380

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Met Ser Thr Asp Leu Thr Ser His Phe Gln Tyr Met Ala Ile Ser Leu
  1             5             10             15

```

```

Phe Val Gly Tyr Lys Ala Leu Leu Asn Asn Glu Thr Pro Val Ser Cys
             20             25             30

```

```

Ile Val Val Asp Ser Lys Ser Asp Lys Ile Ile Ser Ile Gly Tyr Asn
      35             40             45

```

```

Tyr Thr Asn His Ser Leu Asn Gly Thr Gln His Ala Glu Phe Ile Ala
      50             55             60

```

```

Leu Gln Arg Phe Gly Glu Gln Lys Ser Ser Ile Asp Tyr Asn Asp Leu
      65             70             75             80

```

```

Ile Leu Tyr Val Thr Val Glu Pro Cys Ile Met Cys Ala Ser Tyr Leu
             85             90             95

```

```

Arg Gln Leu Gly Ile Lys Lys Val Ile Phe Gly Cys Gly Asn Asp Arg
      100             105             110

```

```

Phe Gly Gly Asn Gly Thr Ile Leu Ser Ile His Ser Asp Ile Thr Leu
      115             120             125

```

```

Pro Asn Ala Ala Tyr Ser Ser Ile Gly Gly Ile Cys Arg Thr Glu Gly
      130             135             140

```

Ile Gln Leu Leu Arg Asn Phe Tyr Ile Gln Gln Asn Glu Ser Ala Pro  
 145 150 155 160

Asn Pro Lys Ile Lys Lys Asn Thr Asp Ile Glu Ser Lys Glu Tyr Pro  
 165 170 175

Glu Asn Gln Phe Cys Ser Ile Ser Lys Asp Glu Phe Ile Glu Phe Tyr  
 180 185 190

Gly Asn Glu Arg Val His Ile Tyr Asp Gly Lys Ile Phe Glu Ile Thr  
 195 200 205

Pro Leu Gln Asn Lys Gly Tyr Asp Ile Lys Glu Leu Ile Ser Leu Asp  
 210 215 220

Met Met Gln Lys Val Pro Phe Leu Glu Asp Glu Leu Gly Gln Ile Thr  
 225 230 235 240

Asp Glu Gln Ile Ile Glu Phe His Asn Leu Phe Phe Asn Ile Asn Asp  
 245 250 255

Asp Gly Thr Val Asn Tyr Lys Lys Pro Ile Gly Lys Tyr Asn Ser Lys  
 260 265 270

Lys Arg His Phe Ala Asn Asp Glu Glu  
 275 280

<210> 381

<211> 1504

<212> DNA

<213> Candida albicans

<400> 381

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 tatcaattat tgttaaattt gtcattggctc gatcaagttg taaattaccc atggataatt 180  
 ctgcttgaga tttattttaat tgattatcca tttcaagtag gactttttgt aatgcttctt 240  
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 agaaaaaaaa aaaaattgaa cagaaagatt catcctttta gatcaaacga aatatatctt 480  
 accatcccc cccctccaaa atgcttagat ttactaggac tactgcttgg aaattaagat 540  
 ctattccaat tgccactatt caatatagac aatttactta ttccactata tgttatcaat 600  
 taaaaaccct tactccatct ttaggaataa ataataccat tgaatccaat ataccttcag 660  
 aaactaatag attagctaaa actggtacta gattttggaa aaaaggtgaa gttaaattca 720  
 ataatgaaac tcaaaaatat gaaattcaat tagatgggaa aactctacgc acaccacttg 780

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ggactcattt acctgatatt aaagtgaat caagtacttt accattaaca gctttagcca 900
ctagagctat agatttgagt caacaacatt tgagtgatat gaagacagaa aaagctgaag 960
aaatgttagc attggaagat attaaattac aaatgttaag atatcttgat actgatactt 1020
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atga 1504

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&lt;210&gt; 382

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 382

```

Met Leu Arg Phe Thr Arg Thr Thr Ala Trp Lys Leu Arg Ser Ile Pro
  1             5             10             15

```

```

Ile Ala Thr Ile Gln Tyr Arg Gln Phe Thr Tyr Ser Thr Ile Cys Tyr
          20             25             30

```

```

Gln Leu Lys Thr Leu Thr Pro Ser Leu Gly Ile Asn Asn Thr Ile Glu
          35             40             45

```

```

Ser Asn Ile Pro Ser Glu Thr Asn Arg Leu Ala Lys Thr Gly Thr Arg
          50             55             60

```

```

Phe Trp Lys Lys Gly Glu Val Lys Phe Asn Asn Glu Thr Gln Lys Tyr
          65             70             75             80

```

```

Glu Ile Gln Leu Asp Gly Lys Thr Leu Arg Thr Pro Leu Gly Phe Pro
          85             90             95

```

```

Leu Glu Leu Pro Ile Asn Lys Lys Gln Leu Ala Tyr Leu Ile Ala His
          100            105            110

```

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Glu Trp Thr His Leu Pro Asp Ile Lys Val Lys Ser Ser Thr Leu Pro
          115            120            125

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Leu Thr Ala Leu Ala Thr Arg Ala Ile Asp Leu Ser Gln Gln His Leu
          130            135            140

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457

Ser Asp Met Lys Thr Glu Lys Ala Glu Glu Met Leu Ala Leu Glu Asp  
 145 150 155 160

Ile Lys Leu Gln Met Leu Arg Tyr Leu Asp Thr Asp Thr Cys Leu Ile  
 165 170 175

Phe Ala Thr Asn Lys Glu Cys Asp Gly Lys Leu Arg Lys Arg Gln Glu  
 180 185 190

Glu Ile Tyr Arg Pro Leu Ile Asn Glu Phe Asn Glu Phe Phe Thr Ile  
 195 200 205

Tyr Ala His Asn Lys Asn Leu Ile Pro Arg Gln Lys Ser Ile Glu Leu  
 210 215 220

Lys Tyr Leu Asp Cys Glu Thr Asp Gly Leu Arg Gly Asn Lys Gln Asp  
 225 230 235 240

Glu Thr Thr Gln Leu Val Val Leu Asp Trp Leu Asn Gln Leu Pro Ile  
 245 250 255

Tyr Asp Leu Ile Ala Leu Glu Lys Thr Ile Leu Thr Thr Lys Ser Phe  
 260 265 270

Leu Cys Gly Ile Thr Leu Leu Arg Ser Asn Val Asn Asp Ile Glu Thr  
 275 280 285

Leu Lys Glu Leu Tyr Gln Phe Asn Lys Asn Ser Ile Asp Glu Asp Tyr  
 290 295 300

Tyr His Lys Thr Leu Glu Glu Leu Val Glu Leu Gly Asn Leu Glu Thr  
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Ile Tyr Gln Thr Glu Glu Trp Gly Glu Val Glu Asp Thr His  
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<210> 383

<211> 3689

<212> DNA

<213> Candida albicans

<400> 383

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 ggaacgcttt ttttaaactg ctgttttatt gtaaaaatta ttgtcgtcct tcttcataac 180  
 attatttgta acagtctcta actgtattgt tgggctgaca gtagagtatt gcggtcattt 240



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&lt;210&gt; 384

&lt;211&gt; 1062

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 384

Met Asp Ser Asn Pro Cys Gln Asp Val Ser Gly Asp Thr Ser Ser Thr  
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Pro Met Ala Asn Asn Asn Pro Thr Asn Asp Ser Thr Ile Ser Ser Gln  
 20 25 30

Asn His Ser Lys Thr Gly Leu Arg Lys His Gln Gln Gln His Tyr His  
 35 40 45

Gln His Ser His Ser Gln Met His Ser His Ser Gln Gln Ser Pro Tyr  
 50 55 60

Ile Asn Gln Leu Glu Tyr Phe Thr Asn Asn Gln Phe Ser Arg Ser Phe  
 65 70 75 80

Asn Ser Leu Ile Leu Glu Asp Ala Asn Asp Ala Asn Thr Asn Asn Ser  
 85 90 95

Ser Thr Thr Thr Leu Asn Lys Lys Thr Ile Asn Lys Ser Pro Pro Phe  
 100 105 110

Asn Ile Lys Gln Asp Leu Leu Asn Asp Ser Ile Asp Thr Phe Leu Asp  
 115 120 125

Asn Ser Asn Thr Glu Thr Ile Glu Asp Gly Asp Val Thr Thr Thr Asp  
 130 135 140

Asp Asp His Asp Phe Asp Asp Glu Asp Ile Glu Asp Pro Glu Ala Val  
 145 150 155 160

460

Gln Tyr Thr Pro Thr Leu Asn Ile Leu Lys Ser Lys Lys Val Asp Ser  
 165 170 175  
 Phe Asn Ile Ile Ser Ser Lys His Arg Lys Ser Asn Ser Gln Ile Thr  
 180 185 190  
 Tyr Asn Ser His Val Arg Lys Pro Ser Glu Glu Asp Thr Ser Ser Ser  
 195 200 205  
 Met Ala Thr Ile Arg Leu Ser Asn Asn Ser Gln Ser Ser Ile Lys Arg  
 210 215 220

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Ser Ser Lys Tyr Leu Asn Leu Ser Ile Asp Ser Asn Leu Lys Thr Val  
 225 230 235 240  
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 245 250 255  
 Ile Asp Val Ala Val Ala Pro Asn Asp Phe Ser Ser Pro Leu Ser Ala  
 260 265 270  
 Arg Lys Pro Asp Ile Phe Ala Ala Ile Thr Ala Ala Asn Gly Asn Ser  
 275 280 285  
 Asn Asn Gln Phe Lys Arg Pro His Lys Leu Val Ser Gln Ser Pro Ser  
 290 295 300  
 Pro Ser Ser Lys Asn Lys Phe Arg Ile Ser Ser Ser Thr Thr Ser Ser  
 305 310 315 320  
 Pro Gln Ser Asn Leu His Ser Pro Ser Lys Leu Gly Ser Lys Gly Phe  
 325 330 335  
 Lys Met Phe Lys Asn Ala Asn Arg Asp Ala Ile Met Ser Ser Ser Arg  
 340 345 350  
 Val Met Thr Pro Glu Lys Pro Lys Met Val Ser Lys Ile Phe Gly Lys  
 355 360 365  
 Ser Ala Lys Ile Arg Arg Ala Tyr Thr Pro Thr His Thr Ser Thr Pro  
 370 375 380  
 Met Ala Val Ser Ser Leu Asn Pro Pro Ser Ser Ser Thr Ser Asn Ser  
 385 390 395 400  
 Thr Thr Ala Ala Ile Thr Ser Thr Ser Pro Ala Ala Asp Glu His Tyr  
 405 410 415

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Asp Ile Asp Asn Asp Cys Asp Ser Pro Ser Lys Asn Arg Lys Ser Ser
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Asn Ile Ser Ala Ser Ser Ile Ile Ile Tyr Gln Asp Glu Asn His Ile
      435                      440                      445

Lys Ser Asn His Ala Arg Lys Ser Ser Asn Pro Ile Pro Tyr Pro Pro
      450                      455                      460

Thr Glu Pro Leu Pro Thr Asn Ile Ser Ala Ser Val Ala Glu Thr Gly
465                      470                      475                      480
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Lys Gly Ser Thr Thr Thr Lys Ser Asn Leu Ser Lys Gly Cys Pro Leu
      485                      490                      495

Phe Asp Asp Lys Glu Asn Lys Ala Ser Tyr Gln Phe Val Lys Pro Leu
      500                      505                      510

Gln Thr Ala Phe Asn Ser Ser Gly Leu Val Lys Lys Asn Ser Ile Ser
      515                      520                      525

Gly Ser Ser Asp Arg Lys Leu Pro Pro Glu Thr Pro Ile Lys Arg Asn
      530                      535                      540

Pro Leu Met Ile Leu Asn Thr Asn Lys Val Val Pro Pro Tyr Ser Ser
      545                      550                      555                      560

Gly Phe Ala Glu Gly Lys Asp Val Met Gly Asp Gln His Asp Ile Tyr
      565                      570                      575

Ser His Ile Pro Cys Gln Asn Gln Arg Phe Pro Gly Ser Val Asn Pro
      580                      585                      590

Asn Thr Thr Thr Asn Asn Asn Asn Thr Gln Gln His His Asp Ser Asp
      595                      600                      605

Leu Ser Ile Glu Val Gly Arg Asn Asn Ser Tyr Asp Ala Ser Ser Ser
      610                      615                      620

Thr Ile Asn Asn Thr Ser Tyr Ile Lys Ile Phe Pro Ser Ser Glu Leu
      625                      630                      635                      640

Lys Lys Glu Gln Val Leu Gln Arg Pro Gln Glu Asp Leu Glu Leu Val
      645                      650                      655

Phe Asn Ser Asp Ile Glu Leu Asp Asp Asn Ile Ile Pro Glu Thr Pro
      660                      665                      670

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Thr Lys Lys Ser Leu Leu Pro Asn Gln His His Gln His His Leu Pro  
 675 680 685

Leu Tyr Thr Gln Ser Lys Ser Pro Leu Leu Lys Phe Asp Thr Glu Lys  
 690 695 700

Asp Gly Arg Arg Asn Leu Ser Ile Val Leu Asp Lys Ser Asn Ala Thr  
 705 710 715 720

Lys Arg Glu Ile Ser Glu Pro Pro Ser Thr Pro Ile Asn Met Ser Phe  
 725 730 735

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Ala Lys Asn Ser Phe Lys Lys Pro Met Asn Asn Ala Glu Arg Gly Asp  
 740 745 750

Asp Pro Asp Ser Ile Ile Ala Gln Arg Ile Asp Ile Met Pro Ser Leu  
 755 760 765

Asp Glu Val Asp Ser Val Ser Val Tyr Pro Ser Lys Ile Asp Glu His  
 770 775 780

Leu Ile Glu Lys Phe Gly Met Lys Asn Ile Lys Tyr Ile Gly Ser Gly  
 785 790 795 800

Ala Phe Ser Ile Ala Phe Glu Cys Leu Phe Asn Asn Glu Lys Phe Ala  
 805 810 815

Ile Lys Arg Thr Lys Lys Pro Leu Ile Gly Lys Leu Glu Lys Gln Thr  
 820 825 830

Ile Lys Arg Glu Ile Glu Ala Leu Arg Val Leu Thr Ser Ile Lys Glu  
 835 840 845

Asp Glu Ala Thr Asn Met Gln Glu Gln Glu Glu Gly Lys Glu Tyr Leu  
 850 855 860

Val Tyr Phe Ile Glu Ala Trp Asp Phe Asn Asn Tyr Tyr Tyr Ile Met  
 865 870 875 880

Thr Glu Phe Cys Glu Gly Gly Thr Leu Phe Asp Phe Leu Glu Glu Asn  
 885 890 895

Lys His Tyr Lys Ile Asp Glu Phe Arg Ile Trp Lys Ile Leu Ile Glu  
 900 905 910

Ile Leu Asn Gly Leu Lys Phe Ile His Ser Lys Asn Tyr Leu His Leu  
 915 920 925

Asp Leu Lys Pro Ala Asn Ile Phe Ile Thr Phe Glu Gly Ser Leu Lys  
 930 935 940

Ile Gly Asp Phe Gly Leu Ala Thr Lys Leu Pro Ile Leu Glu Lys Asp  
 945 950 955 960

Phe Asp Leu Glu Gly Asp Arg Asn Tyr Ile Ala Pro Glu Leu Ile Asn  
 965 970 975

Asp Lys Ile Tyr Thr Pro Phe Ala Asp Ile Phe Ser Leu Gly Leu Ile  
 980 985 990

Ile Leu Glu Ile Ala Ala Asn Ile Ile Leu Pro Asp Asn Gly Thr Pro  
 995 1000 1005

Trp Arg Lys Leu Arg Ser Gly Asp Leu Ser Asp Ala Gly Arg Leu Ser  
 1010 1015 1020

Ser Asp Asn Ile Ser Met Phe Leu Gln His Asn Pro Asn Thr Asn Ser  
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Asn Ile Ser Gly Ser Gly Ser Arg Ser Gly Ser Gly Ser Thr Gly Gly  
 1045 1050 1055

Asn Gly Ser Ala Gly Asp  
 1060

<210> 385

<211> 887

<212> DNA

<213> Candida albicans

<400> 385

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<210> 386  
<211> 51  
<212> PRT  
<213> Candida albicans

<400> 386  
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Leu Gly Ile  
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<210> 387  
<211> 893  
<212> DNA  
<213> Candida albicans

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<210> 388

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 388

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Ala Glu Lys Thr Gly Lys Arg Gln Val Leu Ile Arg Pro Ser Ser Lys  
 20 25 30

Val Ile Ile Lys Phe Leu Thr Val Met Gln Lys His Gly Tyr Ile Gly  
 35 40 45

Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln  
 50 55 60

Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Gln Pro Arg Phe Asn  
 65 70 75 80

Val Lys Ile Asn Asp Ile Glu Arg Trp Thr Asp Asn Leu Leu Pro Ala  
 85 90 95

Arg Gln Phe Gly Tyr Val Ile Leu Thr Thr Ser Ala Gly Ile Met Asp  
 100 105 110

His Glu Glu Ala Arg Arg Lys His Val Ser Gly Lys Ile Leu Gly Phe  
 115 120 125

Val Tyr  
 130

&lt;210&gt; 389

&lt;211&gt; 4619

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 389

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<210> 390

<211> 1372

<212> PRT

<213> Candida albicans

<400> 390

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 35 40 45

Gly Asp Asp Ser Asn Asp Asn Leu Ala Ser Lys Arg Gln Leu Ile Asn  
 50 55 60

Asp Leu Leu His Asn Asp His Phe Glu Glu Gly Thr Glu Arg Tyr Ile  
 65 70 75 80

Ile Pro Gln Asn Phe Leu His Glu Phe Leu Asn Leu Pro Ile Asp Asn  
 85 90 95

Phe Ser Asp Leu Lys Asp Gln Leu Gly Pro Ile Asp Phe His Ser Leu

468

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Leu Asn Glu Gln Gly Asn Leu Tyr Pro Glu Asn Glu Glu Pro Val Thr		
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Phe Cys His Val Ser Pro Glu Val Phe Gln His Leu Gly Glu Trp Phe		
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Gly Ile Leu Gly Gln Pro Ile Ile Arg Ala Ile Ile Ile Asn Pro Asp		
145	150	155
155	160	
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Thr Lys Glu Lys Gln Ile Glu Arg Phe Pro Pro Leu Phe Trp Val His		
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Gln Leu Gly Lys Lys Thr Gln Pro Thr Tyr Leu Arg His Arg His Asn		
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Gly Ser Asn His Asn His His His His Gly His His Asp Ser Pro Ile		
195	200	205
Pro Val Leu Leu Ser Lys Thr Ser Thr Phe His Arg Leu Met Asp Val		
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Ile Arg Tyr Asn Val Leu Lys Ala Pro Arg Lys Ser Thr Lys Asp Phe		
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235	240	
Arg Ile Trp Phe Ile Val Pro Gln Asp Lys Gly Leu Gln Tyr Leu Ile		
245	250	255
Ser Ile Gln Thr Phe Met Phe Asp Ile Ser Lys Lys Thr Leu Val Ser		
260	265	270
Pro Asn Met Leu Glu Asp Ala Leu Lys Asp His Gly Ile Val Ala Ser		
275	280	285
Ser Tyr Asn Ile Met Val Glu Ala Lys Glu Lys His Gln Thr Glu Phe		
290	295	300
Pro Ile Asp Gln Phe Ile Leu Ser His Ser Asn Ala Tyr Glu Glu Val		
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315	320	
Ser Gln Gly Gly Gly His Leu Gly Leu Ser Asn Met Gly Asn Thr Cys		
325	330	335
Tyr Met Asn Ser Ala Leu Gln Cys Leu Leu His Val Pro Glu Ile Asn		
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Tyr Tyr Phe Phe Tyr Asn Ile Tyr Lys Lys Glu Leu Asn Phe Asp Asn		

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Pro Leu Gly Tyr His Gly Asp Val Ala Asn Ala Phe Gly Ser Leu Leu		
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Lys Gln Ala Phe Asp His Val Lys Asn Ser Ser Ser Ile Ser Pro Arg		
385	390	395 400
Glu Phe Lys Ser Thr Ile Gly Arg Tyr Ser Ser Met Phe Ser Gly Tyr		
405	410	415

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Leu Gln Gln Asp Ser Gln Glu Leu Leu Ser Trp Leu Leu Asp Ala Leu		
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Glu Leu Lys Asp Asp Glu Ile Asp Asp Pro Gln Ala Ile Thr Lys Leu		
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Ala Asn Thr Cys Trp Asn Gln His Lys Ala Arg Asn Asp Ser Val Ile		
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Ile Asp Leu Phe Thr Gly Leu Tyr Gln Ser Thr Leu Ile Cys Pro Asp		
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Cys Gly Lys Lys Ser Ile Thr Phe Asp Pro Phe Asn Asp Leu Thr Leu		
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Pro Leu Pro Ile Ser Lys Lys Trp Tyr His Thr Phe Thr Ile Val Asp		
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Leu Ser Asn Gln Gly Val Ile Pro Glu Arg Ile Met Lys Leu Glu Val		
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Glu Leu Asn Lys Thr Ser Asn Phe Asp Asp Leu Leu Ser Tyr Leu Ser		
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Gln Asn Ala Ile Tyr Ser Asp Phe Gln Leu Asp Tyr Thr Lys Asn Lys		
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Phe Leu Pro Ile Ser Asp Ile Ile Arg Asp Thr Asp Asp Val Ile Val		
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Tyr Ile Val Pro His Asn Pro Ala Val Asp Ile Ile Val Pro Val Phe		

470

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Gly Ile Pro Leu Phe Val Val Met Asn Lys Glu Val Asp Val Asn Ser		
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Phe Gly Phe Ile Arg Lys Lys Leu Leu Glu Thr Val Ser Leu Leu Ser		
	660	665 670
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Asp Tyr Val Glu Lys Val Phe Tyr Lys Lys Ser Asp Phe Pro Ala Leu		
	690	695 700
Ser Gln Pro Leu Glu Thr Ser Asp Cys Glu Lys Asn Asn Asn Asn Thr		
	705	710 715 720
Ser Asp Asn Asp Asp Asp Glu Asp Ala Asp Asn Asp Glu Gly Tyr Asp		
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Ser Glu Val Ser Leu Ala Asn Pro Tyr Leu Gly Ala Asn Phe Gly Phe		
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Lys Ile Met Tyr Val His Asp Tyr Ser Pro Lys Leu Asn Ser Asn Leu		
	755	760 765
Arg Ser Arg Tyr Asn His Asp Gln Thr Thr Lys Phe Lys Gln Thr Glu		
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Arg Val Ile Asn Val Pro Thr His Lys Pro Thr Phe Ser Asp Phe Lys		
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Pro Leu Ser Asp Gln Leu Ser Glu Ser Lys Arg Asn Tyr Tyr Phe Tyr		
	805	810 815
Pro Asp Tyr Lys Lys Met Asp Asp Glu Met Asp Gln Leu Val Glu Glu		
	820	825 830
Val Asn Gln Asn Leu Ala Glu Gln Xaa Glu Ala Arg Ser Ser Gly Ser		
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Glu Asn Ser Ser Arg Ala Ser Glu Glu Gln Asp Gly Phe Val Leu Ile		
	850	855 860
Asn Lys Glu Asp Thr Leu Lys Gln Gln Ser Thr Val Pro Ala Ala Ala		

471

472

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Ser Ala Tyr Leu Leu Phe Tyr Arg Arg Arg Ser Ser Lys Gly Ala Gly  
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1250 1255 1260  
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Lys Lys Ser Arg Pro Phe Asp Glu Leu Lys Pro Ser Thr Ser Glu Thr  
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Asp Tyr Asp Tyr Glu Ala Glu Val Glu Asp Ser Asn Ile Arg Lys Gln  
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Arg Leu Leu Ser Lys Glu Asn Asn Ser Asn Lys Leu Val His Ile Lys  
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<210> 391  
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 <212> DNA  
 <213> *Candida albicans*

<400> 391

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&lt;210&gt; 392

&lt;211&gt; 896

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 392

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 20 25 30

Leu Asp Asn Glu Lys Glu Ser Glu Thr Lys Ser Phe Thr Gly Glu Leu  
 35 40 45

Glu Tyr Thr Ser Thr Ser Ser Asn Gly Glu His Asp Thr Thr Thr Thr  
 50 55 60

Ala Thr Lys His Glu Leu Ile Leu Gln Gln Ile Leu Asn Ser Asn Asp  
 65 70 75 80

Glu Ser Tyr Ile Asn Pro Lys Ser Leu Thr Phe Asp Pro Leu Lys Ile  
 85 90 95

Phe Thr Lys Gln Leu Ile Gly Glu Leu Ile Lys Ile Asn Gln Phe Tyr  
 100 105 110

Asn Ser Lys Glu Ser Glu Ile Phe Lys Ile Tyr Asn Asn Leu Ile His  
 115 120 125

Asp Leu Gln Asn Gln Asn Ile Asn Ile Asp Asp Val Phe Lys Phe Thr  
 130 135 140

Gln Ala Tyr Asn Tyr Ser Asp Pro Asn Ile Ile Asn Thr Asp Asp His  
 145 150 155 160

His Gln Tyr His Leu Lys Ser Thr Leu Ser Arg Thr Val Thr Asn Ala  
 165 170 175

Ser Val Phe Asp Thr Ile Asn His Ile Asp Asn Asp Tyr Asp Asn Asn  
 180 185 190

475

Asn Asn Asn Gln Lys Asn Asn Tyr Asp Leu Glu Lys Gln Asn Asn Thr  
195 200 205

Thr Val Ala Ile His Asp Asp Asp Asp Ser Glu Asp Asp Glu Glu Glu  
210 215 220

Glu Glu Glu Glu Thr His Ser His Asp Ser Val Leu Leu Asn His Thr  
225 230 235 240

His Phe Asn Val Lys Gln Gln Leu Lys Ile Thr Leu Lys Arg Lys Ala  
245 250 255

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Ile Thr Leu Phe Ile Asn Leu Ser Glu Leu Lys Ser Phe Ile Glu Leu  
260 265 270

Asn Arg Ile Gly Phe Thr Lys Ile Cys Lys Lys Phe Asp Lys Thr Cys  
275 280 285

Gly Tyr Ser Ile Lys Gln Asp Phe Ile Asn Glu Phe Leu Pro Gln Tyr  
290 295 300

Ser Arg Val Phe Glu Asn Asp Thr Ile Glu Glu Leu Asp Tyr Lys Leu  
305 310 315 320

Asn Gln Ile Ile Lys Ile Tyr Ala Phe Leu Ser Asn Lys Leu Thr Thr  
325 330 335

Gln Ser Thr Thr Lys Glu Asp Leu Asp Asn Ile Lys Phe Glu Leu Arg  
340 345 350

Ser Tyr Leu Arg Asp His Ile Val Phe Glu Arg Asn Thr Val Trp Lys  
355 360 365

Asp Leu Leu Ser Leu Glu Lys Lys Ser Tyr Asn Ile Asp Leu Asp Asn  
370 375 380

Ser Val Val Gln Asn Asn Lys Met Gly Asp Glu Gly His Ile Ile Asn  
385 390 395 400

Ser Met Met Asn Leu Ser Met Lys Arg Ile Asn Leu Pro Gln Cys Leu  
405 410 415

Lys Lys Leu Ile Lys Tyr Asp His Ile Asp Ile Pro Gln Phe Leu Leu  
420 425 430

Thr Thr Gln Met Leu Lys Ile Ile Ile Ile Val Ile Val Phe Ile Ile  
435 440 445

Leu Leu Ala Val Lys Thr Phe Asn Asp Pro Val Gln Gly Arg Cys Leu  
450 455 460

Ala Val Leu Val Ala Ala Ala Met Leu Trp Ala Ser Glu Ala Leu Pro  
465 470 475 480

Leu Tyr Thr Thr Ala Leu Leu Ile Pro Leu Leu Val Val Thr Cys Lys  
485 490 495

Val Cys Lys Thr Pro Gly Thr Asp Asp Pro Met Asp Ala Thr Lys Ala  
500 505 510

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Ser Gln Tyr Ile Phe Gly Thr Met Trp Asn Ser Thr Ile Met Ile Leu  
515 520 525

Ile Gly Gly Phe Thr Leu Ala Ala Ala Leu Ser Lys Tyr Asn Leu Ala  
530 535 540

Lys Ile Leu Ser Ser Tyr Ile Leu Ala Leu Ala Gly Thr Asn Pro Arg  
545 550 555 560

Asn Val Leu Leu Ala Ile Met Cys Val Ser Leu Phe Leu Ser Met Trp  
565 570 575

Ile Ser Asn Val Ala Ala Pro Val Leu Cys Phe Ser Leu Ile Gln Pro  
580 585 590

Val Leu Arg Ser Ile Pro Thr Asp Ser Pro Val Ala Lys Ala Leu Val  
595 600 605

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Ala Ser Pro Gln Asn Val Ile Ala Leu Glu Ser Met Asn Pro Asn Pro  
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Gly Trp Gly Lys Trp Phe Ala Val Ala Leu Pro Val Ala Ile Ile Ser  
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Val Lys Ile Lys Gln Phe Lys Pro Ile Lys Glu Lys Leu Thr Met Lys  
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Gln Trp Phe Val Phe Ala Val Thr Ile Thr Thr Ile Leu Leu Trp Cys  
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Val Met Gln Lys Ile Asp Gly Thr Phe Gly Glu Ser Gly Ile Ile Thr  
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Cys Ile Pro Ile Val Leu Phe Phe Gly Thr Gly Leu Leu Lys Val Asp  
725 730 735

Asp Leu Asn Asn Tyr Pro Trp Ser Ile Val Met Leu Ala Met Gly Gly  
740 745 750

Ile Ala Leu Gly Lys Ala Val Thr Ser Ser Gly Leu Leu Lys Thr Ile  
755 760 765

Ala Leu Ala Leu Gln Lys Arg Ile Met His Tyr Asp Ala Ile Val Val  
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Leu Ile Ile Phe Gly Ala Leu Ile Leu Val Val Ala Thr Phe Val Ser  
785 790 795 800

His Thr Val Ser Ala Leu Ile Ile Ile Pro Leu Val Lys Glu Val Gly  
805 810 815

Asp Ser Leu Pro Lys Pro His Pro Leu Met Leu Ile Met Gly Val Ala  
820 825 830

Leu Ile Ala Ser Gly Ala Met Gly Leu Pro Thr Ser Gly Phe Pro Asn  
835 840 845

Val Thr Ala Ile Gly Met Arg Asp Glu Val Gly Lys Pro Tyr Leu Thr  
850 855 860

Val Asn Leu Phe Ile Thr Arg Gly Val Pro Ala Ser Ile Ile Val Tyr  
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Val Cys Ile Ile Thr Ile Gly Tyr Gly Ile Met Ser Ser Leu Asn Phe  
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<210> 393

<211> 2279

<212> DNA

<213> Candida albicans

<400> 393

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&lt;210&gt; 394

&lt;211&gt; 592

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 394

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Pro	Ser	Glu	Pro	Asn	Ser	Gln	Pro	Gln	Gln	Gln	Gln	Ser	Gln	Pro	Glu
		35					40					45			
Ala	Lys	Thr	Glu	Pro	Gln	Thr	Ile	Arg	Pro	Ala	Thr	Phe	Thr	Thr	Ser
	50					55					60				
Gly	Asn	Ser	Ser	Ser	Ser	Ser	Ile	Ser	Thr	Leu	Ser	Ala	Asp	Ile	Ile
65					70					75				80	

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Gln	Pro	Leu	His	Gln	Leu	Ser	Ile	Asn	Asn	Asn	Asn	Ser	Thr	Val	Thr
			85					90						95	
Gln	Pro	Ala	Pro	Gln	Ser	Ser	Ser	Phe	Gln	Arg	Arg	Asn	Asn	Pro	Gln
		100						105					110		
Arg	Phe	Asn	Arg	Asn	Gln	Leu	Asn	Val	Tyr	Thr	Asp	Phe	Asn	Ser	Thr
	115						120					125			
Thr	Ser	Ser	Ala	Ser	Ser	Ile	Ser	Ser	Ser	Pro	Lys	Asp	Phe	Phe	Thr
	130					135					140				
Arg	Glu	Pro	Pro	Arg	Ile	His	Ser	Lys	Leu	Ile	Cys	Glu	Glu	Ile	Ala
145					150					155					160
Ser	Ala	Asn	Asn	Arg	Ala	Ala	Lys	Glu	Val	Leu	Ser	Arg	Leu	Ser	Thr
				165					170					175	
Asp	Glu	Leu	Arg	Ser	Val	Lys	Ser	His	Thr	Glu	Leu	Ala	Glu	Thr	Ala
		180						185					190		
Asn	Gly	Val	Arg	Met	Leu	Ala	Lys	Asn	Leu	Ser	Arg	Ala	Thr	Ile	Gln
	195						200					205			
Leu	Asp	Val	Arg	Ala	Ile	Met	Ile	Ile	Thr	Lys	Ala	Arg	Asp	Asn	Gly
	210					215					220				

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Leu	Ile	Tyr	Leu	Thr	Lys	Glu	Val	Val	Glu	Trp	Ile	Leu	Asp	Gln	His
225					230					235				240	
Pro	His	Ile	Thr	Ile	Tyr	Ala	Asp	Glu	Lys	Leu	Ala	Lys	Ser	Lys	Arg
			245						250					255	
Phe	Asn	Pro	Glu	Ser	Ile	Ile	Ala	Asn	Tyr	Pro	Asn	Gly	Cys	Lys	Lys
			260					265					270		

480

Leu Lys Tyr Trp Asn Lys Lys Leu Thr Thr Lys Asn Pro Glu Ile Phe  
 275 280 285  
 Asp Leu Val Leu Thr Leu Gly Gly Asp Gly Thr Val Leu Phe Ala Ser  
 290 295 300  
 Asn Leu Phe Gln Lys Ile Val Pro Pro Ile Leu Ser Phe Ser Leu Gly  
 305 310 315 320  
 Ser Leu Gly Phe Leu Thr Asn Phe Glu Phe Ser Ala Phe Arg Thr Val  
 325 330 335

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Leu Ser Lys Cys Phe Asp Ser Gly Val Lys Ala Asn Leu Arg Met Arg  
 340 345 350  
 Phe Thr Cys Arg Val His Thr Asp Glu Gly Lys Leu Ile Cys Glu Gln  
 355 360 365  
 Gln Val Leu Asn Glu Leu Val Val Asp Arg Gly Pro Ser Pro Tyr Val  
 370 375 380  
 Thr His Leu Glu Leu Tyr Gly Asp Gly Ser Leu Leu Thr Val Ala Gln  
 385 390 395 400  
 Ala Asp Gly Leu Ile Ile Ala Thr Pro Thr Gly Ser Thr Ala Tyr Ser  
 405 410 415  
 Leu Ser Ala Gly Gly Ser Leu Val His Pro Gly Val Ser Ala Ile Ser  
 420 425 430  
 Val Thr Pro Ile Cys Pro His Thr Leu Ser Phe Arg Pro Ile Leu Leu  
 435 440 445  
 Pro Asp Gly Met Phe Leu Lys Val Lys Val Pro Ser Ser Ser Arg Ala  
 450 455 460  
 Thr Ala Trp Cys Ser Phe Asp Gly Lys Val Arg Thr Glu Leu Lys Lys  
 465 470 475 480  
 Gly Tyr Tyr Val Thr Ile Gln Ala Ser Pro Phe Pro Leu Pro Thr Val  
 485 490 495  
 Met Ser Ser Lys Thr Glu Tyr Ile Asp Ser Val Ser Arg Asn Leu His  
 500 505 510  
 Trp Asn Ile Arg Glu Gln Gln Lys Pro Phe Ser Ser Tyr Leu Lys Pro  
 515 520 525

481

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Glu Thr Arg Gln Ser Ile Ala Glu Ser Glu Arg Leu Asp Asn Leu His
530                               535                               540

Ile Ser Ser Glu Gln Asp Glu Ser Asn His Glu Glu Pro Glu Ile Thr
545                               550                               555                               560

Glu Asp Phe Asp Ile Asn Tyr Thr Asp Asn Glu Arg Asp Ser Ser Ser
565                               570                               575

Ser Thr Pro Ser Glu Glu Ser Asn Glu Glu Cys Ala Asn Thr Thr Thr
580                               585                               590

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&lt;210&gt; 395

&lt;211&gt; 1042

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 395

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atagcggccg cgcatataat agagaatatg tcattaccag cttcatttga ctttaactcca 60
gaagatgcta aattgttatt agctgccaac gtccatttgg gtgctaagaa cgttcaagtt 120
cacaacaaac catatgttta caaaaccaga ccagatggta tgaacatcat caacattggg 180
aaaacttggg aaaaaattgt tttggctgcc agaattattg ctgctgttcc aaacgcttct 240
gatgttgctg tttgttcttc aagaactttc ggtcaaagag ctgttttgaa atttgctgct 300
cacactgggtg ctactgccat tgctggtaga ttcactccag gtaactttac caattatata 360
actcgttcat tcaaagaacc aagattagtt gttgttactg acccaagaac cgatgctcaa 420
gccatcaaag aatcatctta tgttaacatt ccagttattg ccttgactga catgcagtct 480
ccatctgaat acgttgatgt tgccattcca tgtaacaaca aaggtaaaca ctgtattggg 540
ttaatctggt ggttgcttgc tagagaagtc ttgagattaa gaggtattat ccagacaga 600
actaccgaat ggtcagttat gccagatttg tacttctaca gagaccaga agaaattgaa 660
caaaatgccg tcgaagaagc taaaactgaa ggagttgaag gagctccagt tgctgaagct 720
gaaaccgaat ggactgggtga aactgaagat gttgattggg ctgattctgg tgctaccccc 780
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gaagtagaag tagaagaaga aacaataaca acaataacaa ccaaaataaa aaaaagggtt 900
aatgatgtat attatcgata aggagaaaga agagattttc tttttaata atgaggatgc 960
cattttatac aaatccaaaa ttgtaattaa gaaagattaa taaatataaa atatatatat 1020
ataagtaaaa aaaaaaaaaa aa 1042

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&lt;210&gt; 396

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Candida albicans



&lt;400&gt; 396

```

Met Ser Leu Pro Ala Ser Phe Asp Leu Thr Pro Glu Asp Ala Lys Leu
 1              5              10              15

Leu Leu Ala Ala Asn Val His Leu Gly Ala Lys Asn Val Gln Val His
      20              25              30

Asn Lys Pro Tyr Val Tyr Lys Thr Arg Pro Asp Gly Met Asn Ile Ile
      35              40              45

Asn Ile Gly Lys Thr Trp Glu Lys Ile Val Leu Ala Ala Arg Ile Ile
      50              55              60

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Ala Ala Val Pro Asn Ala Ser Asp Val Ala Val Cys Ser Ser Arg Thr
 65              70              75              80

Phe Gly Gln Arg Ala Val Leu Lys Phe Ala Ala His Thr Gly Ala Thr
      85              90              95

Ala Ile Ala Gly Arg Phe Thr Pro Gly Asn Phe Thr Asn Tyr Ile Thr
      100             105             110

Arg Ser Phe Lys Glu Pro Arg Leu Val Val Val Thr Asp Pro Arg Thr
      115             120             125

Asp Ala Gln Ala Ile Lys Glu Ser Ser Tyr Val Asn Ile Pro Val Ile
      130             135             140

Ala Leu Thr Asp Met Gln Ser Pro Ser Glu Tyr Val Asp Val Ala Ile
      145             150             155             160

Pro Cys Asn Asn Lys Gly Lys His Cys Ile Gly Leu Ile Trp Trp Leu
      165             170             175

Leu Ala Arg Glu Val Leu Arg Leu Arg Gly Ile Ile Pro Asp Arg Thr
      180             185             190

Thr Glu Trp Ser Val Met Pro Asp Leu Tyr Phe Tyr Arg Asp Pro Glu
      195             200             205

Glu Ile Glu Gln Asn Ala Val Glu Glu Ala Lys Thr Glu Gly Val Glu
      210             215             220

Gly Ala Pro Val Ala Glu Ala Glu Thr Glu Trp Thr Gly Glu Thr Glu
      225             230             235             240

Asp Val Asp Trp Ala Asp Ser Gly Ala Thr Pro Ser Cys
      245             250

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483

<210> 397  
 <211> 1335  
 <212> DNA  
 <213> Candida albicans

<400> 397  
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 atgcatgctc cacgagggtga aaataccgag gcaatggcgt tggttgtgcc atggactaat 120  
 tctgacaacg agtacaatga aggtgctatg agttttggcg tggctttggc acgggtacttt 180  
 acaaagatgt cgatctgggtc gaaaaacatt atttttgtat ttcctgagac gggccacaga 240  
 ccgttgaggt cgtgggttga ggcataccat acgggtgttg acgatactgc ggggtcgatt 300  
 gaggcggcga ttattatgga gtacggcaag aacgggtgatt attttgagta ttacgatatg 360  
 ttctacgaag ggttgaatgg gcagttgccg aatttggact tgttgaatac ggccaatgta 420  
 atgacgtatc atgaacagat cccctgtgcc atgcaaggga tgtcggatag ggttatcaat 480  
 tatagcaccg ggttcgagac tttgtttagg ggtatcctca aattgacgct tgtcgggttg 540  
 actgatgaag ttcattgggtg tgaagcattt tcgggggtggc agatccaggc atttacgac 600  
 aaggtaaggg ggactgaagg gaaagatgtt acgcagtttg gccggattgt cgattctacg 660  
 tttaggctcg ttaacaattt gcttgaagaag tttcaccaat cgtttttctt ttacttgatg 720  
 ttgtcgccaa aacactttgt gtctattggg acgtacttgc cgtcggcgat tttgttggca 780  
 gtatcgatg cggtgagctc tgtcagtgcg gtggtggttg ccgggtttga ttttcgaaag 840  
 ctatattttg tgggtggtggt tgaaattgcy tgtgctattt tggcgtttg gccggtgaac 900  
 cagggtgatgc ttgtagcgat tctggcggtg gtgttgttgc cgcgccaagc catcttttcc 960  
 aagcaggcgg cgttttcgct aatttctatt gcgttgttgg cagtggcatt acttattacc 1020  
 gccctcttga ttgtacattt tgcattggcg ttagtattg ggatttttag ccttccattg 1080  
 acatttgtcc cgacattaat gaagaacaag tctaggctaa cagctttttg tttggcgggtg 1140  
 tcgaatccgt tttttgtgat tttcgttgcg gggaaagtgc ttggccaccg cgagctattt 1200  
 gaccgggttg tcaactgcctg gtcggacata cagtgttggc catggtttat cgttgttttg 1260  
 ggggtggttcc cagcgtgggt gattatcaca ctaagctact gtggctacaa gccagttaag 1320  
 gaaaaaagtg aatag 1335

<210> 398  
 <211> 444  
 <212> PRT  
 <213> Candida albicans

<400> 398  
 Ser Gly Leu Gln Ile Ser Ser Met Lys Ile Gly Phe Ala Thr Asn Thr  
 1 5 10 15  
 Leu Tyr Ala Ile Met His Ala Pro Arg Gly Glu Asn Thr Glu Ala Met  
 20 25 30  
 Ala Leu Val Val Pro Trp Thr Asn Ser Asp Asn Glu Tyr Asn Glu Gly  
 35 40 45

484

Ala Met Ser Leu Ala Val Ala Leu Ala Arg Tyr Phe Thr Lys Met Ser  
 50 55 60  
 Ile Trp Ser Lys Asn Ile Ile Phe Val Phe Pro Glu Thr Gly His Arg  
 65 70 75 80  
 Pro Leu Arg Ser Trp Val Glu Ala Tyr His Thr Val Leu Asp Asp Thr  
 85 90 95  
 Ala Gly Ser Ile Glu Ala Ala Ile Ile Met Glu Tyr Gly Lys Asn Gly  
 100 105 110

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Asp Tyr Phe Glu Tyr Tyr Asp Met Phe Tyr Glu Gly Leu Asn Gly Gln  
 115 120 125  
 Leu Pro Asn Leu Asp Leu Leu Asn Thr Ala Asn Val Met Thr Tyr His  
 130 135 140  
 Glu Gln Ile Pro Cys Ala Met Gln Gly Met Ser Asp Arg Val Ile Asn  
 145 150 155 160  
 Tyr Ser Thr Arg Leu Gln Thr Leu Phe Arg Gly Ile Leu Lys Leu Thr  
 165 170 175  
 Leu Val Gly Leu Thr Asp Glu Val His Gly Cys Glu Ala Phe Ser Gly  
 180 185 190  
 Trp Gln Ile Gln Ala Phe Thr Ile Lys Val Arg Gly Thr Glu Gly Lys  
 195 200 205  
 Asp Val Thr Gln Phe Gly Arg Ile Val Asp Ser Thr Phe Arg Ser Val  
 210 215 220  
 Asn Asn Leu Leu Glu Lys Phe His Gln Ser Phe Phe Phe Tyr Leu Met  
 225 230 235 240  
 Leu Ser Pro Lys His Phe Val Ser Ile Gly Thr Tyr Leu Pro Ser Ala  
 245 250 255  
 Ile Leu Leu Ala Val Ser Tyr Ala Leu Ser Ser Val Ser Ala Val Val  
 260 265 270  
 Val Ala Gly Phe Asp Phe Arg Lys Leu Tyr Phe Val Val Val Val Glu  
 275 280 285  
 Ile Ala Cys Ala Ile Leu Ala Phe Val Pro Val Asn Gln Val Met Leu  
 290 295 300

485

Val Ala Ile Ser Ala Val Val Leu Leu Pro Arg Gln Ala Ile Phe Ser  
305 310 315 320

Lys Gln Ala Ala Phe Ser Leu Ile Ser Ile Ala Leu Leu Ala Val Ala  
325 330 335

Leu Leu Ile Thr Ala Leu Leu Ile Val His Phe Ala Leu Ala Phe Ser  
340 345 350

Ile Gly Ile Leu Ala Leu Pro Leu Thr Phe Val Pro Thr Leu Met Lys  
355 360 365

Asn Lys Ser Arg Leu Thr Ala Phe Cys Leu Ala Val Ser Asn Pro Phe  
370 375 380

Phe Val Ile Phe Val Ala Gly Lys Val Leu Gly His Pro Glu Leu Phe  
385 390 395 400

Asp Arg Leu Val Thr Ala Trp Ser Asp Ile Gln Cys Trp Thr Trp Phe  
405 410 415

Ile Val Val Leu Gly Trp Phe Pro Ala Trp Val Ile Ile Thr Leu Ser  
420 425 430

Tyr Cys Gly Tyr Lys Pro Val Lys Glu Lys Ser Glu  
435 440

<210> 399

<211> 1190

<212> DNA

<213> Candida albicans

<400> 399

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caaaaccctt tgttctcat agttaatccg actaaagaag tgttttttt ttcttttctt 120  
ttttgctata tcctagttgc cttaacgaca gtaatagtta aagcgttggg aagtaatggt 180  
gaactcgaac catttggttg acgctgacga ttaataatgt gaatttctt tttctttttg 240  
gttgtagtaa ttgctttggt ttgttgctta aattaggaaa atgtcgtgac cttacgtaca 300  
gcacacacat accactgtcg tgcactgacc aacaacaatg cgggtgtaat cgataaccaa 360  
aagattataa atagggggtg gaaggctgcc actgtttgaa atgaatcaac acagtttttt 420  
ttcttcttgc tttttcttct tattttacat tacaaattct gacaatcgtc aactaacata 480  
tatatacaaa tctacaagca atgcaaattt tcgttaaaac tttgactggt aaaaccatta 540  
ccttagaagt cgaatcttct gacaccatcg ataacgtcaa atccaagatc caagacaaag 600  
aaggatttcc accagaccaa caaagattga ttttcgccgg taaacaatta gaagatggca 660  
gaaccttgct tgactacaac atccaaaaag aatctacttt acatttggtt ttaagattga 720

gaggtggtat gcaaatcttt gttaaaactt taactggtaa gactatcact ttggaagtcg 780  
 aatcttctga caccatcgat aacgtcaaat ccaagatcca agacaaagaa ggtattccac 840  
 cagaccaaca aagattgatt ttcgccggtg aacaattgga agacggtaga acctgtctg 900  
 actacaacat ccaaaaagaa tctactttac atttggtttt aagattgaga ggtggtatgc 960  
 aaatctttgt taaaacttta actggtaaga ctatcacttt ggaagtcgaa tcttctgaca 1020  
 ccatcgataa cgtaaatcc aagatccaag acaaagaagg tattccacca gatcaacaaa 1080  
 gattgatttt tgctggtaaa caattagaag atggcagaac cttgtctgac tacaacatcc 1140  
 aaaaagaatc taccttgac ttggtcttga gattgagagg tggtttctaa 1190

<210> 400

<211> 229

<212> PRT

<213> Candida albicans

<400> 400

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
 1 5 10 15

Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp  
 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
 65 70 75 80

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
 85 90 95

Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile  
 100 105 110

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
 115 120 125

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
 130 135 140

Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu  
 145 150 155 160

Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp  
 165 170 175

487

Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln  
 180 185 190

Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu  
 195 200 205

Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg  
 210 215 220

Leu Arg Gly Gly Phe  
 225

<210> 401  
 <211> 2390  
 <212> DNA  
 <213> Candida albicans

<400> 401

tccagaatag	taattaggga	ctttaatttt	attaggagtg	gattgcatag	aatatgctat	60
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gcccgaagta	gtgcacacaa	caaactagtt	tacaaagtaa	aattcgaagt	tacgtcaaag	180
cttagaatgg	ttcttatagt	agttgtctac	tctatcaaaa	aacccataat	ttgtctatat	240
aacgtaagga	tcactatatg	ctgttgagta	agaaatatgt	tgcgagccgt	accgacaatg	300
gattggctga	aacttgttct	catcaaactt	gcaaaacact	tggagacgcg	cgcgcgtttc	360
aacacacaat	aaacaacacg	aaaaataagg	tagaaaacaa	aaaaaaaaata	aaaggaactt	420
taaacaagaa	gtaatcccca	ttaaaacttg	atcaaacactt	ttagggtttc	cgatttcccc	480
attttcttga	ctaaaataat	atgagaatac	tatgtgttgc	cgaaaaacca	tcgatttcaa	540
aagaggtggc	aaacattttg	ggaggagggc	gaaaaaaagt	aagaaactca	cgagaaaaat	600
tcatcaaaaa	ctacgatttc	accttcactt	tcaactctga	agatgggcca	tgtcaagtaa	660
ccatgacttc	ggtggctgga	catatcacag	gacttgattt	tgggtctgcc	ttttcgtagg	720
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ctatttatga	aaatattgca	gaagaggcaa	gaaacgctga	taagttgatg	atctggacag	840
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cattctggta	tattgagatt	gaaactagga	aagagaataa	aaagacaatt	ttcaattggg	1260
ttcgagggtca	ttttttcgac	aagatgtatg	tggttatgct	ttatgatcga	tgctgcaaaa	1320
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agacggcggt	ggcagctgct	gaaagacttt	ataacctagg	gtatttgtcg	tatcctagaa	1500
ctgaaactga	caggtttgcc	aaagaaaccg	atttcaagag	cttactagag	gtgcacaaac	1560
aagatccgcy	atggggaagc	tatacaacaa	agcttttgaa	cgaaggtttc	gaaactcctc	1620

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gaagcgggtc tcatgatgat aaggcgcata ctccaatcca tcctatcaaa tatgtttctt 1680
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ttgcctgttg ctccaaagat gctgttggtg cgcaaaccgt ggtgacttta aaatggggag 1800
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agttgtcgag tggaatattg aaagacggta aaacaagtcc acccaatcat atgaccgagc 1980
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aagatgtatc actatcgaaa ccatttttgc ggaagtcgtt ggaacgatca cttgaggaca 2220
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aegettatat tgtttgttct catcagatac ttgttttgtg caatgaatgt aggagaatta 2340
tacttggaag tagcagtaac aacaacaaca acaataataa taatagtaa 2390

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&lt;210&gt; 402

&lt;211&gt; 629

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 402

```

Met Arg Ile Leu Cys Val Ala Glu Lys Pro Ser Ile Ser Lys Glu Val
  1             5             10             15

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```

Ala Asn Ile Leu Gly Gly Gly Arg Lys Lys Val Arg Asn Ser Arg Glu
      20             25             30

```

```

Lys Phe Ile Lys Asn Tyr Asp Phe Thr Phe Thr Phe Asn Ser Glu Asp
      35             40             45

```

```

Gly Pro Cys Gln Val Thr Met Thr Ser Val Ala Gly His Ile Thr Gly
      50             55             60

```

```

Leu Asp Phe Gly Ser Ala Phe Ser Trp Gly Asn Cys Val Pro Gly Arg
      65             70             75             80

```

```

Leu Phe Glu Ala Asp Ile Lys Thr Ile Ile Thr Lys Lys Ser Ile Tyr
      85             90             95

```

```

Glu Asn Ile Ala Glu Glu Ala Arg Asn Ala Asp Lys Leu Met Ile Trp
      100             105             110

```

```

Thr Asp Cys Asp Arg Glu Gly Glu Tyr Ile Gly Phe Glu Ile Met Asn
      115             120             125

```

```

Ala Ala Arg Lys Tyr Asn Arg Asn Leu Gly Leu Asn Asn Ile Trp Arg
      130             135             140

```

489

Ala Arg Phe Ser His Leu Glu Arg Asn His Ile Ile Arg Ala Ala Lys  
 145 150 155 160

Asn Pro Val Asn Leu Asp Met Ser Ala Val Ser Ala Val Ser Cys Arg  
 165 170 175

Met Glu Ile Asp Leu Arg Val Gly Thr Ser Phe Thr Arg Leu Leu Thr  
 180 185 190

Asp Gln Leu Arg Gln Lys Gly Ile Ile Glu Lys Asn Glu Leu Ala Ser  
 195 200 205

---

Tyr Gly Thr Cys Gln Phe Pro Thr Leu Gly Phe Val Val Asp Arg Tyr  
 210 215 220

Lys Arg Val Lys Ser Phe Thr Pro Glu Pro Phe Trp Tyr Ile Glu Ile  
 225 230 235 240

Glu Thr Arg Lys Glu Asn Lys Lys Thr Ile Phe Asn Trp Val Arg Gly  
 245 250 255

His Phe Phe Asp Lys Met Tyr Val Val Met Leu Tyr Asp Arg Cys Cys  
 260 265 270

Lys Ser Gly Glu Phe Gly Thr Ile Ser Lys Ile Glu Ser Lys Arg Lys  
 275 280 285

Pro Asn Phe Arg Pro Phe Pro Leu Thr Thr Val Glu Leu Gln Lys Asp  
 290 295 300

Cys Ala Arg Phe Phe Lys Met Ser Ala Lys Thr Ala Leu Ala Ala Ala  
 305 310 315 320

Glu Arg Leu Tyr Asn Leu Gly Tyr Leu Ser Tyr Pro Arg Thr Glu Thr  
 325 330 335

Asp Arg Phe Ala Lys Glu Thr Asp Phe Lys Ser Leu Leu Glu Val His  
 340 345 350

Lys Gln Asp Pro Arg Trp Gly Ser Tyr Thr Thr Lys Leu Leu Asn Glu  
 355 360 365

Gly Phe Glu Thr Pro Arg Ser Gly Ser His Asp Asp Lys Ala His Pro  
 370 375 380

Pro Ile His Pro Ile Lys Tyr Val Ser Leu Asp Thr Leu Asn Thr Leu  
 385 390 395 400



Asp Glu Lys Lys Val Tyr Glu Tyr Val Val Arg Arg Phe Ile Ala Cys  
 405 410 415

Cys Ser Lys Asp Ala Val Gly Thr Gln Thr Val Val Thr Leu Lys Trp  
 420 425 430

Gly Asp Glu Phe Phe Thr Ala Ser Gly Leu Met Val His Glu Lys Asn  
 435 440 445

Tyr Leu Glu Val Tyr Thr Tyr Lys Lys Trp Glu Ser Ser Lys Gln Leu  
 450 455 460

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Pro Lys Phe Thr Glu Gly Glu Gln Val Lys Leu Ser Ser Gly Ile Leu  
 465 470 475 480

Lys Asp Gly Lys Thr Ser Pro Pro Asn His Met Thr Glu Pro Glu Leu  
 485 490 495

Ile Ala Leu Met Asp Ala Asn Gly Ile Gly Thr Asp Ala Thr Ile Ala  
 500 505 510

Glu His Ile Asn Lys Ile Glu Thr Arg His Tyr Ile Asn Lys Leu Lys  
 515 520 525

Lys Gly Lys Asn Glu Tyr Ile Leu Pro Thr Pro Leu Gly Met Gly Leu  
 530 535 540

Ile Glu Gly Leu Glu Lys Met Glu Phe Glu Asp Val Ser Leu Ser Lys  
 545 550 555 560

Pro Phe Leu Arg Lys Ser Leu Glu Arg Ser Leu Glu Asp Ile Ala Thr  
 565 570 575

Gly Ser Arg Pro Lys Val Asp Val Leu Asn Thr Thr Ile Gly Val Tyr  
 580 585 590

Val Asp Ala Tyr Ser Val Cys Ser His Gln Ile Leu Val Leu Cys Asn  
 595 600 605

Glu Cys Arg Arg Ile Ile Leu Gly Asn Ser Ser Asn Asn Asn Asn Asn  
 610 615 620

Asn Asn Asn Asn Thr  
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<210> 403

491

&lt;211&gt; 3098

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 403

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gttaaccact tttattacat atgatagaca atataatcaa taatttgcaa atcatactac 540
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&lt;210&gt; 404

&lt;211&gt; 865

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 404

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Asp Asp Asn Phe Thr Ser Pro His Asp Asp Val Ile Tyr Arg Pro His
      20             25             30

Ser Ala Arg Val Ala Arg Tyr Gln Val Ile Ile Ala Ser Thr Leu Gly
      35             40             45

Leu Thr Ala Leu Leu Leu Phe Ser Ile Leu Arg Leu Lys Tyr Pro Lys
      50             55             60

Ile Tyr Val Ala Asn Phe Asn His Leu Asn Phe Ser Leu His Ser Thr
      65             70             75             80

Ser Arg Arg Asn Leu Pro Glu Leu Pro Ser Asn Ser Leu Phe Gly Trp
      85             90             95

Ile Pro Thr Val Tyr Lys Ile Thr Glu Gln Glu Ile Leu Glu His Ala
      100            105            110

Gly Leu Asp Ala Val Val Phe Leu Glu Phe Phe Lys Met Cys Ile Arg
      115            120            125

Ile Ile Ser Ile Cys Leu Val Phe Ala Ile Ile Ile Ile Ser Pro Ile
      130            135            140

Arg Tyr Lys Phe Thr Gly Arg Val Asp Glu Asp Tyr Pro Asp Asp Asp
      145            150            155            160

Ser Asp Asn Asp Asp Asp Asp Gly Ser Asn Asn Asn Gly Thr Thr Ile

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	165		170		175
Ile Lys His	Ile Val Ser Ala Gly	Ile Ser Val Ala Ser	Lys Asn Asn		
180		185	190		
Asp Gly Glu Gln Tyr Gln Gln Phe Leu Trp Leu Tyr Thr	Ile Phe Thr				
195	200	205			
Tyr Val Phe Thr Phe Val Thr Val Tyr Phe Leu Phe Lys Gln Thr Asn					
210	215	220			
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Arg Ile Ile Ser Met Arg Gln Lys Tyr Leu Gly Ser Gln Asn Ser Val					
225	230	235	240		
Thr Asp Arg Thr Val Lys Ile Ser Gly Ile Pro Gly Ser Leu Arg Asp					
245	250	255			
Glu Val Ala Leu Ala Arg His Ile Asp Arg Leu Asn Ile Gly Glu Val					
260	265	270			
Asp Ser Val Leu Ile Val Lys Glu Trp Gln Asn Leu Asn Lys Leu Phe					
275	280	285			
Lys Arg Arg Arg Arg Ile Val Arg Lys Leu Glu Glu Ser Trp Val Glu					
290	295	300			
Tyr Phe Glu Lys Asn Gly Ile Thr Asn Lys Ser Asp Leu Ile Ser Leu					
305	310	315	320		
His Pro Gln Val Gly Glu Ser Tyr Arg Phe Ser Asn Arg Tyr Thr Asp					
325	330	335			
Asp Ala Glu Glu Ser Pro Asp Trp Gly Ser Gln Asn Ser Asn Ser Ala					
340	345	350			
Gln Ala Ser Ile Ile Asp Gln Asp Ser Glu Ser Val Glu Gly Asp Ser					
355	360	365			
Ser Asp Thr Leu Asn Arg Leu Leu Asn Asp Glu Ser Arg Thr Arg Pro					
370	375	380			
Ser Leu Arg Lys Gly Trp Phe Gly Leu Phe Gly Pro Lys Val Asp Ser					
385	390	395	400		
Ile Asn Tyr Tyr Thr Asp Lys Leu Glu Val Ile Asp Lys Glu Ile Thr					
405	410	415			
Arg Ala Arg Thr Arg Glu Tyr Pro Ala Thr Ser Thr Ala Phe Leu Thr					

494

420

425

430

Met Lys Thr Val Ala Glu Ala Gln Met Leu Ala Gln Ala Val Leu Asp  
435 440 445

Pro Lys Val Asn His Leu Ile Thr Asn Leu Ala Pro Ala Pro His Asp  
450 455 460

Ile Arg Trp Asp Asn Leu Ser Leu Thr Arg Gln Asp Arg Asn Thr Lys  
465 470 475 480

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Ile Leu Ala Val Thr Ile Phe Ile Gly Ile Met Ser Leu Leu Leu Val  
485 490 495

Tyr Pro Val Arg Phe Met Ala Ser Phe Leu Asn Thr Lys Ser Ile Ser  
500 505 510

Lys Ile Trp Pro Ser Leu Gly Lys Ala Ile Glu Ser His Lys Trp Ala  
515 520 525

Glu Thr Leu Ile Thr Gly Leu Leu Pro Thr Tyr Leu Phe Thr Ile Leu  
530 535 540

Asn Ile Val Ile Pro Phe Phe Tyr Val Trp Ile Ser Glu Lys Gln Gly  
545 550 555 560

Tyr Leu Ser His Ser Asp Glu Glu Leu Ser Ser Val Ser Lys Asn Phe  
565 570 575

Phe Tyr Ile Phe Val Asn Leu Phe Leu Val Phe Thr Thr Phe Gly Thr  
580 585 590

Ala Ser Phe Val Asp Thr Thr Lys Ile Ala Phe Asp Leu Ala Arg Ser  
595 600 605

Leu Arg Asp Leu Ser Met Phe Tyr Val Asp Leu Ile Ile Leu Gln Gly  
610 615 620

Leu Gly Ile Phe Pro Phe Lys Leu Leu Leu Val Gly Asn Leu Leu Arg  
625 630 635 640

Phe Leu Val Asn Ser Leu Phe Arg Cys Lys Thr Pro Arg Asp Tyr Leu  
645 650 655

Asn Leu Tyr Lys Pro Pro Val Phe Asn Phe Gly Leu Gln Leu Pro Gln  
660 665 670

Pro Ile Leu Ile Phe Ile Ile Thr Leu Val Tyr Ser Val Met Ser Ser

495

675

680

685

Lys Ile Leu Thr Ala Gly Leu Leu Tyr Phe Ile Ile Gly Tyr Phe Val  
 690 695 700

Ser Lys Tyr Gln Leu Leu Tyr Ala Cys Val His Pro Pro His Ser Thr  
 705 710 715 720

Gly Lys Val Trp Pro Ile Ile Phe Arg Arg Ile Ile Leu Gly Leu Phe  
 725 730 735

~~Leu Phe Gln Ile Thr Met Val Gly Thr Leu Ala Leu Gln Asp Ala Ile~~  
 740 745 750

Thr Cys Ala Thr Phe Leu Ala Pro Leu Pro Phe Leu Thr Leu Tyr Phe  
 755 760 765

Trp Trp Ser Phe His Lys Gln Tyr Ile Pro Leu Ser Thr Phe Ile Ala  
 770 775 780

Leu Arg Ala Ile Glu Ser Asn Glu Asn Ile Asn Pro Thr Asp Leu Glu  
 785 790 795 800

Gln Ile Ile Glu Asn Asn Asn Asn Lys Thr Leu Asp Glu Arg Arg Glu  
 805 810 815

Leu Asn Thr Lys Tyr Glu Tyr Pro Asn Leu Val Asn Asp Leu Asp Gly  
 820 825 830

Pro Met Ile Ala Leu Asp Gly Glu Asp Val Leu Ile Val Asn Arg Asp  
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Gly Thr Thr Val Arg Lys Pro Pro Gln Tyr Phe Ser Ser Glu Trp Asp  
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Tyr  
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<210> 405

<211> 1559

<212> DNA

<213> Candida albicans

<400> 405

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&lt;210&gt; 406

&lt;211&gt; 352

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 406

Met Ala Thr Ser Gln Glu Leu Thr Ala Asp Ile Gln Ala Leu Ala Thr  
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Ser Phe Pro Lys Arg Leu Ala Asn Asp Ser Asp Asn Ser Leu Leu Ile  
20 25 30

Asn Val Ala Pro Thr Gly Arg Gln Ala Lys Arg His Ile Gln Gln Ile  
35 40 45

Asn Tyr Ser Glu Glu Phe Gly Asp Asp Leu Asp Phe Asp Glu Phe Pro  
50 55 60

Ser Ser Thr Pro Gly Thr Arg Ser Leu Asn Glu Asn Lys Ala Gln Ile  
65 70 75 80

Glu Ala Gln Arg Tyr Ser Leu Ala Lys Asn Thr Pro Thr Pro Lys Arg

498



340

345

350

<210> 407  
 <211> 737  
 <212> DNA  
 <213> Candida albicans

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<400> 407  
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<210> 408  
 <211> 78  
 <212> PRT  
 <213> Candida albicans

<400> 408  
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 Arg Ser Asp Ile Lys Ser Ala Ile Val Lys Val Asn Ala Lys Val Asn  
 20 25 30  
 Ala Asn Gly Lys Lys Phe Lys Gln Thr Lys Phe Lys Val Arg Gly Ser  
 35 40 45  
 Arg Tyr Gln Tyr Thr Leu Val Val Asn Asp Ala Ser Lys Ala Lys Lys  
 50 55 60  
 Leu Gln Gln Ser Leu Pro Pro Thr Leu Lys Ile Thr Asn Leu  
 65 70 75

499

<210> 409  
 <211> 1348  
 <212> DNA  
 <213> Candida albicans

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<210> 410  
 <211> 127  
 <212> PRT  
 <213> Candida albicans

<400> 410  
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 Lys Ala Tyr Phe Thr Ala Ser Ser Val Glu Arg Arg Val Leu Leu Ser  
 20 25 30  
 Ala Pro Leu Ser Lys Glu Leu Arg Gln Gln Tyr Asn Val Lys Ser Leu  
 35 40 45

500

Pro Ile Arg Gln Asn Asp Glu Val Leu Val Val Arg Gly Ser Lys Lys  
 50 55 60

Gly Ser Glu Gly Lys Val Asn Ser Val Tyr Arg Leu Lys Phe Ala Ile  
 65 70 75 80

Gln Val Asp Lys Leu Gln Lys Glu Lys Ser Asn Gly Ala Ser Val Pro  
 85 90 95

Ile Asn Ile His Pro Ser Lys Val Val Ile Thr Lys Leu His Leu Asp  
 100 105 110

Lys Asp Arg Lys Ala Leu Ile Gln Arg Lys Gly Gly Lys Ala Glu  
 115 120 125

<210> 411

<211> 1631

<212> DNA

<213> Candida albicans

<400> 411

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&lt;210&gt; 412

&lt;211&gt; 376

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 412

Met Phe Val Tyr Trp Ile Asn Asn Leu Cys Glu Ile Ile Gln Cys Ile  
 1 5 10 15

Cys Trp Arg Arg Arg Arg Gln Gly Arg Thr Phe Phe Pro Ser Tyr Phe  
 20 25 30

Phe Phe Ser Leu Ser Leu Phe Phe Gln Ser His Cys Ser Ser Val Lys  
 35 40 45

Gly Trp Leu Phe Cys Ala Glu Pro Cys Gly Ser Val Asn Ala Arg His  
 50 55 60

Arg Val Ile Phe Gly Glu Thr Lys Arg Ile Leu Lys Asn Arg Gly Leu  
 65 70 75 80

Asn Ser Thr Thr Asp Trp Leu Asp Asp Lys Met Gln Ser Val Phe Ile  
 85 90 95

Arg Thr Phe Ala Thr Ser Arg Ile Glu Phe Gln Arg Tyr Gln Pro Arg  
 100 105 110

Phe Val Asn Thr Ile Lys Glu Thr Val Lys Ser Ala Gln Glu Lys Ser  
 115 120 125

Tyr Ser Ile Thr Arg Pro Leu Gly Leu Ser Lys Pro Val Leu Leu Asn  
 130 135 140

His Lys Leu Ser Asp Thr Tyr Ser Leu Ser Asn Ile Tyr Glu Glu Leu  
 145 150 155 160

Phe Gly Gln Lys Ser Lys Glu Arg Arg Gln Lys Gln Leu Asp Tyr Asp  
 165 170 175

Leu Lys His Ser Pro Ile Tyr Glu Val Lys Ser Phe Glu Asn Thr Lys  
 180 185 190

Gly Lys Ile Phe Thr Pro Pro Val Ser Tyr Phe Arg Gln Asp Lys Ser  
 195 200 205  
 Leu Tyr Phe Pro Asp Phe Ile Ala Lys Thr Leu Ala Gly Asn Gln Arg  
 210 215 220  
 Ser Leu Tyr Asp Ser Leu Asp Asn Arg Leu Ser Ile Val Lys Leu Phe  
 225 230 235 240  
 Ser Ser Val Ala Gly Glu Gln Cys Thr Arg Ser Tyr Phe Lys Val Glu  
 245 250 255  


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 Asn Lys Asp Tyr Tyr Ser Gln Asp Tyr Asp Thr Phe Val Glu Glu Tyr  
 260 265 270  
 Pro His Thr Gln Ile Leu Asp Val Asn Met Pro Gln Ser Trp Ile Lys  
 275 280 285  
 Gly Phe Val Thr Asn Leu Ser Thr Gly Asn Leu Arg Lys Thr Leu Lys  
 290 295 300  
 Pro Ala Ser Arg Tyr Glu Asn Tyr Phe Ile Leu Pro Gly His Ile Met  
 305 310 315 320  
 Ser Ala Glu Ile Arg Glu Gln Leu Tyr Cys Asp Asn Gln Cys Ser Gly  
 325 330 335  
 Tyr Ile Tyr Ile Val Asp Ser Met Gly Lys Ile Arg Trp Ala Thr Ser  
 340 345 350  
 Gly Tyr Ala Thr Pro Glu Asp Leu Lys Leu Met Trp Lys Val Val Lys  
 355 360 365  
 Gly Val Gln Arg Glu Met Thr Lys  
 370 375

<210> 413  
 <211> 1271  
 <212> DNA  
 <213> Candida albicans

<400> 413  
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 cattttgaga cttcaggtac gacccagggt tgcgacaaag tttaggtagt ttgtcgtctg 120  
 aatgtcgcaa caaaataggg ctgtagccct agtcatgtga tgtgaattaa cataacaaga 180  
 agaattgctg gtgcgcacaaa agattatgtg tattttatgt gcgttggttat cctgcacact 240

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aaaattgagc agtgtacaca cacacatatt gggctgtatt tttattcttg tttttctgct 300
gttctctcac tgttaagctc taagtgaatt tgtgtgtgct gtaatagtgt gtgtgttcca 360
agtcccagct ctcacagata ctcacgcacg cccatactac tgaaaatttc ctgactttct 420
gtatctaaaa attttttact aggaattttt ttcttttacg tttttcactt gtttcatata 480
atcaccaact caagtacaac atggctgtcg gtaaaaaacaa gagattgtcc aaaggaaaaga 540
aaggattaaa aaagaaggtc gttgacccat tcaccagaaa agattgggtt gacatcaaag 600
ctccaaccac ttttgaaaac agaaatgttg gtaaaacttt gatcaacaga tctaccggtt 660
taaagaatgc cgtgatggc ttgaaaggta gagttttcga agtttgttg gccgacttac 720
aaggttccga agaccactct tacagaaaaa tcaaattgag agttgatgaa gttcaaggta 780
aaaacttggt gaccaacttc catgggttgg atttcacttc tgacaaaatta agatcattgg 840
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aagtcaaatt gttgaaacaa caaaattcg acttgggttc attattggct ttgcacggtg 1200
aaggttcaac cgaagaaaaa ggtaagaaag tttcttctgg tttcaaagat gttgttttag 1260
aatctgttta a 1271

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&lt;210&gt; 414

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 414

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Leu  
1 5 10 15

Lys Lys Lys Val Val Asp Pro Phe Thr Arg Lys Asp Trp Phe Asp Ile  
20 25 30

Lys Ala Pro Thr Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Ile  
35 40 45

Asn Arg Ser Thr Gly Leu Lys Asn Ala Ala Asp Gly Leu Lys Gly Arg  
50 55 60

Val Phe Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser  
65 70 75 80

Tyr Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu  
85 90 95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Ser Asp Lys Leu Arg Ser  
100 105 110

Leu Val Arg Lys Trp Gln Ser Leu Val Glu Ala Asn Val Thr Val Lys

115

120

125

Thr Ser Asp Asp Tyr Val Leu Arg Val Phe Ala Ile Ala Phe Thr Lys  
 130 135 140

Arg Gln Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Gln Ser Ser Lys  
 145 150 155 160

Leu Arg Glu Val Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Val  
 165 170 175

Ser Asn Cys Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val  
 180 185 190

Ile Gly Arg Glu Ile Glu Lys Ser Thr Gln Thr Ile Phe Pro Leu Gln  
 195 200 205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp  
 210 215 220

Leu Gly Ser Leu Leu Ala Leu His Gly Glu Gly Ser Thr Glu Glu Lys  
 225 230 235 240

Gly Lys Lys Val Ser Ser Gly Phe Lys Asp Val Val Leu Glu Ser Val  
 245 250 255

&lt;210&gt; 415

&lt;211&gt; 1517

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 415

tgatatggat ttttcaaaac taagaaacaa taccaactac aacaacaaga aacataagtg 60  
 tttgcttaat tcaatgacct cgagtcatat tcccacgttt taagtatgag tgttttacga 120  
 agttgtggat cctattttta ataaaacaat aatagtaata aaaaaaaaaa ctttctttgc 180  
 ttttcgagaa tttgtaacac attgtttctt tcttcccaca gcaaccaaatt tttattttat 240  
 tttttctttt gggacttacc cacagttgct caattatgta taacaagggt agaaactctg 300  
 tgggattccc tccttaaaaa tatagcaatc ctttttcttc acaacgattg ctatatgacc 360  
 cccccctaa gcattcattg cttttatata tatttaataa tgtattttctc ttgttcagga 420  
 taattatcac tatttgtgac gtttaatttt tacatttctt cttcttcttc ttctatttc 480  
 aacattaaag aacatttaat atgtatttcc caatcattgt atgggtatat gtatctatca 540  
 cttttgtggg tgccaattat ggttttgatc aatggacaaa tgatgattta aaacaatttt 600  
 taaaagaacg taaagttgca ttcaatgatg ctttgagaa tccaaaatta attagtttgg 660

505

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ctaatagaaga agctaagaaa ttagaaaaaag gttacaagaa agttactgaa gaattaaata 720
acaatttgaa tcctccagat gattcattaa atgattatgt gaattttgat tacttatttg 780
ggaaaagaaa agaaaattat tcaattaaag aatggatttt tgaaagttgg ccagtaacca 840
gtttgcaaac ttttttaact caaaataata tccaatatag tgcaaaggat accaaagatg 900
atttaatacaa taagggttaa gatcaatttg attctatttc taagaaaaat catgggtcta 960
gtttttatcc tggcaattgg ttatatgaat cttggtcaga aaatgatttg aaagattggg 1020
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agtctcaacc ttggatcaca aagggagaac aaaagtctca gaaaaagaag ggtagtaatt 1440
tgattaatga tacattcttt gttggtatta ataattgggc caaggataaa ttgcgtgaat 1500
tgggcaatct tgactaa 1517

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&lt;210&gt; 416

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 416

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Met Tyr Phe Pro Ile Ile Val Trp Leu Tyr Val Ser Ile Thr Phe Val
  1             5             10             15

Val Ala Asn Tyr Gly Phe Asp Gln Trp Thr Asn Asp Asp Leu Lys Gln
          20             25             30

Phe Leu Lys Glu Arg Lys Val Ala Phe Asn Asp Ala Leu Glu Asn Pro
          35             40             45

Lys Leu Ile Ser Leu Ala Asn Glu Glu Ala Lys Lys Leu Glu Lys Gly
          50             55             60

Tyr Lys Lys Val Thr Glu Glu Leu Asn Asn Asn Leu Asn Pro Pro Asp
          65             70             75             80

Asp Ser Leu Asn Asp Tyr Leu Asn Phe Asp Tyr Leu Phe Gly Lys Arg
          85             90             95

Lys Glu Asn Tyr Ser Ile Lys Glu Trp Ile Phe Glu Ser Trp Pro Val
          100            105            110

Thr Ser Leu Gln Thr Phe Leu Thr Gln Asn Asn Ile Gln Tyr Ser Ala
          115            120            125

Lys Asp Thr Lys Asp Asp Leu Ile Asn Lys Val Lys Asp Gln Phe Asp

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130	135	140
Ser Ile Ser Lys Lys Asn His Gly Ser Ser Phe Tyr Pro Gly Asn Trp		
145	150	155 160
Leu Tyr Glu Ser Trp Ser Glu Asn Asp Leu Lys Asp Trp Leu Lys Ser		
	165	170 175
Tyr Gly Ile Glu Phe Asn Pro Ser Ser Thr Lys Asp Gln Leu Val Glu		
	180	185 190
Lys Leu Lys Glu Phe Ser Tyr Gln Ala Thr His Ser Ile Arg Asp Ser		
195	200	205
Lys Glu Ser Leu Phe Asp Ser Leu Asp Leu Phe Asp Lys Thr Ile Phe		
210	215	220
Asp Lys Lys Gly Gln Ile Glu Asp Glu Phe Phe Gln Thr Trp Ser Tyr		
225	230	235 240
Ser Gln Leu Arg Glu Trp Leu Tyr Leu His Gly Phe Ile Asp Thr Lys		
	245	250 255
Pro Gly Ile Tyr Val Glu Asp Leu Asp Lys Glu Lys Leu Val Lys Ile		
	260	265 270
Ala Gln Ser Tyr Lys Lys Cys Leu Leu Ser Asp Ile His Thr Trp Leu		
	275	280 285
Ala Asn Thr Glu Lys Lys Ser Gln Pro Trp Ile Thr Lys Gly Glu Gln		
	290	295 300
Lys Ser Gln Lys Lys Lys Gly Ser Asn Leu Ile Asn Asp Thr Phe Phe		
305	310	315 320
Val Gly Ile Asn Asn Trp Ser Lys Asp Lys Leu Arg Glu Leu Gly Asn		
	325	330 335
Leu Asp		

&lt;210&gt; 417

&lt;211&gt; 2243

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 417

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atgagttcat agatgatctg tttcactttc aaataacgtg tcaacaaaaa taaagttaga 60
gcatagattt tgccgccact tgtacagatg gatagaattg aatgcaaatt ctgcataaag 120
attaaagtga aaaacaattt ccgaaaaaag aagaaaatcg aacacattag aaaaagaaac 180
gaacaaaaga aaaaaaattt caaattgtag ttgcatgtat ataaaaataat ataaaagata 240
tatcaccagc acaactgatt actttttatt tatatcacct gtcaacaaca aatttccaaa 300
taaatacaac tcagaaaaaa cacttactat cttttcttag tttggtttct ataactttat 360
taaacattct tgcctttcat ccttgattat catattagat cttatcttta atttgtttga 420
aaaaataata ccaataatct tcccattaga acttacaaca caacaacaaa aaaacccatt 480
ctaaatcact attctccatt atgaaaattt tcagattatt ttcactacta atcgtaacaat 540
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caaatgttgt gtttaatact tccaacttgt ttgataatag caatttgagg gatgaattta 1560
gatcaagatt tagaaacatt tctgccatta tggattgtgt tggttgtgat agatgcagaa 1620
tgtgggggaa aatccaaacc attggttatg gtaccgctct caagatttta tttgaagatg 1680
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aacaccttaa agatattgct gaaggattaa cccaacctgg tgtttacgac aaaatacaaa 1860
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aattgcttgg taaaccaaca gtttatgatt accaaagttc ttttgatgtt gatgccctac 2220
aatacagtca agtccttgga taa 2243

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&lt;210&gt; 418

&lt;211&gt; 580

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 418

Met Lys Ile Phe Arg Leu Phe Ser Leu Leu Ile Val Gln Phe Ile Ile

1	5	10	15
Asn Thr Thr Val Ala Val Ser Pro Val Ser Ala Val Leu Pro Lys Ser	20	25	30
Ser Phe Ser Pro Phe Asp Ser Pro Glu Phe Cys Ser Gln Ile Ile Thr	35	40	45
Pro Thr Cys Asn Thr Thr Phe Thr Tyr Ile Asp Glu Leu Asn Lys Asp	50	55	60
Ile Arg Pro Tyr Leu Ser Glu Leu Val Lys Thr Ser Tyr Phe Arg Tyr	65	70	75
Phe Lys Val Asn Leu Asp Lys Gln Cys Arg Phe Trp Asn Ala Gln His	85	90	95
Phe Cys Ala Ser Glu Asn Cys Ala Val Glu Ile Leu Glu Asp Phe Asn	100	105	110
Trp Ser Gln Val Thr Asn Glu Ser Leu Lys Pro Ser Gly Leu Gly Lys	115	120	125
Ile Ser Leu Pro Asp Lys Ser Ser Ile Asp Asn Ser Ile Glu Thr Glu	130	135	140
Glu Val Gln Thr Cys Glu Asp Leu Asp Tyr Ser Glu Ile Asp Asp Asp	145	150	155
His His Cys Val Tyr Val Asn Leu Val Asn Asn Pro Glu Arg Phe Thr	165	170	175
Gly Tyr Gly Gly Asn Gln Ser Phe Asp Val Trp Lys Ala Ile Tyr Ser	180	185	190
Glu Asn Cys Phe Pro Asn Thr Asn Pro Met Ser Val Thr Asn Asp Ala	195	200	205
Asp Asn Gly Gly Glu Gln Cys Ile Glu Lys Asn Leu Phe Tyr Arg Val	210	215	220
Val Ser Gly Met His Ala Ser Ile Ala Val His Leu Ser Arg Glu Tyr	225	230	235
Leu Asn Ser Glu Thr Gly Glu Phe Tyr Pro Asn Leu Lys Val Phe Met	245	250	255
Glu Arg Val Gly Met His Asn Asp Arg Leu Ser Asn Ile Tyr Phe Asn			

509

260	265	270
Tyr Ala Leu Val Ser Gln Ala Ile Val Lys Leu Ser Glu Ile Leu Pro		
275	280	285
Leu Arg Glu Phe Ile Gln Ser Gly Tyr Asp Asp Ile Thr Pro Ala Gln		
290	295	300
Lys Gln His Leu Leu Ala Asn Asn Asp Val Glu Ser Val Glu Val Tyr		
305	310	315 320
<hr/>		
Asp Arg Leu Leu Leu Asp Asp Ile Ile Pro Ser Leu Glu Ala Asn Val		
325	330	335
Val Phe Asn Thr Ser Asn Leu Phe Asp Asn Ser Asn Leu Arg Asp Glu		
340	345	350
Phe Arg Ser Arg Phe Arg Asn Ile Ser Ala Ile Met Asp Cys Val Gly		
355	360	365
Cys Asp Arg Cys Arg Met Trp Gly Lys Ile Gln Thr Ile Gly Tyr Gly		
370	375	380
Thr Ala Leu Lys Ile Leu Phe Glu Asp Asp Asn Tyr Asp Asn His Asn		
385	390	395 400
Leu Lys Phe Arg Arg Ile Glu Ile Val Ala Leu Ile Asn Thr Phe Asp		
405	410	415
Arg Leu Ser Lys Ser Ile Glu Ser Ile Asn Met Phe Lys Glu Met Tyr		
420	425	430
Leu Gln His Leu Lys Asp Ile Ala Glu Gly Leu Thr Gln Pro Gly Val		
435	440	445
Tyr Asp Lys Ile Gln Asn Asn Lys Pro Gly Asn Gly Phe Ala Phe Pro		
450	455	460
Phe Val Ser Pro Leu Pro Gln Lys Lys Pro Asp Gln Thr Asn Thr Pro		
465	470	475 480
Lys Asn Gln Gln Gln Lys Gln Pro Gln Glu Thr Asp Lys Lys Arg Leu		
485	490	495
Thr Leu Glu Glu Ile Ala His Thr Lys Pro Glu Asp Arg Thr Phe Ile		
500	505	510
Glu Asp Phe Arg Leu Ser Phe Asp Glu Val Trp Gln Ala Leu Arg Phe		

510

515

520

525

Val Leu Thr Ser Tyr Gln Arg Phe Pro Ala Val Leu Ser Arg Phe Thr  
 530 535 540

Leu Val Gln Leu Asn Glu Trp Trp Asn Lys Leu Leu Gly Lys Pro Thr  
 545 550 555 560

Val Tyr Asp Tyr Gln Ser Ser Phe Asp Val Asp Ala Leu Gln Tyr Ser  
 565 570 575

Gln Val Leu Gly  
 580

&lt;210&gt; 419

&lt;211&gt; 1004

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 419

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tgtgaaaaaa aattgtggtg tggatgttgt tgctgttggt gcgttggtcca caacaaaaaa 60
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acacagctca ttcaccactc atgccccgaa gttctactgc tcaaaagcgt ttactaacag 540
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ataatttata caaatgggaa tgtttattag aaggaccatc cgatactcca tatgcaaatg 660
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ctgaaagtgg ggctaataatc gatgcttgta aattatggag agataatcgt gctgaatatg 960
accgacaaat tagacaacat gtcaaggagt cattaggatt atga 1004

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&lt;210&gt; 420

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 420

Met Pro Arg Ser Ser Thr Ala Gln Lys Arg Leu Leu Thr Glu Tyr Gln

511

1                      5                      10                      15  
 Gln Leu Ser Arg Asp Pro Pro Pro Gly Ile Ile Ala Gly Pro Val Ser  
                     20                      25                      30  
 Glu Asp Asn Leu Tyr Lys Trp Glu Cys Leu Leu Glu Gly Pro Ser Asp  
                     35                      40                      45  
 Thr Pro Tyr Ala Asn Gly Val Ser Pro Ala Val Leu Thr Phe Pro Lys  
                     50                      55                      60  


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 Asp Tyr Pro Leu Ser Pro Pro Thr Leu Lys Phe Asp Pro Pro Leu Leu  
                     65                      70                      75                      80  
 His Pro Asn Ile Tyr Ala Asp Gly Thr Val Cys Ile Ser Ile Leu His  
                     85                      90                      95  
 Pro Pro Gly Glu Asp Pro Asn Gln Tyr Glu Arg Pro Glu Glu Arg Trp  
                     100                      105                      110  
 Ser Pro Val Gln Ser Ile Glu Lys Ile Leu Leu Ser Val Met Ser Met  
                     115                      120                      125  
 Leu Ala Glu Pro Asn Pro Glu Ser Gly Ala Asn Ile Asp Ala Cys Lys  
                     130                      135                      140  
 Leu Trp Arg Asp Asn Arg Ala Glu Tyr Asp Arg Gln Ile Arg Gln His  
                     145                      150                      155                      160  
 Val Lys Glu Ser Leu Gly Leu  
                     165

&lt;210&gt; 421

&lt;211&gt; 1031

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 421

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 aatcagttct gcacgtgata taatctccta tcgctagtag taagttttaa tttttttgat 180  
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 attgttaaca agtctttttt ttccccggga ttgaatccgg aaactacat taattcactc 360  
 attctactca ctcaccttac accctcactc actcaaaca ttatatcaac ccaaaaaaaaa 420  
 aaaatcttca ctacaccaat aacaagaac caatagttca atctaataaa ccatccttcc 480

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ctacttcaat tttaaatatt ccatttgata ctactacttt agtatctgca ttcaccacat 840
taccaacatt tgctcaatat ggtatcaaag ctatttggtgc ttatccattt gtttatcata 900
ttggtaatgg gattagacat ttggtttggg attttggtaa agaattaacc atccctggtg 960
tttatagaac tgggtatgct gttttggctg ctactgctgt cattggaagt tatttagctt 1020
tcttatggta a 1031

```

&lt;210&gt; 422

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 422

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Met Ile Ser Arg Ile Gly Leu Leu Lys Arg Pro Thr Val Ser Thr Leu
  1             5             10             15

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Asn Asn Tyr Val Lys Leu Gln Ser Thr Leu Ala Leu Lys Arg Tyr Thr
      20             25             30

```

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Ser Thr Val Pro Ala Thr Ser Asn Gln Glu Gln Glu Ile Leu Val Ala
      35             40             45

```

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Gln Arg Lys Asn Arg Pro Thr Ser Pro His Leu Gln Ile Tyr Glu Pro
      50             55             60

```

```

Gln Leu Thr Trp Ile Met Ser Ser Phe His Arg Ile Thr Gly Val Ala
      65             70             75             80

```

```

Met Ala Gly Ala Phe Tyr Ala Leu Thr Cys Gly Phe Ala Ala Thr Ser
      85             90             95

```

```

Ile Leu Asn Ile Pro Phe Asp Thr Thr Thr Leu Val Ser Ala Phe Thr
      100            105            110

```

```

Thr Leu Pro Thr Phe Ala Gln Tyr Gly Ile Lys Ala Ile Cys Ala Tyr
      115            120            125

```

```

Pro Phe Val Tyr His Ile Gly Asn Gly Ile Arg His Leu Val Trp Asp
      130            135            140

```

```

Phe Gly Lys Glu Leu Thr Ile Pro Gly Val Tyr Arg Thr Gly Tyr Ala
      145            150            155            160

```

Val Leu Ala Ala Thr Ala Val Ile Gly Ser Tyr Leu Ala Phe Leu Trp  
 165 170 175

&lt;210&gt; 423

&lt;211&gt; 1176

&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 423

```

aaaagcaaga agagaaggac tcgttggcca atttcttcgg caatttcaag aagaaaagag 60
tagctgttta gaactatata tatatgtact cgcgctttaa tgtttatagc aataatgaaa 120
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aacacaactt gcaaagcaat ggtagtttct ttgattttgt gtttctatta gattcctgtt 240
tctattagat tcccgccttt ttttttttgg cagacattaa acctcagggc tatagcccta 300
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caatcaacta gagtcacagc atgttaattc caaaagaaga cagaaagaag atccaccaat 540
acctcttcca aggtatgtaa atatgaatta taaactggaa cagaatatgg catttcaagg 600
gatgcacgat aagtcaagag ttcataaaaa agcacagatt ataacagtcg taaagaaaaa 660
tttactacc aacaacaata agaagatata aaagagattc agtaatcact acttacaaga 720
aacatataac atcatggaga gttaatttg aaatacgaat gaatatacaa atgaactata 780
ccctttttat ggccatatca cgtttcaaga aatattttaa caaaaataaa atgaagaata 840
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aaccaaccaa agcacgatga aattgatact agaaacttgt tcgtcatcaa agctttacaa 960
tctttgactt cttaaaggta cgtcaagact caattctcat ggcaatacta ctactacacc 1020
ttgactgatg aagggtgtga attcttgaga accgaattga acattccaga aggtatcttg 1080
ccattgacca gattgaagaa tgctccagct gaaagaccaa gaccatcaag aggcgggtcca 1140
agaagagggtg gttacagagg tagagctaga gactaa 1176

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&lt;210&gt; 424

&lt;211&gt; 118

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 424

Met Leu Ile Pro Lys Glu Asp Arg Lys Lys Ile His Gln Tyr Leu Phe  
 1 5 10 15

Gln Glu Gly Val Val Val Ala Lys Lys Asp Phe Asn Gln Pro Lys His  
 20 25 30





```

gccaacagca accacaaccg caaccacagc cgcaaccaca gcaaccacaa ctacatactc 1380
tgtctcctct aaatcagata caagcagcga catcagcaac accttctgtg tccactaaaa 1440
acgcgtctaa aagaaattac aaaacctcat ccacttcctc aaaattaaga tcaactacat 1500
caaaactttt cgataaaaaa gggtcacaac caagaagata cagtaccatt cctgatgata 1560
ttgacattga agatttcgat gatgagctta tatactatga caacacagct aggttcccag 1620
cgaacgaatc aacttcatta ctaaatacaa accaaagaat cccccattat agatcactta 1680
atgtgaatgt ccctcaggtg aagcgccaaa gcaagcggtt tttgtcaact ggccaacctt 1740
tagagagttc tgatcgtggc tctaacaaag atggtactga taatggaaac aacagtgate 1800
acaatattaa ttctcctttg actgctaata ataataataa taacgtcaat cacaacgate 1860
atggtgataa caaaaagagt aataccaaca acaacaacat tgctaataat agagcatttc 1920
catttcctta tcaagatcaa caacatcatt attactacga ctacgatgat tttgaccaag 1980
aatcacaaat caatggacee aattttgatt tgcagacct ccctataaac agatcagctt 2040
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caagaaagac agatcagtat agtcaaagaa caagctttct aaagtcatgc atttatacct 2160
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cagtcgtggg tagaaaaact gggatatatt atcctacctt attcgttaata ccacaaggag 2820
agaataatat ttcaatttag                                     2840

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&lt;210&gt; 426

&lt;211&gt; 779

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 426

Met Leu His Pro Asn Asn Ser Val Val Asp Met Ser Ser Thr Gly Asn  
 1 5 10 15

Met Asn Glu Asn Thr Asp Ala Pro Pro Lys Gln Gln Thr Lys Lys Lys  
 20 25 30

Ile Ser Lys Gln Asn Ser Thr Lys Thr Asp Phe Phe Ala Ala Arg Leu  
 35 40 45

Ala Ser Ala Val Asp Asp Ile Glu Ser Ser Asp Ser Asp Glu Thr Phe  
 50 55 60

Ile Tyr Glu Asn Asn Asp Thr Glu Leu Asp Asp Asn Ala Ser Asn Ile  
 65 70 75 80

516

Asn Asn Asn Asn Asn Asn Ser Thr Asn Asn Ile Ile Asn Leu Asp Asn  
85 90 95

Ala Ser Val Asn Gly Ser Met Ile Ala Ser Ser Asn Ala Met Val Thr  
100 105 110

Gly Pro Pro Gly Thr Ser Ile Ala Leu Gly Ser Gly Leu Arg Ser Pro  
115 120 125

Ser Ile Leu Glu Gly Glu Gln Leu Gln Tyr Phe His Asp Pro Val Arg  
130 135 140

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Gln Gln Gln Phe Lys Leu Pro Ser Thr Lys Ala Pro Ser Ile Ser Asn  
145 150 155 160

Ser Ile Ser Ser Ser Asn Asn Ile Asp Ser Ile Leu Lys Arg Pro Val  
165 170 175

His Leu Arg Glu Ala Ser Thr Tyr Ser Val Asn Asp Asn Asp His Arg  
180 185 190

Asn Leu Val Leu Pro Asn Ser Thr Glu Arg Phe Thr Ala Ser Pro Ser  
195 200 205

Asn Asn Ile Gly Asn Glu Asn Ile Pro Gln Tyr Gln Lys Thr Ser Ser  
210 215 220

Val Ala His Ser Ile Asn Glu Gly Tyr Asn Asp Asp Thr Phe Ser Tyr  
225 230 235 240

Asn Glu Val Glu Asp Asn Leu Ile Asp Glu Asp Ser Thr Asp Asp Gly  
245 250 255

Asp Leu Thr Lys Asn Thr Ile Thr Asn Asn Asn Asn Pro Pro Thr Thr  
260 265 270

Ser Ser Gln Gln Gln Pro Gln Pro Gln Pro Gln Pro Gln Gln  
275 280 285

Pro Gln Leu His Thr Ser Ser Pro Leu Asn Gln Ile Gln Ala Ala Thr  
290 295 300

Ser Ala Thr Pro Ser Val Ser Thr Lys Asn Ala Ser Lys Arg Asn Tyr  
305 310 315 320

Lys Thr Ser Ser Thr Ser Ser Lys Leu Arg Ser Thr Thr Ser Lys Leu  
325 330 335

517

Phe Asp Lys Lys Gly Ser Gln Pro Arg Arg Tyr Ser Thr Ile Pro Asp  
 340 345 350  
 Asp Ile Asp Ile Glu Asp Phe Asp Asp Glu Leu Ile Tyr Tyr Asp Asn  
 355 360 365  
 Thr Ala Arg Phe Pro Ala Asn Glu Ser Thr Ser Leu Leu Asn Gln Asn  
 370 375 380  
 Gln Arg Ile Pro His Tyr Arg Ser Leu Asn Leu Asn Phe Pro Gln Val  
 385 390 395 400

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Lys Arg Gln Ser Lys Arg Tyr Leu Ser Thr Gly Gln Pro Leu Glu Ser  
 405 410 415  
 Ser Asp Arg Gly Ser Asn Lys Asp Gly Thr Asp Asn Gly Asn Asn Ser  
 420 425 430  
 Asp His Asn Ile Asn Ser Pro Leu Thr Ala Asn Asn Asn Asn Asn Asn  
 435 440 445  
 Val Asn His Asn Asp His Gly Asp Asn Lys Lys Ser Asn Thr Asn Asn  
 450 455 460  
 Asn Asn Ile Ala Asn Asn Arg Ala Phe Pro Phe Pro Tyr Gln Asp Gln  
 465 470 475 480  
 Gln His His Tyr Tyr Tyr Asp Tyr Asp Asp Phe Asp Gln Glu Ser Gln  
 485 490 495  
 Ile Asn Gly Pro Asn Phe Asp Leu Pro Asp Leu Pro Ile Asn Arg Ser  
 500 505 510  
 Ala Ser Arg Asn Phe Asn Asn Asn Asn Asn Pro Lys Arg Phe Gly Asp  
 515 520 525  
 Ser His Phe Phe Leu Pro Arg Lys Thr Asp Gln Tyr Ser Gln Arg Thr  
 530 535 540  
 Ser Phe Leu Lys Ser Cys Ile Tyr Thr Phe Val Cys Ile Leu Ile Val  
 545 550 555 560  
 Leu Thr Ile Gly Phe Val Leu Gly Phe Val Leu Ala Thr Thr Lys Asp  
 565 570 575  
 Leu Thr Asp Val Gly Ile Thr Ser Ile Glu Asn Pro Ile Val Ser Lys  
 580 585 590

518

Asp Glu Leu Val Phe Asn Val Val Ile Glu Ala Phe Asn Pro Gly Trp  
 595 600 605  
 Phe Ser Val Asp Ile Asn Glu Val Glu Leu Asp Leu Phe Ala Arg Ser  
 610 615 620  
 Gly Tyr Leu Pro Asp Thr Asp Asn Ser Lys Ile Ser Asn Met Gly Gly  
 625 630 635 640  
 Ser Gln Lys Val Glu Thr Val Lys Leu Gly Thr Ile Leu Asn Phe Glu  
 645 650 655  


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 Ser Val Leu Asn Phe Lys Gly Gly Phe Leu Ser Arg Glu Pro Thr Ile  
 660 665 670  
 Gln Lys Gly Gly Ile Arg Leu Leu Tyr Pro Gly Lys Asn Val Thr Ala  
 675 680 685  
 Glu Ala Lys Leu Val Val Asn Met Ala Asp Ile Lys Ile Ala Ala Ser  
 690 695 700  
 Asn Ser Ile Ala Lys Glu Ser Thr Thr Ser Asn Asp Thr Asn Asp Asn  
 705 710 715 720  
 Asp Asn Ser Lys Lys Trp Glu Ile Ile Ser Ser Asn Pro Phe Asp Leu  
 725 730 735  
 Ile Ile Thr Gly Val Leu Lys Tyr Asp Leu Pro Phe Ser Arg Thr Ser  
 740 745 750  
 Arg Ser Val Val Val Arg Lys Thr Gly Tyr Ile Asp Pro Thr Leu Phe  
 755 760 765  
 Val Ile Pro Gln Gly Glu Asn Asn Ile Ser Ile  
 770 775

&lt;210&gt; 427

&lt;211&gt; 1352

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 427

cccacagacc aataacgttt taccaaccaa aacctctgat atcaatgatt cgaaaagatt 60  
 cattcaaccc cggtagctg tttgagtatt ggatagcaac actttcaatt agtgcaacac 120  
 aatcaaatta ccaatacttg tttacctttc atctgattct aattggttca tagcaatata 180

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gtctcttctg ttgtttgata ttaatatataa taaaacttat ttatcacgtt gtttagtagt 240
ctcgcaaatt tgaaccatg gatgagtaaa cttgttgtgt tagatgagct caaatatctg 300
gtggaacaat tgtgtagtag ctctttgata aatatccaag aacagtcgtg caagtttcaa 360
aataccatcg caaaaatcct aacaaaaaaaa aaaaattaat aaagaaaaga aataattcta 420
taatagctca tcacaacaat tcgtctacac ttcccacctg atttgttggg ttaaatataa 480
taagacaaac ctcaagaagct atgataagaa aacaggctag agaaagaaga gagtatcttt 540
atagaaaggc ttacagctt caggaatctt ccttaacaga aaaaagacaa caattgaaag 600
cagctctagc aagtggaaaa tcattatcaa aggagcttgc cgaagatgaa aaattacaac 660
gtgattttat ttacgatgaa agtgaacaaa tagaaattga tgacgaatac agtcggttgt 720
cggaatatc tgatccaaaa gttgttatta ccacatcccg tgatccatct gtcaagttgc 780
tacaattcct gaaagaaatc aagttaatgt ttccaaatag cttgaagttg aatcgaggaa 840
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tattgcacga gcatcgtggt gtcccatcaa gtttaactgt aagccacttt cctcatggcc 960
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ctaaggattc agtggagttg agtgagattg gccacggtt cgaaatgaga ttgtatgaaa 1260
tcagactagg attacctgac acaaagatg ctgatgtcga gtggcagatg agaagattca 1320
taagaacagc taatagaaag aattacttgt aa 1352

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&lt;210&gt; 428

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 428

Met Ile Arg Lys Gln Ala Arg Glu Arg Arg Glu Tyr Leu Tyr Arg Lys  
1 5 10 15

Ala Leu Gln Leu Gln Glu Ser Ser Leu Thr Glu Lys Arg Gln Gln Leu  
20 25 30

Lys Ala Ala Leu Ala Ser Gly Lys Ser Leu Ser Lys Glu Leu Ala Glu  
35 40 45

Asp Glu Lys Leu Gln Arg Asp Phe Ile Tyr Asp Glu Ser Glu Gln Ile  
50 55 60

Glu Ile Asp Asp Glu Tyr Ser Arg Leu Ser Gly Ile Ser Asp Pro Lys  
65 70 75 80

Val Val Ile Thr Thr Ser Arg Asp Pro Ser Val Lys Leu Leu Gln Phe  
85 90 95

Ser Lys Glu Ile Lys Leu Met Phe Pro Asn Ser Leu Lys Leu Asn Arg  
100 105 110

520

Gly Asn Tyr Ile Ile Ser Asp Leu Val Ser Thr Cys Asn Arg Val Gln  
 115 120 125

Val Ser Asp Met Ile Leu Leu His Glu His Arg Gly Val Pro Ser Ser  
 130 135 140

Leu Thr Val Ser His Phe Pro His Gly Pro Thr Ala Ile Phe Thr Leu  
 145 150 155 160

His Asn Val Lys Leu Arg His Asp Leu Pro Asn Leu Gly Asn Val Ser  
 165 170 175

Glu Ser Tyr Pro His Leu Ile Phe Glu Asn Phe Gln Ser Asp Leu Gly  
 180 185 190

Lys Arg Val Val Lys Ile Leu Gln His Leu Phe Pro Pro Gly Val Lys  
 195 200 205

Lys Asp Ser Ser Arg Val Ile Thr Phe Val Asn Asn Asp Asp Tyr Ile  
 210 215 220

Ser Val Arg His His Val Tyr Val Lys Thr Lys Asp Ser Val Glu Leu  
 225 230 235 240

Ser Glu Ile Gly Pro Arg Phe Glu Met Arg Leu Tyr Glu Ile Arg Leu  
 245 250 255

Gly Leu Pro Asp Asn Lys Asp Ala Asp Val Glu Trp Gln Met Arg Arg  
 260 265 270

Phe Ile Arg Thr Ala Asn Arg Lys Asn Tyr Leu  
 275 280

<210> 429

<211> 1061

<212> DNA

<213> Candida albicans

<400> 429

tccttttgggttttttttttctgtgttactccagaaatgtgcataataatgataatagta 60  
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 cttagaacagaaaaataaaaacgaataaa caaaaacccc ccaatcggca tgcacgga 180  
 ttctttcagcccaattactttatttttgcc cacttcttttggattagggc aatagcccta 240  
 aagctcgtgttttagccctttatattgcagtctattttatttttcttttttttttggt 300  
 gttggtaaac ttttttttttttcgcaggtgttgaaaaaaa aatcattttt acagtttaca 360

```

tttctctaac ctgcaaaaag ctctcgtttt tttgtagtga gagttactcg ttcacaatag 420
tatacttttac aggggagttc ttttcttttg gaatagtcaa ccaacagcaa atagccaagg 480
atcaagcttc atcattaatc atgtcctcta agatcttatac agaaaacca actgaattag 540
aattaaaagt tgctcaagct ttcggttgatt tggaatctca agctgattta aaagctgaat 600
tgagaccatt acaattcaaa tctatcaaag aaattgatgt taatggaggt aaaaaagctt 660
tagctgtttt cggtccacca ccaagtttac aagcttacag aaaagttcaa actagattaa 720
ctagagaatt agaaaaaaaa ttcccagata gacatgttgt ctttttagct gaaagaagaa 780
tcttaccaaa accagctaga aaagctagaa aacaacaaaa aagaccaaga tcaagaactt 840
tgactgctgt tcatgataaa attttggaag atttagtttt cccaactgaa atcattggta 900
aaagagttag atacttggtt ggtggttaaca aaatccaaaa agtcttggtg gattctaaag 960
attcaactgc tgttgattac aaattggatt ctttccaaca attgtactca aaattgactg 1020
gtaaacaagt tgtttttgaa atcccagggtg aatctcatta g 1061

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&lt;210&gt; 430

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 430

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Met Ser Ser Lys Ile Leu Ser Glu Asn Pro Thr Glu Leu Glu Leu Lys
  1             5             10             15

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Val Ala Gln Ala Phe Val Asp Leu Glu Ser Gln Ala Asp Leu Lys Ala
          20             25             30

```

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Glu Leu Arg Pro Leu Gln Phe Lys Ser Ile Lys Glu Ile Asp Val Asn
          35             40             45

```

```

Gly Gly Lys Lys Ala Leu Ala Val Phe Val Pro Pro Pro Ser Leu Gln
          50             55             60

```

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Ala Tyr Arg Lys Val Gln Thr Arg Leu Thr Arg Glu Leu Glu Lys Lys
          65             70             75             80

```

```

Phe Pro Asp Arg His Val Val Phe Leu Ala Glu Arg Arg Ile Leu Pro
          85             90             95

```

```

Lys Pro Ala Arg Lys Ala Arg Lys Gln Gln Lys Arg Pro Arg Ser Arg
          100             105             110

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```

Thr Leu Thr Ala Val His Asp Lys Ile Leu Glu Asp Leu Val Phe Pro
          115             120             125

```

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Thr Glu Ile Ile Gly Lys Arg Val Arg Tyr Leu Val Gly Gly Asn Lys
          130             135             140

```

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Ile Gln Lys Val Leu Leu Asp Ser Lys Asp Ser Thr Ala Val Asp Tyr

```

522



145

150

155

160

Lys Leu Asp Ser Phe Gln Gln Leu Tyr Ser Lys Leu Thr Gly Lys Gln  
 165 170 175

Val Val Phe Glu Ile Pro Gly Glu Ser His  
 180 185

&lt;210&gt; 431

&lt;211&gt; 1256

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 431

tggttttgttt ttgcaatcaa cataatagaa gaccaaacaa ataatttcta ttttttttga 60  
 ctctcccgtta gttttacact tctagcctct cttgtaaata tacacctaat tgacagtacc 120  
 attaggaccc catcttattg ttaaggataa tacttcttct tcttcttctt ctttgtttaa 180  
 tcaaatgtgc aataaataaa aaaaaaaaaa aaacaaagcc gcacaagttt tcctaaaatg 240  
 acttattttg tgtaacgcat tcacgtgatc ataatttttt taaattcaaa aactgaacca 300  
 aattcctgca tattgagggt gaaaaaaaaa agaaaaagaa aattttttca atcttgtttg 360  
 aggagagaga ggtgaaaaat ttttctctct ctctttcttt ctttcattct catataccat 420  
 aaacttaaac aacttctttt actttttcct ttcttttctt ttcaaacctc tacaacagat 480  
 ccaattaatt aacaaaaaaaa atggttaacg ctatcttate taagaaaaag aaattagtag 540  
 ctgacggtgt cttctacgct gaattgaacg aattcttcac cagagaatta gctgaacaag 600  
 gttatgctgg tggtgaagtt agaaaaactc catctaaatt ggaagttatt gttaaagctt 660  
 ctaacactca aggtgtttta ggtgaacaag gtagaagaat ccatgaatta acttcattga 720  
 ttgttaaaag attcaaatta tctccagaag gtattgccat ttatgctgaa agagttgaag 780  
 aaagagggtt atctgctgct gttcaagctg aagctttgaa agccaaatta ttgtctgggt 840  
 taccaattag aagagctgct tatggtgttt taagatttgc tatgggtgcc ggtgctaaag 900  
 gtgttgaagt tggtatctct ggtaaattaa gagctgctag agctaaatct caaaaatatg 960  
 ctgatggttt tatgattcat tctggtcaac caactagaga tttcattgat attgccatta 1020  
 gacatgtttt aatgagacaa ggtgttttgg gtatcaaagt taaaattatg aaagatccag 1080  
 ctgctaatag atttgggtcca agagctttac cagatgctgt taaaattgct gaagctaaag 1140  
 atgaagatga agttattcca gctccaactg ttaaattctta taaacaaact gctgaagatg 1200  
 aaactgaaac tgatgctcca gttgaagctg aagctgaagt tgaagctact gcttaa 1256

&lt;210&gt; 432

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 432

Met Val Asn Ala Ile Leu Ser Lys Lys Lys Lys Leu Val Ala Asp Gly  
 1 5 10 15

Val Phe Tyr Ala Glu Leu Asn Glu Phe Phe Thr Arg Glu Leu Ala Glu  
20 25 30

Gln Gly Tyr Ala Gly Val Glu Val Arg Lys Thr Pro Ser Lys Leu Glu  
35 40 45

Val Ile Val Lys Ala Ser Asn Thr Gln Gly Val Leu Gly Glu Gln Gly  
50 55 60

Arg Arg Ile His Glu Leu Thr Ser Leu Ile Val Lys Arg Phe Lys Leu  
65 70 75 80

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Ser Pro Glu Gly Ile Ala Ile Tyr Ala Glu Arg Val Glu Glu Arg Gly  
85 90 95

Leu Ser Ala Ala Val Gln Ala Glu Ala Leu Lys Ala Lys Leu Leu Ser  
100 105 110

Gly Leu Pro Ile Arg Arg Ala Ala Tyr Gly Val Leu Arg Phe Ala Met  
115 120 125

Gly Ala Gly Ala Lys Gly Val Glu Val Val Ile Ser Gly Lys Leu Arg  
130 135 140

Ala Ala Arg Ala Lys Ser Gln Lys Tyr Ala Asp Gly Phe Met Ile His  
145 150 155 160

Ser Gly Gln Pro Thr Arg Asp Phe Ile Asp Ile Ala Ile Arg His Val  
165 170 175

Leu Met Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Lys Asp  
180 185 190

Pro Ala Ala Asn Arg Phe Gly Pro Arg Ala Leu Pro Asp Ala Val Lys  
195 200 205

Ile Ala Glu Ala Lys Asp Glu Asp Glu Val Ile Pro Ala Pro Thr Val  
210 215 220

Lys Ser Tyr Lys Gln Thr Ala Glu Asp Glu Thr Glu Thr Asp Ala Pro  
225 230 235 240

Val Glu Ala Glu Ala Glu Val Glu Ala Thr Ala  
245 250

&lt;210&gt; 433

02-07-1999

<211> 2105  
 <212> DNA  
 <213> Candida albicans

EP99870141.1

&lt;400&gt; 433

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 agtaagtaat attagttgtg tcataaacac ttcccatgc agcaagagtt atgtctcgtt ccacgtatt 240  
 accactggtc ccaccagtaa acttggctcc tgggaatcacc tctggcccat caaacacaac 360  
 ggtggcacca tggaaataat ggtcccaata tgggaatcacc tcttctgtcc caatttctt 480  
 aggtcccatat tctttaattt ggtcccaata tgggaatcacc tcttctgtcc caatttctt 480  
 actagttaaa aaatttctgc gcataattg cctttttatt tgaataaatt caatttctt 480  
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 ttacatacat ccatttctcc acgttgataa accatccaa ttcactgctt atcccgatc 600  
 acgttactgc cataactggt tcatcgtctt ataacacag tcaagaatca caatttctt 480  
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 taattactgc agtgagggtt ttttactatc ccatcagctt ataacacag tcaagaatca 600  
 tttatgacaa ccatcagctt ttttactatc ccatcagctt ataacacag tcaagaatca 600  
 cactactgaa cagcagctt ttttactatc ccatcagctt ataacacag tcaagaatca 600  
 cttcagaaga cagcagctt ttttactatc ccatcagctt ataacacag tcaagaatca 600  
 tcgggttga taacgttctt gtaagatcaa ttctttata ttctataaag agcctgtt 1500  
 cagtgttga aagtattgca ggcagatcaa ttctttata ttctataaag agcctgtt 1500  
 taaagagac aagtattgca ggcagatcaa ttctttata ttctataaag agcctgtt 1500  
 tggtagaa aagtattgca ggcagatcaa ttctttata ttctataaag agcctgtt 1500  
 gcagagtgtt agcttatatt tcttttgac attgtgaaa ctatccctga tgaatttgc aataactt 1680  
 actctccaat taccactaat aagcagca accggcaata atcagatatt ctggacatt caatttaa 1800  
 ctactactgc aagcagca accggcaata atcagatatt ctggacatt caatttaa 1800  
 gagtactgc aagcagca accggcaata atcagatatt ctggacatt caatttaa 1800  
 ccaccgaa attacaattt aaaaacctt ctggaataaa ctctattgca caacaggtt 1980  
 aatctgaaga tgtatcgat ctggaataaa ctctattgca caacaggtt 1980  
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 aatag

<210> 434  
 <211> 534  
 <212> PRT  
 <213> Candida albicans

525

Printed: 17-08-2000

525

&lt;400&gt; 434

Met Tyr Val Leu Lys Lys Lys Asn Phe Val Gln Phe Leu Val Leu Val  
 1 5 10 15  
 Leu Pro Leu Ile Ser Ser Leu Ser Tyr Lys Phe Thr Asn Met Asp Glu  
 20 25 30  
 Val Val Phe Tyr Ile Ala Gln Gly Asp Pro Ala Asp Lys His Ser Gln  
 35 40 45  
 Glu Ser Tyr Gly Tyr Val Thr Ser Ile His Ser Ser Lys Gln Tyr Ala  
 50 55 60

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Ser Tyr Arg Gln Ala Asp Ser His Ile Asn Gly Thr Ala Ile Thr Gly  
 65 70 75 80  
 Ile Gly Pro Gly Glu Arg Ile Phe Thr Ala Val Pro Asn Lys Ala Leu  
 85 90 95  
 Ile Asn Val Tyr Ser Trp Gly Lys Glu Ser Val Asp Gln Arg Ile Pro  
 100 105 110  
 Ile Pro Glu Ala Leu Thr Cys Ile Thr Leu Ile Asn His Pro Asn Gly  
 115 120 125  
 Ser Asn Asn Asn Ser Asp Asn Asp Asp Asn Gln Leu Tyr Lys Leu Pro  
 130 135 140  
 Asn Tyr Arg Val Pro Trp Leu Leu Ala Gly Gly Ser Lys Ser Gly Lys  
 145 150 155 160  
 Leu Tyr Ile Trp Glu Leu Ser Ser Gly Asn Leu Leu Cys Val Arg Asp  
 165 170 175  
 Ala His Tyr Gln Gly Ile Thr Thr Ile Lys Gly Ser Ser Cys Gly Thr  
 180 185 190  
 Phe Leu Ile Thr Gly Gly Glu Asp Ala Arg Cys Leu Val Trp Asn Leu  
 195 200 205  
 Ala Glu Leu Ile Ser Ile Tyr Asp Lys Ser Asp His Gln Val Lys Pro  
 210 215 220  
 Tyr Trp Gln Ile Thr Asp Asn Thr Leu Pro Leu Thr Asp Leu Cys Leu  
 225 230 235 240  
 Asn Asp Thr His Asn Ile Asn Asp Leu Lys Leu Tyr Thr Thr Ser Glu  
 245 250 255

526

Asp	Ser	Thr	Val	Arg	Ile	Tyr	Asp	Ile	Val	Thr	Lys	Ser	Leu	Leu	Thr	260	265	270	
Thr	Phe	Ile	Leu	Pro	Ser	Ser	Ala	Glu	Cys	Ile	Thr	Lys	Asp	Pro	Ala	275	280	285	
Asn	Arg	Ala	Leu	Tyr	Val	Gly	Leu	Asn	Asn	Gly	Leu	Val	Arg	Ser	Ile	290	295	300	
Pro	Leu	Tyr	Ser	Ile	Asn	Ser	His	Thr	Ser	Val	Leu	Glu	Ser	Ile	Gly	305	310	315	320

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Gly	Met	Asn	Lys	Ile	Ile	Thr	Val	Asp	Ala	Asp	Gln	Asn	Leu	Lys	Glu	325	330	335	
Thr	Phe	Val	Ala	His	Gln	Gln	Lys	Thr	Lys	Thr	Gly	Asp	Asp	Lys	Pro	340	345	350	
Val	Val	Val	Thr	Lys	Leu	Thr	Ile	Ser	Phe	Asp	Gly	Thr	Ser	Ile	Ile	355	360	365	
Ser	Gly	Asp	Ser	Glu	Gly	Arg	Val	Phe	Val	Ser	Asp	Ile	Val	Thr	Lys	370	375	380	
Gln	Val	Val	Lys	Ser	Phe	Thr	Pro	Cys	Asn	Ser	Pro	Ile	Ala	Tyr	Ile	385	390	395	400
Ala	Val	Glu	Thr	Ile	Pro	Asp	Asp	Phe	Val	Asn	Asn	Leu	Ala	Thr	Ser	405	410	415	
Thr	Thr	Thr	Asn	Lys	Ala	Asp	Lys	Lys	His	Arg	Met	Ile	Pro	Gln	Phe	420	425	430	
Lys	Arg	Val	Leu	Ala	Ser	Thr	Asn	Ser	Glu	Glu	His	Gln	Ile	Phe	Leu	435	440	445	
Asp	Ile	Pro	Gly	Lys	Thr	Thr	Ala	Thr	Thr	Asn	Ala	Thr	Gly	Asn	Ile	450	455	460	
Asp	Phe	Ala	Thr	Trp	Leu	Gln	Gly	Lys	Gln	Ser	Glu	Glu	Leu	Gln	Phe	465	470	475	480
Lys	Asn	Leu	Ser	Gly	Ile	Asn	Ser	Ile	Val	Lys	Gln	Val	Gly	Asn	Glu	485	490	495	
Asn	Val	Ser	Asp	Leu	Glu	Glu	Arg	Leu	Gln	Arg	Val	Ser	Gln	Ala	Tyr	500	505	510	

527

Thr Glu Leu Arg Asn Lys His Glu Glu Leu Ile Lys Glu His Ala Lys  
 515 520 525

Leu Leu Asp Lys Leu Glu  
 530

<210> 435

<211> 896

<212> DNA

<213> Candida albicans

<400> 435

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 ttgtgtaata aggttatgtc atcgggtatt acagattgca gggccatctt gtcttcatca 180  
 gttatagcat ttcaataaaa ataagccaca tatgtgtaca gcgctgagtc tactcaacat 240  
 gtgtaaatag aataaatcaa ttgacacagt cttttgagat ctgttattct ggcctatagc 300  
 gtttttaggaa attgcggtat tttcttgtct gtttttcttt tatctatttt cgcacgactt 360  
 ggggtggttt gtgtgacttt tttagcaaat taattttgtc ggtcttcgca gtaaaaaataa 420  
 aaaattcaaa aaaaaaaaca aattgacttt ttttttact ttctttcttt tctatcaaca 480  
 atactaatca caagccaacc atgaaattca ctactgttgc cactgttttt gctatttcct 540  
 cattagctgc cgctaaaggt ggtgaaaaag atcacggtaa agcttctact gtcaccaaatt 600  
 atgtcactga aactaccac agatacggtc gttttgacaa aaccagtaga tctaaaaagc 660  
 caaaggaaac tgggtactcac agatacggta aattcaacaa gactccacgt ccagttacca 720  
 caactgtctt ggtcaaagaa agcgaccttc caaagaaaag agatgctgtt gttgctagag 780  
 attctaaaaa cgcttcttcc aactctacca cctctagtgg taacaatggt gtcgccactg 840  
 gtgtcagctt ggggtcttgc ggtgtcttag ctgttggtgc tgctttggtc atctaa 896

<210> 436

<211> 131

<212> PRT

<213> Candida albicans

<400> 436

Met Lys Phe Thr Thr Val Ala Thr Val Phe Ala Ile Ser Ser Leu Ala  
 1 5 10 15  
 Ala Ala Lys Gly Gly Glu Lys Asp His Gly Lys Ala Ser Thr Val Thr  
 20 25 30  
 Lys Tyr Val Thr Glu Thr Thr His Arg Tyr Gly Arg Phe Asp Lys Thr  
 35 40 45  
 Ser Arg Ser Lys Lys Pro Lys Glu Thr Gly Thr His Arg Tyr Gly Lys

528

50                      55                      60  
 Phe Asn Lys Thr Pro Arg Pro Val Thr Thr Thr Val Leu Val Lys Glu  
 65                                      70                                      75                                      80  
 Ser Asp Leu Pro Lys Lys Arg Asp Ala Val Val Ala Arg Asp Ser Lys  
                                     85                                      90                                      95  
 Asn Ala Ser Ser Asn Ser Thr Thr Ser Ser Gly Asn Asn Gly Val Ala  
                                     100                                      105                                      110  
 Thr Gly Val Ser Leu Gly Leu Ala Gly Val Leu Ala Val Gly Ala Ala  
                                     115                                      120                                      125

---

Leu Val Ile  
 130

<210> 437  
 <211> 1076  
 <212> DNA  
 <213> Candida albicans

<400> 437  
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 ctcttgtttc ggttctactt gttccttttt tttattctcc tcgttaatcc taattttgtg 120  
 taacaaatta attataggga gttggaaaat taaaagcttg aaaagaaaga aagaaagaaa 180  
 taccaacgtg gaatttctat tacgtaagtc actataactt gcatagaaat ttcagggtttt 240  
 caatttaaga aagtattaat caactgaatt aagcaattga aacgaattga accagctcag 300  
 cattttatttt tcgttttctt tttttttcaa ggggggtgggt gaaagaaaaa tctaaaaata 360  
 tataaatact ccacttatct cctctcttcc tctctttctc tctctaactc aatttcaatt 420  
 tttcccaaac caaaatttcc tttctttctt tctttcttta ttttttactc aattgaatca 480  
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 acagaggggtt attatctact gtcgccggtg gtggttgctgg tggttatggt ggtcacaaat 660  
 taggtgaaaa ggcacaacat ggtacttttg gtactgtatt aggtgccatt gggggtgcca 720  
 ttggtgccaa taaactagaa gatgcttatg aagaccgtaa agaacataaa aaacacgagc 780  
 aacaatatgg tggtagtggt aaacacgaag gcggaagaca tgaagggtgg tttggtggtg 840  
 gtagaccaga tgatcgttat gaaggcgata gaagaaatga taattacggt ggtggttaca 900  
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 gacacgaagg tggtttcggc ggtggcagac cagatgaccg ttttgggtggc ggtagaccag 1020  
 atgaccgttt tggaggtgac agaagagatg atagaagaga tgaccgtaga tggtaa 1076

<210> 438  
 <211> 191  
 <212> PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 438

Met Ser Ala Asn Asp Phe Tyr Ser Ser Gly Asp Gln Ser Asn Tyr Asp  
 1 5 10 15

Pro Lys Arg Ser Ser Asn Gln Gly Ser Ser Ser Ser Asn Asp Glu Gln  
 20 25 30

Gln Asp Arg Gly Leu Leu Ser Thr Val Ala Gly Gly Val Ala Gly Gly  
 35 40 45

Tyr Gly Gly His Lys Leu Gly Glu Lys Ala Gln His Gly Thr Leu Gly  
 50 55 60

Thr Val Leu Gly Ala Ile Gly Gly Ala Ile Gly Ala Asn Lys Leu Glu  
 65 70 75 80

Asp Ala Tyr Glu Asp Arg Lys Glu His Lys Lys His Glu Gln Gln Tyr  
 85 90 95

Gly Gly Ser Gly Lys His Glu Gly Gly Arg His Glu Gly Gly Phe Gly  
 100 105 110

Gly Gly Arg Pro Asp Asp Arg Tyr Glu Gly Asp Arg Arg Asn Asp Asn  
 115 120 125

Tyr Gly Gly Gly Tyr Asn Asp Arg Arg Asp Asp Gly Tyr Gly Gly Gly  
 130 135 140

Tyr Gly Gly Gly Arg Pro Asp Asp Arg Arg His Glu Gly Gly Phe Gly  
 145 150 155 160

Gly Gly Arg Pro Asp Asp Arg Phe Gly Gly Gly Arg Pro Asp Asp Arg  
 165 170 175

Phe Gly Gly Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Trp  
 180 185 190

&lt;210&gt; 439

&lt;211&gt; 1745

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 439

ttggtattga agacaccgaa gacttggtga aagatattga acaagcttta caaaaggctg 60



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atattgtgat aaaaaatttg aaagacaatc cgaatgtagt gcttgtctta tttctgcttg 240
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caggtcaaga tataccacct gggttacacg ttagattaaa tatagatacg ttggaaaaag 720
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gcgaattgca ggatcattcg aggggaagcca tcactgagaa tctacaaaag ttgcatgagc 840
tgaaacatcc tgaagtaaaa caggagcacg ctcatcgtac aaaggttagc caggggagatt 900
tgagtaattt tgacgcagct tgtctggaaa ttgagagttt caagccacat gagagtgatg 960
tggaaggtt gcatttgga ctagatactt tagaggaatt aagtcatgat atcgaatttg 1020
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gagcacgtca tgaagtattt ggcaatccaa tgggattaag aaaggcaatt gccgacgagt 1740
tgtag
1745

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&lt;210&gt; 440

&lt;211&gt; 414

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 440

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Met Lys Phe Ser Val Leu Val Leu Leu Ala Ser Tyr Leu Val Gly Val
  1             5             10             15

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Asn Ser Ser Ile Val Asp Thr Ser Glu Glu Leu Ile Cys Pro Asp Pro
      20             25             30

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Glu Asn Pro Leu Asp Cys Tyr Pro Lys Leu Phe Val Pro Thr Asn Glu
      35             40             45

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Trp Gln Thr Ile Lys Pro Gly Gln Asp Ile Pro Pro Gly Leu His Val
      50             55             60

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531

Arg Leu Asn Ile Asp Thr Leu Glu Lys Glu Ala Lys Leu Met Ser Ala  
 65 70 75 80  
 Asp Glu Lys Asp Glu Pro Val Gln Glu Val Val Val Gly Gly Glu Leu  
 85 90 95  
 Gln Asp His Ser Arg Glu Ala Ile Thr Glu Asn Leu Gln Lys Leu His  
 100 105 110  
 Glu Ser Lys His Pro Glu Val Lys Gln Glu His Ala His Arg Thr Lys  
 115 120 125  
 Val Ser Gln Gly Asp Leu Ser Asn Phe Asp Ala Ala Cys Ser Glu Ile  
 130 135 140  
 Glu Ser Phe Lys Pro His Glu Ser Asp Val Glu Arg Leu His Leu Ala  
 145 150 155 160  
 Leu Asp Thr Leu Glu Glu Leu Ser His Asp Ile Glu Phe Gly Val Lys  
 165 170 175  
 Leu Thr Ser Asp Lys Ala Ile Phe Gln Ser Phe Val Asn Ile Ala Asn  
 180 185 190  
 Gly Ala Ser Asp Pro Lys Ile Thr Glu Lys Val Tyr Arg Val Met Gly  
 195 200 205  
 Ser Ser Leu Arg Asn Asn Pro Glu Ala Ile Ser Asn Ile Leu Thr Asn  
 210 215 220  
 Phe Asp Lys Ser Tyr Val Asp Asn Leu Phe Glu Gln Leu Ala Asn Glu  
 225 230 235 240  
 Asn Asp Val Leu Gln Lys Arg Ile Leu Gly Ile Ile Gln Ala Leu Val  
 245 250 255  
 Gln Asn Ser His Phe Ala Arg Gln Tyr Phe Ser Phe Asp His Ser Ser  
 260 265 270  
 Gly Leu Asn Asp Leu Ile Ala Ile Phe Pro Lys Leu Gly Pro Asn Ser  
 275 280 285  
 Lys Ser Arg Ala Ser Asn Ile Leu Glu Asp Leu Gln Leu Phe Pro Val  
 290 295 300  
 Thr Asn Asp Arg Arg Ser Leu Glu Asp Gln Asp Pro Glu Ser Gln Val  
 305 310 315 320

532

Ser Lys Phe Ile Gln Asn Ser Phe Val Gly Asn Lys Leu Asp Glu Lys  
 325 330 335

Asn Phe Lys Ser Tyr Phe Asp Gln Leu Val Asn Leu His Gln Ser Asn  
 340 345 350

Lys Ser Leu Arg Pro Ser Gly Asp Phe Leu Asn Trp Leu Ala Glu Glu  
 355 360 365

Val Glu Ser Arg Lys Glu Asn Lys Lys Arg Asp Asp Tyr Ser Gln Glu  
 370 375 380

Asp Lys Asp Phe Asp Glu Tyr Met Leu Arg Ala Arg His Glu Val Phe  
 385 390 395 400

Gly Asn Pro Met Gly Leu Arg Lys Ala Ile Ala Asp Glu Leu  
 405 410

<210> 441

<211> 1244

<212> DNA

<213> Candida albicans

<400> 441

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 atatattttca ataacaggag cagtaattag cttcaacatc aagggtactct tttatttttc 180  
 taccaaaaac acatctgaag tagctcttat ccatagatcc aaatatttta accttttttt 240  
 tttctacttc tcactacttt ttttttgcaa cacttactgc tcacaacgcc aatgaccata 300  
 ccattaattt caataatcaa atcaagagct tatttgtatc ctctcaagggt atgttaatgt 360  
 attaacaaca ccgatttctat ttcaccaact aacacgacag aaaggggttg tactatttttg 420  
 taacacatcc caccgtttgg cccttttaca taaccatatt gatacctcaa ttggtcctta 480  
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&lt;210&gt; 442

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 442

Met Phe Ser Leu Phe Phe Pro Pro Gln Ala Ile Val Tyr Thr Leu Leu  
 1 5 10 15

~~Met Gly Pro Leu Gly Val Ile Gly Ala Trp Tyr Ser Leu Ile Ser Gln~~  
~~20 25 30~~

Ala Ser Thr Leu Ser Ile Phe Val Val Thr Ile Ser Leu Met Pro His  
 35 40 45

Ile Gln Arg Val Ala Tyr Asp Ala Ile Leu Ser Arg Glu Cys Ala Asn  
 50 55 60

Asp Val Val Leu Met Gly Lys Leu Arg Arg Tyr Arg Lys Leu Pro Ile  
 65 70 75 80

Arg Val Arg Ala Arg Glu Tyr Leu Lys Ala Ile Pro Asp Phe Ser Ile  
 85 90 95

Phe Pro Phe Ser Leu Leu Lys Leu Leu Val Phe Phe Gly Ile Tyr Phe  
 100 105 110

Ile Pro Phe Val Gly Pro Ile Ile Val Leu Phe Phe Gln Ser Ser Lys  
 115 120 125

Arg Gly Leu Lys Ala His Ala Arg Tyr Phe Lys Leu Lys Gly Phe Ser  
 130 135 140

Arg Ser Asp Ile Arg Thr Ile His Lys Leu Asn Arg Pro Ala Tyr Met  
 145 150 155 160

Gly Tyr Gly Val Val Ala Leu Trp Leu Glu Ser Phe Pro Phe Ile Asn  
 165 170 175

Met Phe Phe Met Phe Thr Asn Thr Leu Gly Ala Ala Leu Trp Ala Val  
 180 185 190

Asp Ile Glu Gln Gln Glu Lys Ala Val Thr Glu Asn Val Ala Ala Ala  
 195 200 205

Thr Thr Thr Ala Thr Asp Thr Asn Ser Val Asn Gln Gln Gly Leu Val

534

210

215

220

Ile Pro Val His Asn Glu Pro Ala Thr Asn Ile Pro Glu Ala Thr Pro  
 225 230 235 240

Lys Thr Ala Thr Asn Thr Ile  
 245

&lt;210&gt; 443

&lt;211&gt; 2270

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 443

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 tgtattatac aatattttaa ttatagtaat catcctataa atttcaaagt caaaagacag 180  
 atcttaagggt ctaattaata actctctatg gccttctgtg tcaaattggt gtcgtttgat 240  
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 aatcagttga atctgcttta tcatctggtg gtggtgatga caaggattta ggatttggtg 900  
 aaattttaaa tgatcctaatt ctttatacta aattgaaaaa taatcctaaa acaagtgaat 960  
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 ccttatacaa gaaacgtcaa tttgatgaag caattgccgc ctataataag gcttggggaat 1380  
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 attataaatt gattgctaaa tcatttgcta gattaggtaa tattttattg aaaaaagatg 1560  
 aattacccga agcagtgaaa aattttgaaa aatctttaac tgaacatcgt acccctgatg 1620  
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 tagatccaga aaaggctgaa gaagcaagat tacaaggtaa agaataattc accaaaggag 1740  
 attggccaaa tgccgttaag gcttatactg aaatgattaa aagagcacca gaagatgcta 1800  
 gaggatattc taatcgtgct gctgcattgg caaaattggt atcatttcct gatgctatac 1860  
 aagattgtaa taaagccatt gaaaaagatc caaatttcat tagagcttat attagaaaag 1920

535

ctaagtctca attggcaatg aaagaatata gtcatgtcat ggatacttta accgaggcaa 1980  
 gaactaaaga tgttgaattg ggtggtaaat caattcatga aattgatgaa ttaatgaata 2040  
 aagctactta tcaaagattt caagccattg aagggtgaaac tcctgaacaa actatggaaa 2100  
 gagtttctaa agatccagaa attgttcaaa ttttacaaga tccagtaatg caaggaattt 2160  
 tagctcaagc tagagaaaat cctgctgctt tacaagatca tatgaaaaat cctgaagttt 2220  
 ataaaaaat taatatgttg attgctgctg gtgttattcg taccagataa 2270

&lt;210&gt; 444

&lt;211&gt; 589

&lt;212&gt; PRT

<213> ~~Candida albicans~~

&lt;400&gt; 444

Met Thr Thr Ala Asp Glu Tyr Lys Ala Glu Gly Asn Lys Tyr Phe Ala  
 1 5 10 15

Ala Lys Asp Phe Glu Lys Ala Ile Glu Ala Phe Thr Lys Ala Ile Glu  
 20 25 30

Ala Ser Pro Glu Pro Asn His Val Leu Tyr Ser Asn Arg Ser Gly Ser  
 35 40 45

Tyr Ala Ser Leu Lys Asp Phe Asn Asn Ala Leu Lys Asp Ala Gln Glu  
 50 55 60

Cys Val Lys Ile Asn Pro Ser Trp Ala Lys Gly Tyr Asn Arg Ile Ala  
 65 70 75 80

Gly Ala Glu Phe Gly Leu Gly Asn Phe Asp Gln Ala Lys Ser Asn Tyr  
 85 90 95

Glu Lys Cys Leu Glu Leu Asp Pro Asn Asn Ala Met Ala Lys Glu Gly  
 100 105 110

Leu Lys Ser Val Glu Ser Ala Leu Ser Ser Gly Gly Gly Asp Asp Lys  
 115 120 125

Asp Leu Gly Phe Gly Lys Ile Leu Asn Asp Pro Asn Leu Tyr Thr Lys  
 130 135 140

Leu Lys Asn Asn Pro Lys Thr Ser Glu Phe Met Asn Asp Pro Gln Phe  
 145 150 155 160

Val Ala Lys Leu Glu Arg Leu Lys Thr Asn Pro Gln Leu Gly Asn Pro  
 165 170 175

Asp Met Phe Ser Asp Pro Arg Leu Leu Thr Ala Phe Ala Ala Leu Met

180

185

190

Gly Ile Asp Met Asp Leu Pro Asn Met Gly Phe Thr Ala Pro Asn Glu  
 195 200 205

Ser Gln Ser Asn Ala Ser Glu Pro Lys Ser Glu Pro Lys Ser Val Pro  
 210 215 220

Glu Ser Lys Pro Glu Pro Lys Ala Glu Gln Lys Glu Glu Glu Ser Thr  
 225 230 235 240

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Ser Ala Lys Asp Glu Asp Thr Pro Met Thr Asp Ala Gln Asp Asp Thr  
 245 250 255

Asn Asp Asn Asp Ala Lys Thr Gln Ala Asp Asn Ala Lys Ala Glu Gly  
 260 265 270

Asn Ala Leu Tyr Lys Lys Arg Gln Phe Asp Glu Ala Ile Ala Ala Tyr  
 275 280 285

Asn Lys Ala Trp Glu Leu His Lys Asp Ile Thr Tyr Leu Asn Asn Arg  
 290 295 300

Ala Ala Ala Glu Tyr Glu Lys Gly Asp Tyr Asp Ala Ala Ile Ala Thr  
 305 310 315 320

Cys Glu Lys Ala Ile Asp Glu Gly Arg Asp Met Arg Ala Asp Tyr Lys  
 325 330 335

Leu Ile Ala Lys Ser Phe Ala Arg Leu Gly Asn Ile Tyr Leu Lys Lys  
 340 345 350

Asp Glu Leu Pro Glu Ala Val Lys Asn Phe Glu Lys Ser Leu Thr Glu  
 355 360 365

His Arg Thr Pro Asp Val Leu Asn Lys Leu Arg Ser Thr Gln Arg Glu  
 370 375 380

Ile Lys Thr Arg Glu Leu Asn Ala Tyr Ile Asp Pro Glu Lys Ala Glu  
 385 390 395 400

Glu Ala Arg Leu Gln Gly Lys Glu Tyr Phe Thr Lys Gly Asp Trp Pro  
 405 410 415

Asn Ala Val Lys Ala Tyr Thr Glu Met Ile Lys Arg Ala Pro Glu Asp  
 420 425 430

Ala Arg Gly Tyr Ser Asn Arg Ala Ala Ala Leu Ala Lys Leu Leu Ser

537

435

440

445

Phe Pro Asp Ala Ile Gln Asp Cys Asn Lys Ala Ile Glu Lys Asp Pro  
 450 455 460

Asn Phe Ile Arg Ala Tyr Ile Arg Lys Ala Asn Ala Gln Leu Ala Met  
 465 470 475 480

Lys Glu Tyr Ser His Val Met Asp Thr Leu Thr Glu Ala Arg Thr Lys  
 485 490 495

~~Asp Val Glu Leu Gly Gly Lys Ser Ile His Glu Ile Asp Glu Leu Met~~  
 500 505 510

Asn Lys Ala Thr Tyr Gln Arg Phe Gln Ala Ile Glu Gly Glu Thr Pro  
 515 520 525

Glu Gln Thr Met Glu Arg Val Ser Lys Asp Pro Glu Ile Val Gln Ile  
 530 535 540

Leu Gln Asp Pro Val Met Gln Gly Ile Leu Ala Gln Ala Arg Glu Asn  
 545 550 555 560

Pro Ala Ala Leu Gln Asp His Met Lys Asn Pro Glu Val Tyr Lys Lys  
 565 570 575

Ile Asn Met Leu Ile Ala Ala Gly Val Ile Arg Thr Arg  
 580 585

&lt;210&gt; 445

&lt;211&gt; 1019

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 445

ccactaacaa actttttttt gactatacac cactgaaaaa aaaaaaaaaa tttttgtaaa 60  
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 cgttataata gaatagaata agagcatgac aacaaaggga tacaagcttg aaaaaagaaa 180  
 aagggtggga tatcttaaaa ttattaaaga gtttttttta taacatgtca ttgagattga 240  
 gattgggaat actgaattcg attttaaagt cattggatgg gagagttaat tattcgtttt 300  
 attattagga ttaccaatga atagtaatga agtgatggag agatagaatg aaagtattca 360  
 gaagagcatc aagtccctta taagtttgtg agacataata tgtctacccc cttgtcaact 420  
 tgtcataaat tttattgctc gtccttttaa agaaatgaat aaaaagattt actaacttaa 480  
 tttcaattat ttatagaaag atgtctagat taaacgaata tcaagttatt ggtcgtaatt 540  
 taccaactga atccgttcca gaaccaaagt tggttcagaat gagaattttt gtcctcaaca 600  
 ccgttggtgc caaatcaaga tattggtatt tcttgcaaaa attgcataaa gttaaaaaag 660

538



cttctggtga aattgtatct gtcaacatta tttctgaagc taaaccaact aaagttaaaa 720  
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 acagagatgt tactagagtt ggtgctgttg aaaccatgta ccaagattta gctgctagac 840  
 acagagctag atttagaagt atccatattt tgaaagttgt tgaattagaa aaaactgatg 900  
 atgttaaaaag acaatacgtt aaacaatttt tgactaaaga tttgaaattc ccattaccac 960  
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<210> 446

<211> 172

<212> PRT

<213> *Candida albicans*

<400> 446

Met Ser Arg Leu Asn Glu Tyr Gln Val Ile Gly Arg Asn Leu Pro Thr  
 1 5 10 15

Glu Ser Val Pro Glu Pro Lys Leu Phe Arg Met Arg Ile Phe Ala Pro  
 20 25 30

Asn Thr Val Val Ala Lys Ser Arg Tyr Trp Tyr Phe Leu Gln Lys Leu  
 35 40 45

His Lys Val Lys Lys Ala Ser Gly Glu Ile Val Ser Val Asn Ile Ile  
 50 55 60

Ser Glu Ala Lys Pro Thr Lys Val Lys Thr Phe Gly Ile Trp Leu Arg  
 65 70 75 80

Tyr Glu Ser Arg Ser Gly Ile His Asn Met Tyr Lys Glu Tyr Arg Asp  
 85 90 95

Val Thr Arg Val Gly Ala Val Glu Thr Met Tyr Gln Asp Leu Ala Ala  
 100 105 110

Arg His Arg Ala Arg Phe Arg Ser Ile His Ile Leu Lys Val Val Glu  
 115 120 125

Leu Glu Lys Thr Asp Asp Val Lys Arg Gln Tyr Val Lys Gln Phe Leu  
 130 135 140

Thr Lys Asp Leu Lys Phe Pro Leu Pro His Arg Val Gln Lys Ser Lys  
 145 150 155 160

Lys Leu Phe Gln Ala Thr Ala Pro Thr Thr Phe Tyr  
 165 170

<210> 447  
 <211> 932  
 <212> DNA  
 <213> Candida albicans

<400> 447  
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 acaatattaa catacctttg tcacaagcaa ttatattgaa gttttttgat acaagtgtgt 120  
 tgtttttttg tgtacatgtg agatatataa ttgtgtatat acagtcacgt gaatagagca 180  
 gaaaaattac gaagtagaaa tattggtagc gcggttagggc tatagcccta tttagtttgt 240  
~~gcaccacaag aettacaatt tttttttttt tttttcttag aatccttgag gcactgacac 300~~  
 tgtactctct ctctctctct ctctctctcg taggtagtga aaaatttcca ctagtcttcc 360  
 cataaccac ctaggttctt tcttttgga accactgagc agtaaatcaa tttacttgac 420  
 gaagaagtct atacataaat ataaacttgt cccctcccc ccctttttt ttaactaact 480  
 aagaagaaaa aattaataaa atgtctgacg ttgaacaaga acaaattgtt gaagaagttg 540  
 ttgttgaaga acaatccggt gccatcacca ttgaagatgc tttaaaagtt gttttaagaa 600  
 cttctttagt ccatgatggt ttagctagag gtttaagaga agcttctaaa gctttatcta 660  
 aaagagaagc tcaattatgt gttttgtgtg actctgttac tgaagaatca atcatcaaat 720  
 tggttgaagc tttatgtaat gaaccagaag aaaaaatccc attgattaaa gtttccgatg 780  
 ctaaattatt ggggtgaatgg gctggtttat gtcaattaga tagagatggt aatgctagaa 840  
 aagttgttgg tgcctcttgt gttgttgtca aaaactgggg tgctgattct gatgaaagaa 900  
 acatcttggt ggaacacttt tctcaacaat aa 932

<210> 448  
 <211> 143  
 <212> PRT  
 <213> Candida albicans

<400> 448  
 Met Ser Asp Val Glu Gln Glu Gln Ile Val Glu Glu Val Val Val Glu  
 1 5 10 15  
 Glu Gln Ser Gly Ala Ile Thr Ile Glu Asp Ala Leu Lys Val Val Leu  
 20 25 30  
 Arg Thr Ser Leu Val His Asp Gly Leu Ala Arg Gly Leu Arg Glu Ala  
 35 40 45  
 Ser Lys Ala Leu Ser Lys Arg Glu Ala Gln Leu Cys Val Leu Cys Asp  
 50 55 60  
 Ser Val Thr Glu Glu Ser Ile Ile Lys Leu Val Glu Ala Leu Cys Asn  
 65 70 75 80  
 Glu Pro Glu Glu Lys Ile Pro Leu Ile Lys Val Ser Asp Ala Lys Leu  
 85 90 95

540

Leu Gly Glu Trp Ala Gly Leu Cys Gln Leu Asp Arg Asp Gly Asn Ala  
 100 105 110

Arg Lys Val Val Gly Ala Ser Cys Val Val Val Lys Asn Trp Gly Ala  
 115 120 125

Asp Ser Asp Glu Arg Asn Ile Leu Leu Glu His Phe Ser Gln Gln  
 130 135 140

<210> 449  
 <211> 881  
 <212> DNA  
 <213> Candida albicans

<400> 449  
 aaaatttcca atcttgaatt tcatcttcaa cgtcataaac ttgttctggt tgaaatttat 60  
 cgtcctcatt atcgttgtca ttttcattgt cattgtcaat attacggtta cgattttggt 120  
 ttccctttga agtctttgac tctagctggt catctgtcat tacccttggc ttggtttggtc 180  
 ttactgttga gcgatgagac aaactttttg attgattgca actgaacaaa aaaaaatagc 240  
 acagacacac acacacacac acacacacaa ttttcagctc cttccaagtc gtgttttttt 300  
 ggaagaaaaa aaaaacaact tggccctaaa aactctatgc tctaaccgac aacattagat 360  
 tactttgata actcacaacc tttaattaac actatctaca aaatatgaca agtacaccaa 420  
 taacgtacaa gacactagta tgaaaggcaa gcacaaactt gcaaacaaaa aaccctaac 480  
 ttttattata gttttgtttg atgttatttt gttttatact aactaaaatc tgtttttttt 540  
 ttttttcaaa ggccgattct atatttaatg atctaataca caatatcatt aaacaacata 600  
 cattaaccag ttttaaccaat attaaagatc attcctcatt attaaattca tctaatagca 660  
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 atgaaaataa tgaaattgaa aattcaacaa ttcaagataa atcaaaatta aaacaattag 780  
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 catctcatat aagtaagtgt ttagaacgga aacggaaatg a 881

<210> 450  
 <211> 126  
 <212> PRT  
 <213> Candida albicans

<400> 450  
 Met Leu Phe Cys Phe Ile Leu Thr Lys Ile Cys Phe Phe Phe Phe Ser  
 1 5 10 15

Lys Ala Asp Ser Ile Phe Asn Asp Leu Ile Asn Asn Ile Ile Lys Gln  
 20 25 30

His Thr Leu Thr Ser Leu Thr Asn Ile Lys Asp His Ser Ser Leu Leu

35

40

45

Asn Ser Ser Asn Ser Asn Thr Asn Ser Asn Thr Asn Gly Thr Ile Ala  
50 55 60

Ser Asn Gly Gly Asn Gly Thr Thr Ser Asp Glu Asn Asn Glu Ile Glu  
65 70 75 80

Asn Ser Thr Ile Gln Asp Lys Ser Lys Leu Lys Gln Leu Glu Thr Ser  
85 90 95

Arg Tyr Phe Arg Cys Leu Asn Cys Gly Arg Asn Ile Ala Gly Gly Arg  
100 105 110

Phe Ala Ser His Ile Ser Lys Cys Leu Glu Arg Lys Arg Lys  
115 120 125

&lt;210&gt; 451

&lt;211&gt; 5344

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 451

ctctagaagt aggacatcgt atagtgtata aacactcaat aagtaatgaa gaaacacggt 60  
ttgttgtgca atgttagctg gcgagctcaa tattgggtct ctccgccgtc tgtctgcctt 120  
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ctgttgtttg cactttgcac gtagttgttt tcccctcatt ctttcatctg attattctgt 240  
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aaagatgtag cgagagaaat agaattncaa gggttaaggat gattaacttt tttttttttt 540  
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tatagagtaa cctgggtcga ggtgaaccg aattcaatat tggttttcgg ttgttatatg 720  
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cataccacaa aataaattgc ctttacctaa tgccaatgaa gattttgcca cgggtgtgtc 1380

542

gaatggagat gttgactggc tatttcgagg taaatcaaag aaattgggga aaaagatggc 1440  
taacaacaat gccataagg atgaacgaaa gaatagtcac ggtaacatca aaaactcggg 1500  
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cgatttacat caacttggtg acggtaaaca taatggtaat ggtacggtg atcccatggt 5280
tagtgaagtt tatgacaagt tgttaaatga tgctgaacga gtcagactga atagagatat 5340
ataa 5344

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&lt;210&gt; 452

&lt;211&gt; 1364

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 452

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Met Thr Ser Asn Ser Pro Pro Leu Gly Ser Thr Thr Asn Asp Gln Arg
  1             5             10             15

Leu Pro Gln Ser Gly Val Ser Ser Ile Pro Thr Asn Lys Leu Pro Leu
          20             25             30

Pro Asn Ala Asn Glu Asp Phe Ala Thr Gly Val Ser Asn Gly Asp Val
          35             40             45

Asp Trp Leu Phe Arg Gly Lys Ser Lys Lys Leu Gly Lys Lys Met Ala
          50             55             60

Asn Asn Asn Ala Asn Lys Asp Glu Arg Lys Asn Ser His Gly Asn Ile
          65             70             75             80

Lys Asn Ser Glu Lys Thr Thr Ala Lys Pro Asn Glu Thr Lys His Glu
          85             90             95

Ser Asn Gly Glu Lys Leu Glu Phe Asn Val Pro Lys Ser Val Met Pro
          100            105            110

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544

Thr Lys His Thr Ser Ser Gly Asn Pro Lys Ala Pro Thr Asn Gly Gln  
 115 120 125  
 Ile Ser Asn Val Thr Pro Ser Gln Pro Ser Pro Lys Gln Thr Thr Ser  
 130 135 140  
 Gly Ser Thr Asn Ala Asn Asp Ile Pro Pro Ile Ser Pro Lys Gln Pro  
 145 150 155 160  
 Glu Lys Ala Ser Lys Leu Asn Lys Leu Lys Ile Gly Arg Ser Arg Ser  
 165 170 175

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Ser Ser Ala Ser Thr Val Val Pro Ser Ser Thr Thr Ala Ser Thr Thr  
 180 185 190  
 Thr Asn Pro Gly Asp Pro Lys Ser Gln Pro Lys Arg Arg Ser Ser Ser  
 195 200 205  
 Phe Asn Phe Val Thr Pro Ser Leu Thr Ser Asp Leu Ala Tyr Asp Asp  
 210 215 220  
 Pro Ala Leu Val Ser Gln Leu Ser Asn Asn Ser Asn Ser Ser Asn Ser  
 225 230 235 240  
 Ser Ser Pro Asn Val Ser Arg Ser Asn Ser Lys Lys Gly Gly Leu Phe  
 245 250 255  
 Ser Ser Leu Ser Ser Lys Phe Arg Ser Ser Ser Ala Ser Ser Lys Gln  
 260 265 270  
 Pro Gln Ser His Ser Ser Ser Thr Pro Ser Thr Thr Thr Thr Asn Gly  
 275 280 285  
 Gly Gly Asn Ser Ser Ala Ala Pro Lys Ser Ser His His Ser Pro Lys  
 290 295 300  
 Phe Asn Pro Ser Leu Val Gly Pro Val Ser Lys His Asn Arg Glu Ala  
 305 310 315 320  
 Glu Asp Leu Val Ser Leu Thr Asn Thr Leu Pro Ala Gly Ser Gly Ile  
 325 330 335  
 Pro Ile Lys Arg Lys Pro Ser Ile Ser Gly Asn Ser Ile Phe Lys Asp  
 340 345 350  
 Ser Phe Leu Asp Asp Ala Ser Ser Ser Pro Ser Ser Ser Leu Asn Ser  
 355 360 365

545

Asp Gly Gly Leu Lys Phe Phe Arg Arg Arg Ser Ser Val Ala Ser Thr  
 370 375 380  
 Pro Ser Thr His Ala Ser Thr Pro Arg Val Ile Leu Asn Lys Asn Pro  
 385 390 395 400  
 Asn Arg Arg Lys Val Pro Ile Glu Glu Ile Ser Glu Val Arg Leu Arg  
 405 410 415  
 Arg Val Thr Phe Ser Val Asp Lys Leu Glu His Asp Pro Gln Gln Gln  
 420 425 430  


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 Ile Pro Ser Arg Arg Pro Lys Arg Gly Asn Val Leu Ile Pro Gln Asp  
 435 440 445  
 Ile Asn Ala Pro Pro Pro Arg Leu Cys Leu Gly Ile Ser Val Asn Glu  
 450 455 460  
 Pro Asn Asn Lys Asp Asp Gly Lys Ser His Asn His Ser Lys Tyr Ser  
 465 470 475 480  
 Asp His Glu Ile Ala Leu Ala Glu Asp Ala Gln Arg Arg Ala Ile Ile  
 485 490 495  
 Glu Ala Glu Lys His Ala Gln Glu Ala His Arg Gln Ala Lys Lys Ile  
 500 505 510  
 Ala Gln Glu Val Ser Gly Tyr Arg Ser His Arg Phe Ile Ser Ile Lys  
 515 520 525  
 Glu Gly Gly Ser Val Gly Asn Ser Asn Thr Asn Gly Asn Asp Asn Asp  
 530 535 540  
 Glu Asp Asp Asp Glu Val Glu Glu Ala Val Asp Lys Lys Leu Ala Asn  
 545 550 555 560  
 Asp Val Ser Val Asp Gly Pro Leu His Val His Glu Gln His Phe Glu  
 565 570 575  
 Glu Glu Ile Glu Ser Lys Thr Gly Glu Lys Thr Ile Ser Leu Glu Thr  
 580 585 590  
 Ile Tyr Thr Arg Cys Cys His Leu Arg Glu Ile Leu Pro Ile Pro Ala  
 595 600 605  
 Thr Leu Lys Gln Leu Lys Asn Lys Thr Ala Pro Leu Glu Val Leu Lys  
 610 615 620



Met Leu Asn Pro Lys Pro Thr Leu Ile Asp Val Leu Ser Phe Ser Asp  
625 630 635 640

Phe Ile Ala Ile Thr Pro Ile Asn Thr Val Ile Phe Asp Asn Val Thr  
645 650 655

Met Thr Thr Glu Met Leu Lys Asn Phe Leu Gly Ser Leu Thr Tyr Asn  
660 665 670

Lys Gln Leu Glu Lys Leu Ser Leu Arg Asn Val Ser Ile Asp Glu Leu  
675 680 685

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Gly Trp Lys Tyr Leu Cys Glu Phe Leu Ala Thr Asn Lys Thr Val Lys  
690 695 700

Lys Leu Asp Ile Ser Gln Gln Arg Ile Lys Pro Asp Thr Pro Asp Thr  
705 710 715 720

Ser Ile Arg Gly Asn Met Asn Trp Asp Leu Phe Ile Arg Ser Leu Ile  
725 730 735

Leu Arg Gly Gly Ile Glu Glu Leu Val Ile Asn Gly Cys Lys Leu Ser  
740 745 750

Asp Ala Ile Phe Glu Lys Phe Ile Asn Gln Ala Val Lys Lys Ser Thr  
755 760 765

Tyr Arg Leu Gly Ile Ala Gly Ile Asp Leu Asn Val Lys Lys Ser Glu  
770 775 780

Met Val Thr Ser Trp Leu Thr Asp Gly Asn Ser Gln Cys Val Gly Val  
785 790 795 800

Asp Ile Ala Phe Asn Asp Leu Ser Lys Gly Gln Leu Arg Pro Phe Ile  
805 810 815

Asn Ala Phe Asn Thr Gly Lys Val Asn Asn Leu Val Phe Phe Ser Leu  
820 825 830

Asn Ser Thr Asn Leu Ser Asn Ile Glu Glu Thr Ser Asp Leu Ile Lys  
835 840 845

Ser Leu Ile Asn Val Lys Thr Leu Arg Phe Leu Asp Leu Ser Ser Ile  
850 855 860

Pro Asn Ile Phe Pro Lys Ile Ile Thr His Leu Asp Lys Tyr Leu Pro  
865 870 875 880

Arg Tyr Pro Asn Leu Arg Arg Ile His Phe Asp Leu Asn Glu Leu Thr  
 885 890 895  
 Ala Gln Ala Ile Gly Ser Leu Ala Gly Cys Leu Ser Lys Met Pro Gln  
 900 905 910  
 Leu Val His Val Ser Leu Leu Gly Asn Arg Asn Leu Ser Thr Thr Ser  
 915 920 925  
 Ala Ala Thr Leu Tyr Gly Ala Val Lys Gln Ser Lys Thr Leu Phe Ala  
 930 935 940

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Leu Asp Leu Asp Tyr Asp Leu Ile Pro Asp Gln Leu Ser Gln Arg Ile  
 945 950 955 960  
 Ala Phe Tyr Leu Met Arg Asn Leu Glu Tyr Thr Leu Lys Pro Ser His  
 965 970 975  
 Gly Gly Asn Ile Glu Ser Asn Pro Glu Lys Pro Glu Asp Leu Met Tyr  
 980 985 990  
 Asp Gly Ser Leu Leu Met Glu Thr Ala Glu Lys Leu Leu Val Glu Ile  
 995 1000 1005  
 Glu Lys Gly Lys Lys Glu Asp Ile Lys Met Gln Arg Ile Ile Ser Asp  
 1010 1015 1020  
 Ser Val Leu Glu Arg Thr Arg Ser Ile Arg Lys Asp Ile His Lys Thr  
 1025 1030 1035 1040  
 Ile Asp Thr Leu Phe Glu Gln Arg Asn Leu Gly Lys Leu Ser Phe Glu  
 1045 1050 1055  
 Gly Lys Glu Asn Leu Val Arg Phe Cys Leu Leu Asp Ser Ser Leu Glu  
 1060 1065 1070  
 Lys Leu Val Val Met Val Glu Glu His Ala Asn Gly Leu Leu Leu Thr  
 1075 1080 1085  
 Pro Thr Thr Ser Thr Asp Asp Leu Arg Ser Arg Ala Met Ser Pro Ser  
 1090 1095 1100  
 Val Thr Val Asp Thr Ile His Glu Ser Ala Asn Glu Leu Ile Thr Ala  
 1105 1110 1115 1120  
 Gly Pro Ile Leu Ser Pro His Val Asn Arg Lys Ala Glu Gln Ser Ser  
 1125 1130 1135

Tyr Phe Pro Val Phe Ala Asn Asn Asp Asn Leu Thr Pro His Gln Val  
1140 1145 1150

Val Val Glu Ser Asn Asp Glu Gly Arg Asp Val Pro Ile Asp Lys M t  
1155 1160 1165

Thr Gly Arg Pro Val Leu Ile Arg Ser Ile Ser Gln Thr Ser Val His  
1170 1175 1180

Ala Lys Glu Gln Glu Ile Glu Glu Gly Glu Leu His Lys Phe Gly Phe  
1185 1190 1195 1200

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Phe Ile Gln Gln Lys Glu Arg Gln Lys Gln Gln Gln Gln Gln Gln  
1205 1210 1215

Gln Gln Asn Ser His His Gln His Gln Pro Ala Gln Ser Ile Gln Gln  
1220 1225 1230

Glu Asn Gln Ser Pro Ser Pro Gln Gln Gly Lys Tyr Glu Asp Leu Pro  
1235 1240 1245

Ile Leu Asn Thr Leu Pro Ser Gly Pro Glu Leu Arg Asp Ala Ile Met  
1250 1255 1260

Ala Ala Lys Gly Val Ala Asn Val Thr Glu Leu Ile Asp Arg Ile Asn  
1265 1270 1275 1280

Asn His Arg Val Lys Ile Asp Ala Pro Ser Thr Lys His His His Glu  
1285 1290 1295

Leu Asn Lys Pro Asn Ser Asp Lys Val Val Glu Asp Glu Val Glu Val  
1300 1305 1310

Ser Asp Asn Ala Ser Ile Asp Ser Thr Asn Gly Asp Asp Leu His Gln  
1315 1320 1325

Leu Gly Asp Gly Lys His Asn Gly Asn Gly Thr Val Asp Pro Met Val  
1330 1335 1340

Ser Glu Val Tyr Asp Lys Leu Leu Asn Asp Ala Glu Arg Val Arg Ser  
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Asn Arg Asp Ile

<210> 453

549

<211> 1859  
 <212> DNA  
 <213> Candida albicans

<400> 453

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aaggtagaat agaattcaat gtaggtgata tcactttctg agagttctta ttacgatata 180
taaaatacat agccaaaatt ataatgaagt aaaaacatgt aactgtgtaa ttttattcaa 240
gtccaaaggt attgattaat attgtagagt gttgagcatt taaaatatga aggaagaccg 300
ataacctaaa gttttcctca ggggtgctgaa ggctaggagg aataaaatct gagtagagaa 360
ctttcgttta tatcagtttt ttgcaagaaa aaaaggaaaa caaaacaaaa taacaccaca 420
aacgaattac acaagcacat cctaaacacc actctgttgg agcaccaatc aacctgagaa 480
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cgaatggttt gaaagtgtat tatgtaccac tttgggtgat ctatagaagc tcagttttcc 720
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<210> 454  
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 <212> PRT  
 <213> Candida albicans

<400> 454

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Gly Gly Val Glu Phe His Val Tyr His Leu Ser Gln Lys Leu Ile Glu

Leu Gly His Ser Val Val Ile Ile Thr His Asn Tyr Ser Ser Arg Asn  
 35 40 45  
 Gly Val Arg Val Leu Thr Asn Gly Leu Lys Val Tyr Tyr Val Pro Leu  
 50 55 60  
 Trp Val Ile Tyr Arg Ser Ser Val Phe Pro Thr Val Phe Ser Cys Phe  
 65 70 75 80  


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 Pro Ile Leu Arg Asn Ile Phe Ile Arg Glu Asn Ile Glu Ile Ile His  
 85 90 95  
 Gly His Gly Ser Phe Ser Thr Leu Cys His Glu Ala Ile Leu His Gly  
 100 105 110  
 Arg Thr Met Gly Leu Lys Thr Val Phe Thr Asp His Ser Leu Phe Gly  
 115 120 125  
 Phe Ala Glu Ile Gly Ser Ile Met Gly Asn Lys Ala Leu Lys Phe Thr  
 130 135 140  
 Phe Ser Asp Val Gly His Val Ile Cys Val Ser His Thr Cys Lys Glu  
 145 150 155 160  
 Asn Thr Val Leu Arg Gly Ser Ile Asp Pro Ile Lys Val Ser Val Ile  
 165 170 175  
 Pro Asn Ala Val Ile Ser Lys Asp Phe Lys Pro Lys Ser His Cys Val  
 180 185 190  
 Asn Lys Asn Tyr Thr Lys Glu Ile Thr Ile Val Val Ile Thr Arg Leu  
 195 200 205  
 Phe Pro Asn Lys Gly Ala Asp Leu Leu Thr Ala Val Ile Pro Lys Ile  
 210 215 220  
 Cys Gln Leu Lys Pro Lys Val Lys Phe Leu Ile Ala Gly Asp Gly Pro  
 225 230 235 240  
 Lys Phe Leu Asp Leu Glu Gln Met Arg Glu Lys Tyr Phe Leu Gln Glu  
 245 250 255  
 Arg Val Thr Leu Val Gly Ala Ile Lys His Glu Glu Val Arg Asp Val  
 260 265 270  
 Met Val Gln Gly Asp Ile Tyr Leu His Pro Ser Leu Thr Glu Ala Phe

551

275

280

285

Gly Thr Val Ile Val Glu Ala Ala Ser Cys Gly Leu Tyr Val Val Thr  
 290 295 300

Thr Lys Val Gly Gly Ile Pro Glu Val Leu Pro Asn Glu Met Thr Ser  
 305 310 315 320

Phe Ala Glu Pro Glu Glu Asn Ser Leu Ile Asp Ala Ala Ile Asp Ala  
 325 330 335

~~Ile Asn Lys Ile Glu Ser Asn Glu Ile Asp Thr Ser Lys Phe His Asp~~  
 340 345 350

Ala Val Ala Lys Met Tyr Ser Trp Asn Asp Ile Ala Arg Arg Thr Glu  
 355 360 365

Asn Val Tyr Asn Ser Leu Asp Leu Asp Lys Leu Asn Glu Ser Leu Leu  
 370 375 380

His Arg Leu Gln Arg Tyr Tyr Cys Cys Gly Ile Ile Ala Gly Lys Leu  
 385 390 395 400

Tyr Ala Leu Cys Val Ile Val Asp Ile Phe Ile Phe Val Ile Leu Glu  
 405 410 415

Trp Leu Tyr Pro Ala Asp His Ile Asp Lys Ala Thr Lys Trp Pro Ser  
 420 425 430

Ala Ile Lys Glu Glu Asp Glu Ser Glu Glu Glu Thr Phe Ile Phe Pro  
 435 440 445

Asn Lys Val Asn  
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<210> 455

<211> 1231

<212> DNA

<213> Candida albicans

<400> 455

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 cagcctagta actcaagtgt tgttacactc ttgttattat tattattata tcgtttacaa 180  
 gtagatttct cattttgaac agcaaatact gtcgttaata ggaatcagag gcagaaagaa 240  
 agagagagaa aaaaaaaag gacacattta cacgtacacc cttaacttga aggaaaaaaa 300

552

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caaaacaaga ga aagagacaaa gaaaatactt tcaac aagattgaga 360
tattggtgat ttta c caaaaaaaaaa gaatacaciaa cttgt aacagaattt 420
gaacatttct agagtttctt atattcccc caaggtggac aattaataat aacatttgat 480
tatacaagaa catttcaatc atgtggattt ttgactggtg tatgtaatga tttatcttta 540
ccgaatcaat actttattta tgagtgattg gttggttggg tataataacca ccactttatt 600
ctattaacca agtttgatct aattactgat ctgtatatac taaccaaata tttaccttat 660
cacttaatta tttacagttc aagatatatt atcatcatta ggattatgga ataaacatgc 720
caaattatta ttttagggg tagataatgc tggtaaaact actcttttac atatgttaaa 780
gaatgataga ttggccactt tacaaccaac attacatcca acttcagaag aattggccat 840
tggatcagtt agatttacta cttttgattt aggtggacat caacaagcta gaagattatg 900
gaaagattat ttccctgaag tcaatggtat tgtcttttta gtcgatgctg ctgataccga 960
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<210> 456

<211> 190

<212> PRT

<213> Candida albicans

<400> 456

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Trp Asn Lys His Ala Lys Leu Leu Phe Leu Gly Leu Asp Asn Ala Gly  
20 25 30

Lys Thr Thr Leu Leu His Met Leu Lys Asn Asp Arg Leu Ala Thr Leu  
35 40 45

Gln Pro Thr Leu His Pro Thr Ser Glu Glu Leu Ala Ile Gly Ser Val  
50 55 60

Arg Phe Thr Thr Phe Asp Leu Gly Gly His Gln Gln Ala Arg Arg Leu  
65 70 75 80

Trp Lys Asp Tyr Phe Pro Glu Val Asn Gly Ile Val Phe Leu Val Asp  
85 90 95

Ala Ala Asp Thr Glu Arg Phe Ala Glu Ser Lys Ala Glu Leu Glu Ser  
100 105 110

Leu Phe Arg Ile Glu Glu Leu Ser Gln Val Pro Phe Val Ile Leu Gly  
115 120 125

553

Asn Lys Ile Asp Val Pro Thr Ala Val Gly Glu Met Glu Leu Lys Asn  
130 135 140

Ala Leu Gly Leu Tyr Asn Thr Thr Gly Lys Asp Thr Gly Lys Leu Pro  
145 150 155 160

Glu Gly Thr Arg Pro Ile Glu Val Phe Met Val Ser Val Val Met Arg  
165 170 175

Ser Gly Tyr Gly Glu Ala Phe Lys Trp Leu Ser Gln Tyr Ile  
180 185 190

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